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GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

April 22, 2003, 12:48:24 ; Search time 15.7143 Seconds (without alignments) 97.882 Million cell updates/sec US-09-674-716B-3 Title: Perfect score: Run on:

81 1 RSSKSLLYKDGKTYLN 16 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

,		مبر)				
Result No.	Score	uery atch	Leng	DB		Description
-	81	100.0	112	 	KVMS16	у карра
7	81	100.0	113	-	KVMS51	g kappa
e	81	00	120	Н	KVMS67	
4	81	8	120	8	A29775	y kappa chain
ú	81	100.0	120	7	B29775	g kappa
9	99	81.5	112	~	PL0273	g kappa
7	65		133	7	S40324	g kappa
60	64		83	~	834095	g kappa
o	64	79.0	111		820709	m
10	64	79.0			S42267	g kappa
11	64		120		S42268	g kappa
12	64				K2HURP	g kappa
13	63	77.8			S49572	g kappa chain
14	61	75.3			PH1057	g light chain
15	61	75.3			K2HUFR	g kappa
16	19	75.3			S40338	g kappa
17	9	74.1			PL0275	b
18	9				S42611	rotein
13	9	٠			S41374	长
20	29	72.8			S34094	a chain V
21	59		91		S42186	g kappa
22	59	72.8			A33730	a chain V
23	59				PH1055	g light
24	59	72.8			PH1056	g light
25	50				A36259	g kappa
	59	•			F30560	g kappa
27	59	٠			C32513	kappa
28	59	72.8			S23230	g kappa chain
29	59	•			26	Ig kappa chain pre

Ig kappa chain V r Ig kappa chain V r	light	chain	kappa kappa		kappa kappa	kappa	Ig kappa chain V r Ig kappa chain V r
S22902 S42266	PH0090 A55491	S41815 S40322	A24452 B25155	A28762 T26317	H26317 C26317	D26317	PL0274 KVMS7S
142 2 120 2	110 2	120 2	133 1 89 2	92 2	112 2	112 2	112 2
72.8	70.4	70.4	69.1	67.9	67.9	67.9	67.9 67.9
50 00	57	57	56	52.5	ក ភូមិ ភូមិ	20.0	ນ ເນີນ ເນີນ
30	332	34 35	36	8 0	0 4 0 1	4.5	4 4 4 5 4 4

Ig kappa chain V region (M167) - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996

C. Accession: A01908
R. Rudikoff, S.; Potter, M.
Biochemistry 17, 2703-2707, 1970
A; Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma prot
A; Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma prot
A; Reference number: A01908, MUID:79000273; PMID:99160
A; Accession: A01908
A; Molecule type: protein
A; Residues: 1-112 < RUD.
C; Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C; Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C; Comment: This chain heterotetramer subunit consists of two identical light (kap)
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C; Susperfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer
F;16-95/Domain: immunoglobulin homology < IMM>
F;23-93/Disulfide bonds: #status predicted

Gaps ; Length 112; Indels 100.0%; Score 81; DB 1; I ilarity 100.0%; Pred. No. 3.1e-06; Conservative 0; Mismatches 0; Local Similarity Les 16; Conserv Query Match Best Loca Matches

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24 RSSKSLLYKDGKTYLN 39 1 RSSKSLLYKDGKTYLN 16 엄 8

RESULT 2

Ig kappa chain V region (M511) - mouse C.Speciese: Mus musculus (house mouse) C.Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000 C;Accession: A01910

RiAppella, E. Mol. 17, 711-718, 1980
Mol. Immunol. 17, 711-718, 1980
A;Title: Amino acid sequence of the light chain variable region of M511, a phosphorylche A;Reference number: A01910; MUID:81052016; PMID:6776396
A;Accession: A01910

A.Molecule type: protein
A.Residues: 1-113 cARP>
A.Residues: 1-113 cARP>
A.Residues: 1-113 cARP>
A.Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap, hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lacksuperfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer
F.16-95/Domain: immunoglobulin homology < IMM>
F.23-93/Disulfide bonds: #status predicted

DB 1; 100.0%; Score 81; Query Match

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Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PL0273
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A. A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                               C; Species: Wus pahari
C; Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C; Accession: B2-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C; Accession: B2-1, 19-201, 1986
Immunogenetics 24, 191-201, 1986
A; Title: Exolution of a V-kappa gene family.
A; Reference number: A91751; MUID:87006895; PMID:3093373
A; Accession: B29775
A; Molecule type: DNA
A;
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1940324
19 kappa chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 840324
C;Accession: 840324
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-120/Product: Ig kappa chain V region 24.1 #status predicted <MAT>
F;36-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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A,Residues: 1-112 <SHL>
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heteroterramer; immunoglobulin
F;1-23/Region: framework 1
F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 112;
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Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 66, DB 2; Length 112
Pred. No. 0.00097;
4; Mismatches 0; Indels
                                                                                                                  Ig kappa chain precursor V region (mouse 24.1) - shrew mouse
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F;62-93/Region: framework 3
P;94-102/Region: complementarity-determining 3
F;103-112/Region: framework 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;24-39/Region: complementarity-determining 1
F;40-54/Region: framework 2
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24 KSSQSLLYRNGKTYLN 39
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Best Local (
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Matches
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PL0273
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C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Complex: An immunoglobulin serior immunoglobulin homology
C;Keywords: heterotetramer
C;Keywords: heterotetramer #status predicted <SIG>
C;Keywords: heterotetramer
F;120/Domain: signal sequence #status predicted <SIG>
F;21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>
F;36-115/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000
C;Accession: A)01909
R;Selsing, E; Storb, U.
A;Title: Somatic mutation of immunoglobulin light-chain variable-region genes.
A;Reference number: A01909; MUID:82002223; PMID:6791832
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C.Species: Narchesion: A29778
R.Jouvin-Marche, E.; Rudikoff, S.
Immunogenetics 24, 191-201, 1986
A.Title: Evolution of a V-kappa gene family.
A.Reference number: A91751; MUID:87006895; PMID:3093373
A.Accession: A29775
A.Molecule type: DNA
A.Molecule this sequence was determined from the germline gene
                                             Gaps
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroteramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-20/Product: Ig kappa chain V region 24.2 #status predicted <MAT>
F;36-115/Domain: immunoglobulin homology <INM's
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100.0%; Score 81; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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                                        Indels
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A;Residues: 1-120 <SEL>
A;Note: the sequence was determined from the germline gene
C;Genetics:
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Local Similarity 100.0%; Pred. No. 3.4e-06;
ee 16; Conservative 0; Mismatches 0;
100.0%; Pred. No. 3.2e-06;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 16; Conservative
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Ig kappa chain V region (A17) - human
Ig kappa chain V region (A17) - human
C;Date: 30-Apr-1999 #text_change 21-Jan-2000
C;Accession: $42268
R;Lautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zo
Euf. J. Immunol. 22, 1023-1029, 1992
A;Title: The human immunoglobulin kappa locus. Characterization of the duplicated A registacence number: A49043; MUID:92201291; PMID:1551402
A;Reference number: A9043; MUID:92201291; PMID:1551402
A;Reference number: Jeliminary
A;Molecule type: DNA
A;Residues: 1-120 <LAU>
                                                                                                                                                                                              Grappa chain V region (A1) - human (Species Homo sapiens (man) - human (Species Homo sapiens (man) - C; Species Homo sapiens (man) (C; Species Homo sapiens (man) (Species 10-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 (C; Accession: 842267 (R; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zchatr. J. Immunol. 22, 1023-1029, 1992 A; Title: The human immunoglobulin kappa locus. Characterization of the duplicated A reginal A; Reference number: A49043; MUID:92201291; PMID:1551402
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-115/Domain: immunoglobulin homology <IMM>
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75.0%; Pred. No. 0.0022;
ive 2; Mismatches 2; IndelB
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Pred. No. 0.0022;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: X63402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 75.0
Matches 12; Conservative
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Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-120 < LAU>
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A, Status: preliminary
A, Molecule type: DNA
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C; Superfamily: 1
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K2HURP
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: O'rebel-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S20709
R;Brennand, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osh submitted to the EMBL Data Library, April 1992
A;Berence number: S20706
A;Reference number: S20706
A;Recession: S20709
A;Recission: S20709
A;Residues: 1-111 <-RES
A;Residues: 1-111 <-RES
C;Superfamilary
A;Residues: 1-111 <-RES
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <INM>
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Eur. J. Immunol. 23, 3248-3271, 1993
A, Title: Expressed human immunoglobulin chi genes and their hypermutation. A, Reference number: 840312; MUID: 94080891; PMID: 8258341
A, Accession: 840324
A, Status: preliminary; translation not shown
A, Rolled type: mRNA
A, Residues: 1-133 < KLE>
A, Cross-references: EMBL: X72434
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin homology < IMM>
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Pred. No. 0.0021;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 133;
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Pred. No. 0.0015;
2; Mismafches 2; Indels
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Pred. No. 0.0017;
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Best Local Similarity 75.0%;
Matches 12; Conservative
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Best Local'Similarity 75.04
Matches 12; Conservative
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RSSQSLVYSDGNTYLN 24
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Best Local Similarity
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Search completed: April 22, 2003, 12:54:45 Job time : 16.7143 secs
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K2HUFR
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C;Species: Homo sapiens (man)
C;Accession: 849572
R;Giachino, C.; Padovan, E.; Lanzavecchia, A.
R;Giachino, C.; Padovan, E.; Lanzavecchia, A.
R;Giachino, C.; Padovan, E.; Lanzavecchia, A.
A;Accession: 849571
A;Accession: 849571
A;Accession: 849572
A;Accession: 849572
A;Accession: Pape: MRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-114 <GIAS
A;Cross-references: EMBL:Z46626; NID:9575261; PIDN:CNA86596.1; PID:9575262
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <INM>
                                                                                                                                                                                                                                    Cycomplex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la Cysperfamily: immunoglobulin v region; immunoglobulin homology cysperfamily: immunoglobulin immunoglobulin homology cysperfamily: immunoglobulin immunoglobulin homology cysperfamily: ig kappa chain v-II region (RPMI) #status predicted cMAT> F;21-20/Domain: signal sequence #status predicted cSIG> F;21-31/Froduct: Ig kappa chain V-II region (RPMI) #status predicted cMAT> F;21-43/Region: framework I F;60-74/Region: complementarity-determining 1 F;60-74/Region: complementarity-determining 2
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19 light chain V region (clone 178.145) - mouse (fragment)

C; Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

R; Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

S; Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

A; Tille: Both Igh and IgG anti-DNA antibodies are the products of clonally selective B c A; Reference number: PH0971; MUID:92381444; PMID:1512540

A; Rocession: PH1057

A; Statuw nucleic acid sequence not shown

A; Molec:: 'type: mRNA
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A;Molecule type: DNA
A;Realdues: 1-133 <KLO>
A)Octe: the sequence was determined from the differentiated gene
C;Genetics:
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Pred. No. 0.0025;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F:82-111/Region: framework 3
F:114-122/Region: complementarity-determining 3
F:23-113/Region: framework 4
F:43-113/Disulfide bonds: #status predicted
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Local Similarity 75.0%;
hes 12; Conservative
                                                                                                                      A;Gene: GDB:IGKV2
A;Cross-references: GDB:136265
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A; Introns: 17/1
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12;
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A;Gene: GDB:IGKV2
A;Cross-references: GDB:136265
A;Cross-references: GDB:136265
A;Cross-references: GDB:136265
A;Cross-references: GDB:136265
C;Cosplex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-95/Domain: immunoglobulin homology <IMM>
F;23-93/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: A01886
R,Risesen, W.F.; Jaton, J.C.
Biochemistry 15, 3829-3833, 1976
Biochemistry 15, 3829-3833, 1976
A;Title: Variable region sequence of the light chain from a Waldenstroem's IgM with spec A;Reference number: A01886; WUID:76253627; PMID:821524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: A01886
A,Molecule type: protein
A,Residues: 1-113 <RIE>
C,Comment: This chain was isolated from a Waldenstrom's macroglobulin that binds phospho
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C.Species: Homo sapiens (man)
C.Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C.Accession: A01886
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A;Residues: 1-101 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reymords: immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
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80.0%; Pred. No. 0.0059;
iive 2; Mismatches 1; Indels
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Best Local Similarity 62.5
Matches 10; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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Q82h56 yersinia pe P51503 gorilla gor P51504 homo sapien P22045 leishmania P0885 vaccinia vi P32989 varciola vir P43265 euglena gra P60899 saccharomyc Q9G8K4 myxoma viru Q9G872 shope fibro Q03877 trypanosoma

112 AA

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MEDLINE=79000273; PubMed=99160;
Rudikoff S., Potter M.;
"Kappa Chain variable region from M167, a phosphorylcholine binding
                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-Mul-1999 (Rouse).
16 kappa chain V-II region MOPC 167.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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21-JUL-1986 (
15-JUL-1999 (
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P01626;
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                                                                           April 22, 2003, 12:46:53; Search time 8 Seconds (without alignments) 82.953 Million cell updates/sec
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           GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Gaps

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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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DT 101-JAN
DE 19 kapp
CC Mammal
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RA KIODEC
RRT "HUMAN
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                                                                                                                                                                MEDLINE-81052016; PubMed=6776396;
MEDLINE-81052016; PubMed=6776396;
Appella E.;
"Amino acid sequence of the light chain variable region of M511, a phosphorylcholine-binding murine myeloma protein.";
Mol. Immunol. 17:711-718(1980).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A NYELOMA PROTEIN THAT BINDS PROPEGULANEOUS.
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Ig kappa chain V-II region MOPC 511.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK.
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15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-II region VKAPPA167 precursor.
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21-JUL-1986 (Rel. 01, Last sequ
15-JUL-1999 (Rel. 38, Last ann
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HSSP; P80362; 1WTL.
InterPro; 1PR003066; 1g_MHC.
InterPro; 1PR003596; 1g_v.
Pfam; Pf00047; 1g; 1.
SMART; SMO0406; IGv; 1.
Immunoglobulin V region.
POWAIN
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Cell 25:47-58(1981).
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HSSP; P80362; IWTL.
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SEQUENCE FROM N.A.
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P01627;
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KV2B MOD 21-07U-
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DT 21-07U-
DT 21-07U-
DT 15-07U-
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                              IG KAPPA CHAIN V-II REGION VKAPPA167.
PRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=86041852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin Kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo Sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                         COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3. COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                                                                                                                                                                            Length 120;
                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                  BY SIMILARITY.
63BB571F0E4DE3E8 CRC64;
                                                                                                                                                                                                                                                                                                                                    Score 81; DB 1;
Pred. No. 3e-07;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 06, Created)
10-JAN-1988 (Rel. 06, Last sequence update)
10-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-II region RPMI 6410 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 AA.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region; Signal. SIGNAL 1. 20
Pfam; PF00047; ig; 1.
SMART, SM00406; IGv; 1.
Immuncglobulin V region; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                             120 AA; 13280 MW;
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Local Similarity 100.0%;
les 16; Conservative 0
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KV2G MOUSE
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KV2G MOUSE
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"Variable region sequence of the light chain from a Waldenstroms IgM
with specificity for phosphorylecholine.";
Blochemistry 15:3829-3831(1976).
-! MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
HSSP: PO1607; IREL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_W.
PRAN; SM00406; IG'.
Immunoglobulin V region.
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MOUSE STANDARD; PRT; 113 AA.

POL530,
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
17-JUL-1999 (Rel. 38, Last annotation update)
18-JUL-1999 (Rel. 38, Last annotation update)
18-JUL-1998 (Rel. 38, Last annotation update)
18-JUL-1998 (Rel. 38, Last annotation update)
19-JUL-1998 (Rel. 38, Last annotation update)
19-JUL-1998 (Rel. 38, Last annotation update)
19-JUL-1998 (Rel. 38, Last annotation update)
19-JUL-1999 (Rel. 38, Last annotation upd
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 39, Last sequence update)
15-JUL-1999 (Rel. 39, Last annotation update)
16 kappa chain V-II region FR.
17 kappa chain V-II region FR.
18 kappa (Human).
18 kappa (Annan).
19 kappa (Annan).
19 kappa (Annan).
19 kappa (Annan).
19 kappa (Annan).
10 kappa (Annan).
10 kappa (Annan).
10 kappa (Annan).
11 kappa (Annan).
11 kappa (Annan).
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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               Length 133;
             Score 64; DB 1; Length 133
Pred. No. 0.00032;
2; Mismatches 2; Indels
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BY SIMILARITY.
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MEDLINE=83256427; PubMed=6409088;
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=76253627; PubMed=821524;
             79.0%;
Query Match
Best Local Similarity 75.v.
Thes 12; Conservative
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24 RSSQSLVYRBGBTYLB 39
                                                                           1 RSSKSLLYKDGKTYLN 16
                                                                                            44 RSSQSLVYSDGNTYLN 59
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94
103
23
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113 AA;
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KV2B HUMAN
ID KV2B HUMAN
PO1615;
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Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;

"A new isotype sequence (V kappa 27) of the variable region of kappa-
"Ight chains from a mouse hybridoma-derived anti-(streptococcal group
"Ight chains from a mouse hybridoma-derived anti-(streptococcal group
"Application of the dimethylaminoszobenzene isothiocyanate reshidue."
"Thyplication of the dimethylaminoszobenzene isothiocyanate technique
"Thyplication of peptides.";
"Blochem. J. 211:173-180(1983).";
"I Blochem. J. 211:173-181S CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
"MINEDIA AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
"PIRSP: PRO0362; INTL.
"RICEPPO: IPRO03596; Ig_V.
"RICEPPO: IPRO03596; Ig_V.
"REPAIRS FROM 46; IGY; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novotny J., Margolies M.N.;

"Amino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma attibody.";

Biochemistry 22:1153-1158(1983).";

-I.-MISCELLANBOUGS: THIS CHAIN WAS ISOLATED FROM AN IGGZA HYBRIDOMA FROTEIN THAT BINDS DIGOXIN.

PIR; A01914; KWMS26.

HSCP: PR003627; MT.C.

InterPro; IPR003506; Ig MHC.

FEAN; FR0047; ig; I.-

SMART; SM00406; IGV; I.-

Immunoglobulin V region; Monoclonal antibody; Hybridoma.
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21-701.

21-701.

21-701.

21-701.

15-701.

15-701.

19 kappa chain V-II region 26-10.

Mus musculus (Mouse).

Eukaryota; Merazoa; Chordaca; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
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MEDLINE=83178921; PubMed=6404298;
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Les 11; Conservative
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39
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102
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93
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113 AA;
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NON TER SEQUENCE

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Query Match

Best Loca Matches

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Hilschmann N.; "The complete amino acid sequence of Bence Jones protein Cum (kappa-
                                                                                                                                                                                                                        TISSUE=Hybridoma;
MabLINE=8128968; bubMed=6441768;
Aebersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
Ambrine V kappa 25 and V kappa 27 amino-acid sequences of C57B1/6
origin: monoclonal antibodies 17529.1 and 22525.1 specific for the
group A-streptococcal polyasccharide.";
Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig Rappa chain V-II region Cum.
Howo septens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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Pred. No. 0.034;
2; Mismatches 2; Indels
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Hopper Seyler's Z. Physiol. Chem. 348:1718-1722(1967)
REVISIONS TO 50; 52; 96 AND 97.
MEDLINE=70063440; PubMed=4188189;
Milschmann N.;
"Molecular basis of antibody formation.";
Naturaviseenschaften 56:195-205(1969).
                                                23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-II region 17829.1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                 113 AA.
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BY SIMILARITY.
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HSSP; POLGO7; 1REL.
InterPro; IPR003306; 1g_WHC.
InterPro; IPR003596; 1g_V.
Pfam; PR00047; ig_1.
SMART; SM00406; 1GV; 1.
                 PRT;
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MEDLINE=68242259; PubMed=5586923;
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                 STANDARD;
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                                                                                                                         (Mouse).
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es 11; Conserv
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         KVZE MOUSE
P03976;
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P01614;
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KV2A_HUMAN
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MEDLINE=73166538; PubMed=4700495;
Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
"Structural identity of Bence Jones and amyloid fibril proteins in a patient with plasma cell dyscrasia and amyloidosis.";
J. Clin. Invest. 52:1276-1281 (1973)
-I- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
-I- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE (BENCE-JONES PROTEIN TEW).
MEDLINE=74148480; PubMed=4596149;
Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
Maino acid sequence of a kappa Bence Jones protein from a case of primary amyloidosis.";
Biochemistry 12:3763-3780(1973).
                                                                                                                                                                                                                                                                        21-JUL-1996 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 34, Last annotation update)
19 Kappa chain V-II region TEW.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
                                              66.7%; Score 54; DB 1; Length 113; 62.5%; Pred. No. 0.015; 2; Indels :ive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.4%; Score 53; DB 1; Length 113; larity 68.8%; Pred. No. 0.023; Conservative 2; Mismatches 3; Indels
113
12273 MW; F9F39CE949A84C2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12316 MW; 0C3C38F81F1843CA CRC64;
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                                                                                                                                                                                                                                             113 AA.
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BY SIMILARITY.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Bence-Jones
                                                                                                                                                                                                                                           PRT;
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HSSP, P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                               Local Similarity 62.5
les 10, Conservative
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                                                                                                                                         24 RSSQSLVHSNGNTYLN 39
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                                                                                                                                                                                                                                           STANDARD;
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               113 AA;
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wes 11; Conserv
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                                                                                                                                                                                                                          KV2D_HUMAN
ID KV2D_HUMAN
AC P01617;
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DOMAIN NON TER SEQUENCE Query Match

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=84191506; PubMed=6325927;
Klobeck H.G., Solomon A., Zachau H.G.;
"Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                                                                                                                                                                                                                      'n
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Pred. No. 0.32;
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PRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMEMORK-2.
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FRAMEWORK-4.
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                                                                                                                                                                                                                                                                                                      115 AA; 12676 MW; 59E9F90A379569EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-II region GM607 precursor (Fragment).
                                                                                                       InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
Pfam; PPR0047; Ig; 1.
SMART; SM00406; IGv; 1.
DISULFID
24 95 BY SIMILARITY.
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PIR; A01889; KZHUGM.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfaw; PF00047; ig; 1.
SMART; SM00406; IGV, 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                               Query Match 57.4%;
Best Local Similarity 70.6%;
Matches 12; Conservative 1
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                                                         PIR; A01885; K2HUCM.
HSSP; P01607; 1REI.
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117 AA;
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Length 117;

55.6%; Score 45; DB 1;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                              STRAIN-S288C / AB972;
Churcher C.M., Louis E.J., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces
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               Gaps
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MEDLINE=95304651; PubMed=7785338;
Pryde F.E., Huckle T.C., Louis B.J.;
Sequence analysis of the right end of chromosome XV in Saccharomycen cerevisiae: an insight into the structural and functional significance of sub-telomeric repeat sequences.";
Yeast 11:371-382(1995).
-- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate
                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                 Indels
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247 247 MAGNESIUM (BY SIMILARITY).
296 296 MAGNESIUM (BY SIMILARITY).
321 321 MAGNESIUM (BY SIMILARITY).
437 AA; 47312 MW; 143DGEF66FB03D13 CRC64;
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                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update)
15-UTL-1998 (Rel. 36, Last annotation update)
Enolar zerlated protein 1 (EC 4.2.1.11).
ERRI OR YMR323W OR YM9924.15.
Pred. No. 0.59;
4; Mismatches
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EMBL; U23472; AAC48992.1; -...
HSSP; P00924; 4ENL.
SGD; S0005920; ERRI.
INCEPPC; IPR000941; Enclase.
Pfam; PF00113; enclase; 1...
PROSITE; PR00146; ENCLASE.
TICRFAMS; TIGR01060; enc; 1...
PROSITE; PS00164; ENCLASE; 1...
Lyase; Glycolysis; Magnesium, ACT SITE
                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
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56.2%;
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248 SAPSVFYKDGKYDLN 262
                   9; Conservative
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P4222;
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Herbat H., Chang J.Y., Aebersold R., Braun D.G.;
"Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for
                                                                                                                                                                                                                                                                                                                                          MEDLINE 96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., KIrkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Weese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      jannaschii.";
Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
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Pred. No. 6.5;
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8848EDB757FDC233 CRC64;
                                                                                                                                                                                                           Archaea, Buryarchaeota, Methanococci, Methanococcales, Methanocaldococcaceae, Methanocaldococcus.
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21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-II region 281.3
                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000286; His deacetylse.
Pfam: PF00850; Hist deacetyl; 1.
PRINTS; PR01270; HDSAUPER.
Hypothetical protein; Hydrolase; Comp.
SEQUENCE 343 AA; 38174 MW; 8848EE
                                           PRT;
                                                                                     (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.9%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U67502; AAB98526.1; -.
                                                                                                   15-JUL-1998 (Rel. 36, Last a 16-OCT-2001 (Rel. 40, Last a Hypothetical protein MJ0535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 69.2
                                                                                                                                                                                               Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                           STANDARD;
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                                                                                   15-JUL-1998 (15-JUL-1998 (16-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KV2D MOUSE
P01629;
                                           METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                           Y535 ME1
057955;
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KV2D MOUSE
                       Y535_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                       HOPDE-Sejler's Z. Physiol. Chem. 363:1069-1076(1992).
-!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- CATALYTIC ACTIVITY: Citrate = cis-aconitate + H(2)O.
-1- CATALYTIC ACTIVITY: Citrate = cis-aconitate + H(2)O.
-1- PATHWAY: Tricarboxylic acid cycle.
-1- SUBUNIT: MONOMER (BY SIMILARITY).
-1- MISCELANBOUS: ACONITASE HAS AN ACTIVE (4FE-4S) AND AN INACTIVE (AFE-4S) PORMS: THE ACTIVE (4FE-4S) CLUSTER IS PART OF THE CATALYTIC SITE THAT INTERCONVERTS CITRATE, CIS-ACONITASE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mengaud J.M., Horwitz M.A., refrequence Legionella pneumophila is an aconitase homologous with the human iron-responsive element-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Legionella pneumophila.
Bacteria, Proteobacteria; gamma subdivision; Legionellaceae group;
Legionellaceae, Legionella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aconitate hydratase (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase)
(Major iron-containing protein) (MICP) (IP210).
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                                                                                                                                                                                                                                                                                                                                       FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 1; Length 112;
Pred. No. 2.8;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12221 MW; BD5EF5E6D789FBEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         891 AA.
streptococcal polysaccharide.";
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                                                                                                                    PIR, A01911; KVMSS1.

HSSP; P01607; IREI.
InterPro; IPR003506; Ig_W.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SWART; SMO0406; IG; 1.
Immunoglobulin V region; Moncelonal ani
DOMAIN
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MEDLINE=93374864; PubMed=8366052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 66.7
hes 10, Conservative
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Search completed: April 22, 2003, 12:51:45 Job time : 9 secs

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Q8tcd0 homo sapien Q9180 homo sapien Q9180 homo sapien Q9598 arabidopsis Q8vci6 mus musculu Q9182 mus musculu Q97182 mus musculu Q90373 methanobact Q90373 mus musculu Q9179 streptomyce Q96876 streptomyce Q96879 streptomyce
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                                                                                                                                                                            April 22, 2003, 12:47:43 ; Search time 32 Seconds (without alignments) 103.024 Million cell updates/sec
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         OM protein - protein search, using sw model
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Q9UL80
Q9C9E8
Q8VCI6
Q9JL82
Q8VC55
Q2C451
Q9Q9M37
Q9L035
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1: sp arches:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
5: sp mammal:*
5: sp phage:*
6: sp phage:*
7: sp phage:*
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Q9P8D3
Q8X096
Q9P8F3
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sp_bacteriap:*
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Maximum DB seq length: 2000000000
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Match Length DB
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489
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O96602 trypanosoma Q56939 yersinia pe Q9cmu7 pasteurella Q67538 aquifex aeo Q23217 caenorhabdi	Q97vh4 sulfolobus O77209 trypanosoma Q9xdt5 clostridium Q8riq5 fusobacteri	υΔ		059233 pyrococus 059234 borrelia bu P78905 schizosacch Q59964 streptomyce Q59968 Bacillus ha	
096602 Q56939 Q9CMU7 O67538 Q23217	Q97VH4 O77209 Q9XDT5 OBRIQ5	Q45820 Q9WYL6 O24781 Q9YWQ6		P 0	Q9M2AQ Q9PQU6 Q918H4 Q9LCJ7 Q9U0H2 Q8U9V9
5 16 16 5	17 16 16	12 16	12 12 16 17 16 17	17 3 3 16 16	
646 822 239 245 434	755 786 418 555	635 651 700 241	249 249 87 127	233 364 465 769 769	489 489 521 761 1016 1928 257
53.1 53.1 51.9 51.9	51.9		50.00 4.90.00 4.40.00	4 4 4 4 4 0 0 0 0 0 0 0	4 4 4 4 4 4 4 9 9 9 9 9 9 8 4 4 4 4 4 5 6
4 4 4 4 4 6 6 6 6 6 6	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	40.5 40.5 40.5 40	44444	6 4 4 4 4 4 4 . 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
11 18 20 21	222 243 243	2222	33 33 33 33 33	6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	2 4 4 4 4 4 4 2 0 1 1 1 1 1 1 2 2

ALIGNMENTS

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Gaps
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region (Fragment).
                                                                                                                                                                                                                                                                        75.3%; Score 61; DB 4; Length 239; 68.8%; Pred. No. 0.029; Live 3; Mismatches 2; Indels
                                                                                                                                                                                       Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. Submitted (FEB-20182; AAH22362.1; -. Hypchetical protein. SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;
             QBTCD0,
01-UNN-2002 (TrEMBLrel. 21, Created)
01-UNN-2002 (TrEMBLrel. 21, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26.2 kDa protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                      114 AA.
239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
PRT;
                                                                                                                                                                                                                                                                                          Best Local Similarity 68.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                                                                                                                                                                                                                     44 RSTQSLVYSDGNTYLN 59
 PRELIMINARY;
                                                                                                                                               [1] _
SEQUENCE FROM N.A.
TISSUE=LÜNG;
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   Q8TCD0
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LISSUE=COLON
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SEQUENCE FROM N.A.

KEDLINE=21016719; PubMed=11130712;

MEDLINE=21016719; PubMed=11130712;

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Cornay A.R., Creagy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Cornay B., Fujii C.Y.,

Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Lid J.H., Li Y.-P.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maitt R., Marziali A.,

Lin S., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

Rakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Who Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                          SEQUENCE FROM N.A.
MEDILINE-88277139; PubMed-9614934;
Nu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 70.4%; Score 57; DB 4; Length 114; I Similarity 68.8%; Pred. No. 0.059; 11; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER 1
NON TER 114 114
SEQUENCE 114 AA, 12775 MW, 070E31E210D1CB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09C9E8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MNR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 84.8 KDa protein.
                                                                                                                                                                                                                                                    Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035034; AAD56270.1; -.
HSSP; P80362; JWTL.
InterPro; IPR003006; Ig WHC.
InterPro; IPR003596; Ig_v.
Pfam; PR00047; ig; 1.
NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AC016529, AAG52586.1, -.
InterPro, IPR002052; N6 Mtase.
InterPro, IPR002035; VWF A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 RSSQSPVYSDGNTYLN 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RSSKSLLYKDGKTYLN 16
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                                                                      NCBI TaxID=9606;
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Q9C9E8
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MEDLINE=20448942; PubMed=10992488;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
Malkiel S., Constant S., Constan
                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
11.1 TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBL-21. 21, Last amotation update)
01-UNN-2002 (TrEMBL-21. 21, Last amotation update)
Hypothetical 26.2 kpa protein.
Hypothetical 26.2 kpa protein.
Hypothetical 26.2 kpa protein.
Elwaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
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                                                                                                                                                                                                      Score 50; DB 10; Length 758; Pred. No. 7.3; 2; Indels 3; Mismatches 2; Indels
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R Strausberg R.;

R Submitted (DEC-2011) to the EMBL/GenBank/DDBJ databases.

R InterPro: IPRO03599; 1g.

R InterPro: IPRO03599; 1g.

R InterPro: IPRO03599; 1g.

R InterPro: IPRO03590; 1g.

R InterPro: IPRO03590; 1g.

R SMART; SM00409; 1G; 2.

R SMART; SM00409; 1G; 1.

R SMART; SM00406; IGV; 1.

R SMART; SM00406; IGV; 1.

R SMART; SM00406; IGV; 1.

R PROSITE; PS00290; 1G. MHC; UNKNOWN_1.

PROSITE; PS00290; 1G. MHC; UNKNOWN_1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2011 (TrEMBLrel.), Last sententation update)
Anti-myosin immunoglobulin light chain variable region
PROSITE; PS50234; VWPA; 1.
Hypothetical protein.
SEQUENCE 758 AA; 84789 MW; 8434F219D227036B CRC64;
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5; Mismatches
                                                                                                                                                                                                           Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 SQKLIYKDGKFHLN 207
                                                                                                                                                                                                                                                                                                                                                                                                                       3 SKSLLYKDGKTYLN 16
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PRELIMINARY;
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43 RSSQSIVHSNGNTYL 57
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| SRELLYRDGKLYDN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 SKSLLYKDGKTYLN 16
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
FROM N.A.
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Matches
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Q99M37
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Q9L035
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Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae; Methanobacter.
[1]
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62.5%; Pred. No. 4.4;
                                                                                                                                                                                                                 59.3%; Score 48; DB 11; Length 104; 56.2%; Pred. No. 1.7; tive 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021781, AAH21781.1;
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 2.
SWART; SM00407; IG; 2.
SWART; SM00406; IGv; 1.
SWART; SM00406; IGv; 1.
PROSTIE; PS00290; IG MHC; UNKNOWN_1.
HYDCHCHical protein
SQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;
                                                                                                                                                                                104 AA; 11360 MW; SDA8BBFD5F0AA1AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         026451;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Magnesium chelatase subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1561 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                      239 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
Infect. Immun. 68:5803-5808 (2000).
EMBL; AF206024; AAF69322.1; -.
HSSP; P01607; IRRI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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Best Local Similarity 62.5
Matches 10; Conservative
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44 KSTKSLLNSDGFTYLD 59
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                                                                                                                                                                                                                                     Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                 1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                                                                                                                                                                                       16 RSSQSLVHTNGNTYLH 31
                                                                                                                                                               104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
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TISSUE=COLON;
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NON TER
SEQUENCE
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026451
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98 VCS 5
10 O8 VCS 6
00 VC O8 VC O8 VC O1 -M
DT 01 -M
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STRAIN=DELTA H;

STRAIN=DELTA H;

MEDLINE=98037514; PubMed=9371463;

MEDLINE=98037514; PubMed=9371463;

Andredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

Andredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

Andredge T., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,

A spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

A Daniels G.J., Mao J.-I., Rice P., Nocelling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155(1997).

EMBL; AE000820; AAB84857.1;

REMBL; AE000820; AAB84857.1;

RITHEFPO; IPRO01589; Actbind_actnin.

RITHEFPO; IPRO01589; CobN/Mg_chltase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.8%; Score 46; DB 11; Length 238; 53.3%; Pred. No. 9.4; ive 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                x Habe; jucios; jelen.

x Habe; jucios; jelen.

x InterPro; IPR003599; Ig.

x InterPro; IPR003500; Ig_like.

x InterPro; IPR003006; Ig_MHC.

x InterPro; IPR003006; Ig_WHC.

x InterPro; IPR00403596; Ig_V.

x Ramar; Sw00409; IG; 2.

x Swar; Sw00406; IG; 1.

x Swar; Sw00410; IG; 1.

x Ramar; Sw00410; IG like; 1.
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1; -.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 26.3 kDa protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02514; cobn-Mg_chel; 1.
PROSTIE; PS00019; ACTININ_1; UNKNOWN_1.
Complete proteome.
SEQUENCE 1561 AA; 170574 MW; 764561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Gaps
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1916;
                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces. NCBI_TaxID=1916;
                                                                                                                                                                             | No. | Comparison | No. | No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Submitted (JAN-1999) to the EMEL/GenBank/DDBJ databases.
EMBL; Y13601; CAA73926.1; -.
HSSP; P29957; LAQM.
InterPro; IPR000461; Alpha_amylase.
InterPro; IPR00128; alpha-amylase.
Pfam; PF00128; alpha-amylase.
Pfam; PF00186; alpha-amylase.
Pfam; PF00186; CBM 20; 1.
Pfam; PR00110; Alpha-amylase.
Pram; PR00110; Alpha-amylase.
Primy; PR00110; Alpha-amylase.
Primy; PR00110; Alpha-amylase.
Probom; PD001568; CBD 4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.8%; Score 46; DB 2; Length 573; 57.1%; Pred. No. 25; 3; Indels ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 AA.
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Best Local Similarity 57.1-
Conservative
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les 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Q9CG26
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086876
006877
AC 08687
DT 01-NO
DT 01-NO
DT 01-JU
DE Alpha
GN AML.
OC Bacte
OC Bacte
OC Actin
OX NCBI
RN [1]
RN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.; "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
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STRAIN=A3[2] / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                     Streptomyces coelicolor.
Bacteria, Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of the model actinomycete Streptomyces coelicolor {\rm A3}\,(2).";
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EMBL; AL352966; CAB88153.1; -.
HSSP; P2957; 1AQM.
InterPro; 1PR002046; Alpha_amylase.
InterPro; IPR0020044; CBD 4.
Pfam; PP02186; alpha-amylase; 1.
Pfam; PP02806; alpha-amylase; 1.
Pfam; PP02806; alpha-amylase; 1.
Pfam; PP00866; CBM 20; 1.
Pfam; PP0010; ALPHAAMYLASE.
ProDom; PD001169; 41.
SEQUENCE 506 AA; 53868 MW; PCC92A3BED9D2DAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seeger K.J, Harris D.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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    506 AA.
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P97179;
01-MAY-1997 (TrEMBLE1. 03, C:
01-MAY-1997 (TrEMBLE1. 03, L:
01-JUN-2002 (TrEMBLE1. 21, L:
Alpha-amylase.
                                                                                                                                                                                     Secreted alpha-amylase.
AMLB OR SCO7020 OR SCIH10.09.
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    PRELIMINARY;
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Best Local Similarity
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RESULT 10 P97179 ID P97177 AC P97177 DT 01-MA DT 01-MA DT 01-MA DT ALPHA

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EMBL; Z73637; CAA98018.1; -.
EMBL; Z75302; CAA99728.1; -.
HSSP; P00924; 4EML.
SGD; 80005920; ERRI.
SGD; 80006202; ERRI.
InterPro; IPR000941; Enclase.
Pfam; PP00113; enclase; 1.
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Best Local Similarity
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Q8X096
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MEDLINE=21235186; PubMed=11337471;
MEDLINE=21235186; PubMed=11337471;
MEDLINE=21235186; PubMed=11337471;
MEDIANE=21235186; PubMed=11337471;
Meissenbach J., Bhrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis sup. lactis IL1403.";
Genome Res. 11:731-753(2001).
EMBL; AE066360; AAK05382.1; -
InterPro; IPR00183; Decarbxy18e2.
Ffam; PF00778; Orn DAP_Arg_dec_N; 1.
Pfam; PF00778; Orn DAP_Arg_dec_N; 1.
Pfam; PF00778; Orn DAP_Arg_dec_N; 1.
PRINTS; PR01179; ODADCRENKIASE.
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-1- PATHMAX: GLYCOLYSIS.
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-1- SUBCELLULAR TO CATO THE ENOLASE FAMILY.
EMBL; Z75301; CAA99725.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Duesterhoeft A., Floeth M., Fritz M., Hilbert H., Moestl D.;

Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

Submitted ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2002 (TrEMBLrel. 21, Last annotation update)
Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
                                                                                                                                 Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Streptococcaceae; Lactococcus.
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(ERRI OR YOR393W) AND (ERRZ OR YPL281C).

Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Delius H., Hebling U., Hofmann B.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delius H., Hebling U.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wambutt R., Wedler H.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 AA; 47279 MW; F8305C3E1FAD71E9 CRC64;
          01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MRR-2002 (TrEMBLrel. 20, Last annotation update)
Diaminopimelate decarboxylase (EC 4.1.1.20).
LYSA OR LI1284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 16;
Pred. No. 38;
2; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RSSKSLLYKDGKTYL 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 419 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                           NCBI_TaxID=1360;
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STRAIN=3346, TISSUE=MYCELIUM;
STRAIN=3346, TISSUE=MYCELIUM;
Nowrousian M., Kuck U., Loser K., Weltring K.M.;
Nowrousian acl1 and acl2 genes encode two polypeptides with homology to the N- and C-terminal parts of the animal ATP citrate lyase polypeptide. The polypeptide. Curr. Genet. 0.0-0(0).

Curr. Genet. 0.0-0(0).
EMBL; AJ243817; CAB76164.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Bukaryota; hungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Sordaria.
NCBI_TaxID=5147;
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Sordariales; Sordariaceae; Neurospora.
NCB_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.1%; Score 43; DB 3; Length 481; 60.0%; Pred. No. 65; ive 2; Mismatches 4; Indels
                                                                                                                                                            Score 43; DB 3; Length 437;
Pred. No. 59;
2; Mismatches 4; Indels
                                                                                                                     FAF09C00BE0E711C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ATP citrate lyase, subunit 2 (EC 4.1.3.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     487 AA
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01-MAR-2002 (TrEMBLrel. 20, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
Probable ATP citrate lyase subunit 2.
B14D6.320.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
PRINTS; PRO0148; ENOLASE.
ProDom; PD000902; Enolase; 1.
TIGREAMs; TIGR01060; eno; 1.
PROSITE; PS00164; ENOLASE; 1.
Glycolysis; Lyase; Magnesium.
SEQUENCE 437 AA; 47327 MW; E
                                                                                                                                                                      53.1%;
60.0%;
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                248 SAPSVFYKDGKYDLN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                 Query Match 53.1%; Score 43; DB 3; Length 487; Best Local Similarity 60.0%; Pred. No. 66; Matches 9; Conservative 2; Mismatches 4; Indels
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
German Neurospora,
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL356173; CAB91741.2; -.
Lyase.
SEQUENCE 487 AA; 52969 MW; 56BC196FCCE4CBA2 CRC64;
                                                                                                                                                                                                                                    2 SSKSLLYKDGKTYLN 16
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Search completed: April 22, 2003, 12:53:45 Job time : 35 secs

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April 22, 2003, 12:45:19; Search time 40.5714 Seconds (without alignments) 52.550 Million cell updates/sec
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                     1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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81
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Perfect score:
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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

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23: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1997.DAT:*

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23: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA2000.DAT:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Mouse germline kap Humanised anti-CD2 Mouse anti-CD23 MA Light chain CDR1 o Light chain of the Variable domain of Mouse MAD 2812 L c Light (kappa) chai Light chain CDR1 o Light chain CDR L1 Description AAW39882 AAW39804 AAR12232 AAR12354 AAW39815 AAY32254 AAE06969 AAY32262 AAY32261 AAY32261 ij DB Length Query Match I 1000.0 1000.0 1000.0 95.1 95.1 95.1 95.1 93.8 Score 81 81 81 77 77 77 76 76

Light chain CDR1 o	chain of t)le	able domain	ole dom	chain	chain	Light chain of the	ole dom	- 1		appa ligh	ide	germline	germline	οĘ	Human kappa light	kappe	Light chain variab	топо	Mouse HBV pre-Sl a	sed	Humanised HBV pre-	anti-gar		The kappa chain of	Insulin/insulin-li	BLyS b	9	Human Kappa II lig	appa lic	CDR-	11 pr	tapp	Murine derived ant
AAW39824	AAW39886	AAW39801	AAW39802	AAW39803	AAW39875	AAW39839	AAW39897	AAW39805	AAY70802	AAY70790	AAE06992	AAY56670	AAE06960	AAE06961	AAW53585	AAE06993	AAE07003	AAR52057	AAU76445	AAB12170	AAB12171	AAB12173	AAY42306	AAY56735	AAY93724	AAU90900	ABP45953	AAW39821	AAU70328	AAE07007	AAY14404	AAY24099	AAE06999	AAB86292
13	19	13	13	13	19	13	13	19	21	21	22	21	22	22	19	22	22	15	21	21	21	21	20	21	21	23	23	13	23	22	20	20	22	22
16	113	113	113	113	16	16	113	114	20	122	112	93	100	100	112	112	112	113	113	113	113	113	132	133	139	247	253	15	16	112	16	112	112	16
95.6	92.6	ď	ď	ä	'n	'n.	85.2	'n	ď.	ď	ö	ę,	ó	ė,	o,	ď.	ď	ď	ď	6.	ė,	ę.	e,	ę.	o,	é,	ų.	77.2	75.3	'n.	74.1	74.1	74.1	72.8
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11	12	13	14	15	16	17	18	19	20	21	22	23	• 24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

CD23, FCERII, IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region, CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; lafabalmacto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; dermatitis; psoriasis; inflammatory bowel disease; glomerulonephritis; crohn's disease; graft-versus-host disease; CoPD; bronchitis; eczema; insultis; B-cell malignancy; therapy. Light chain CDR L1 of mouse anti-CD23 MAb C11. AAY32254 standard, Peptide, 16 AA. (first entry) W09958679-A1. Mus musculus. 15-FEB-2000 AAY32254;

98GB-0009839 09-MAY-1998; 07-MAY-1999; 18-NOV-1999

(GLAX) GLAXO GROUP LTD.

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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The comprisions are useful for inhibiting the interaction of a call expressing CR2. They are useful for inhibiting the interaction of a call expressing CR2. They are useful for inhibiting of treating CR2 mediated disorders such as shewcyte trafficking, for treating CCR2-mediated disorders such as rheumatorid arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating allergy, anaphylaxis, and in the manufacture of a medicament for treating allergy, anaphylaxis, and in the manufacture of a medicament for treating allergy, anaphylaxis, consistent allergy and allergic reaction, shock, seroosis, allograft rejection, ender fibrotic disease, asthma, inflammatory glomenlopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular threevention, including angioplasty and/or stent placement in a mammal. The present sequence is mouse germline kappa light chain variable of the present sequence is mouse germline kappa light chain variable
                                                          Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD23; FCERII; IgB receptor; monoclonal antibody; C11; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; inflammation; arthritis; lupus erythematosus; multiple sclerosis; urflammation; they providate; diabetes; uvaitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; drohn's disease; inflammatory bowel disease; ulcerative colitis; Crohn's disease; graft-versus-host disease; CDP; bronchitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised anti-CD23 MAD C11 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 81; DB 22;
100.0%; Pred. No. 3.9e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "framework region 1"
24..39
                                                                                                                                                                Disclosure; Page 151; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY32262 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 RSSKSLLYKDGKTYLN 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RSSKSLLYKDGKTYLN 16
                    WPI; 2001-488888/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 AA;
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ID AAY3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .<del>.</del>
                                                                                                                                                                                               This sequence represents complementarity determinating region 1 (CDR L1) of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11 (see also AAY32262). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY3224-59) to render them capable of binding to the CD23 type II molecule expressed on heematopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, are used to block soluble CD23 formation for treatment of arthritis, clubus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, dabetes, uvatis, demantils, psoriasis, multiple sclerosis, diabetes, graftome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogrem's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, COPD, insulitis, bronchitis diabetes, and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; hoos; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasia; VK; kappa light chain variable region.
                                                                                                    Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Keefe T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse germline kappa light chain variable (VK) region, 167/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 81; DB 21; Length 16; 100.0%; Pred. No. 5e-07;
  Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Brien S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
  Rapson NT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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  Ellis JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE06969 standard; Protein; 100 AA.
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                                                                                                                                                                Claim 1; Page 40; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         determining the binding agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-FEB-2000; 2000US-0497625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-FEB-2001; 2001WO-US03537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
nes 16; Conservative
  Crowe SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RSSKSLLYKDGKTYLN 16
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                                        WPI; 2000-053101/04.
N-PSDB; AAZ34739.
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Bonnefoy JMP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
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cD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythemacosus; multiple sclerosis; Hashimoto's thyroiditis; lupus erythemacosus; multiple sclerosis; urticaria; nephrotic syndrome; glomerulonephritis; psoriasis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; slogram's syndrome; allergy; asthma; thinitis; eczema; insultis; graft.vergus-host disease; COPD; bronchitis; diabetes;
Mouse anti-CD23 MAb C11 light chain variable region.
                                                                                                                                                                                                 B-cell malignancy; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-053101/04.
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                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                    WO9958679-A1.
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                                                                                                                                                                                                                                                                                            Region
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                                                                                                                                                                                                                                                                                                                                                                 Region
 This sequence represents the light chain variable region (VL) of humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human framework (HSIGNYII) and the light chain complementarity determining regions (see AAY32254-56) of murine antibody C11. The DNA was constructed by splice overlap PCR. The invention provides attered antibodies, such as chimacis or humanised antibodies, which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on hamanised of binding to the CD23 type II molecule expressed on hamanised of binding to the CD23 for the treatment of arthritis, charactoris, dermatitis, porthas thyrologism scolers, republication in human therapy, for the treatment of arthritis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, crohn's disease, Sjogram's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthma, and secandary type I charactes), and B-cell malignancies (Claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor specific antibodies useful for treating e.g. arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 81; DB 21; Length 116; 100.0%; Pred. No. 4.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                   Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                   Ellis JH, Rapson NT,
                                   'note= "framework region 2"
                                                                                                                                                                              /note= "framework region 4"
                                                                                                           region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetes, multiple sclerosis and psoriasis
                                                                                                       "framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  determining the binding agents.
                                                                       "CDR 2"
                                                                                                                          94..102
/note= "CDR 3"
   "CDR 1"
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Bonnefoy JMP, Crowe SJ,
                                                                                                                                                               103..113
                                                                                                                                                                                                                                                                                                                                                               (GLAX ) GLAXO GROUP LTD
   /note=
40..54
                                                                         note=
                                                                                                           /note=
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Ellis JH, Rapson NT, Shearin J;

Crowe SJ,

Location/Qualifiers "CDR L1"

55..70 /note= 83..92

/note= "CDR L2" 125..134 /note= "CDR L3"

99WO-GB01434.

98GB-0009839

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This sequence represents the light chain variable region (VL) of murine anti-CD23 (FCERII) monoclonal antibody Cll. The invention provides altered antibodies, such as chimeric or humanised antibodies (see AAV32262 and AAV32263), which comprises sufficient of the amino acid sequences of the Cll light and heavy chain complementarity determining regions (see AAV32454-59) to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble complements in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, sjogren's syndrome, allergic asthma, intrinaic asthma, acte asthmatic exacerbation, rhintis, ecema, graft-versue-host disease, COPD, insultis, insultis,
Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (particularly chronic bronchitis) or diabetes (particularly type 1 diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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100.0%; Pred. No. 5.8e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              determining the binding agents
                                                                                                           Claim 8; Fig 2; 81pp; English.
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les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 AA;
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AAY32261 standard; Protein; 145 AA.

15-FEB-2000 (first entry)

AAY32261;

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The present sequence represents the light chain of a catalytic antibody which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAs) were presented and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be
Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue; TSA; benzoic acid, phenyl cocaine; immunogenic conjugate; reduction, cocaine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue, TSA, benzolc acid, phenyl cocaine, immunogenic conjugate, reduction, cocaine, treatment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variable domain of the Kappa light chain of catalytic antibody 2A10.
                                                                                                                                                                                                                                                                                                                                    New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 77; DB 19; Length 113;
Pred. No. 2.1e-05;
.; Mismatches 0; Indels
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93.8%;
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                                             overdose, addiction.
                                                                                                                                                                                                                                                                                        WPI; 1998-077166/07.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 AA;
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                                                                                                      WO9749800-A1,
                                                                                                                                                                 25-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW39818-20 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 6A12, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-bancoic acid from 3H-phenyl cocaine. The 6A12 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 6A12 has a per minute Kcat 60 0.072. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
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                                                                                                                                                        Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Pred. No. 2.4e-06;
1; Mismatches 0; Indels
                                                                                                                              Light chain CDR1 of catalytic antibody 6A12
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                                       AAW39818 standard; peptide; 16 AA.
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                                                                                                                                                                                                                                                                                                                                                                                       (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.1%;
Best Local Similarity 93.8%;
Matches 15; Conservative
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                                                                                                  (first entry)
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                                                                                                                                                                                                       overdose, addiction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             simply binding
                                                                                                  16-JUN-1998
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       RESULT 5
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                                                                                        þe
                             The mouse VL gene product may be used to produce chimeric mouse-human Abs against HIV-1 comprising human Ig constant regions and murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections, and may k produced by a bacterial, yeast or mammalian expression system.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%; Score 76; DB 12; Length 132; 93.8%; Pred. No. 3.7e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                  93.8%; Score 76; DB 12; Length 131; 93.8%; Pred. No. 3.7e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robinson RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Light (kappa) chain variable region of murine 2E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric antibodies; immunoconjugates; HIV; AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                         AAR12354 standard; Protein; 132 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90WO-US06615.
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-1991 (first entry)
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GREC ) GREEN CROSS CORP.
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                                                                                                                                                                                                                              15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Better MD, Horwitz AH,
                                                                                                                                                                                                                                                                                               44 RSSKSLLYKDGKTYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1991-178044/24.
N-PSDB; AAQ12056.
                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                   131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR12354;
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                                                                                                                                                                                      Query Match
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                $$666655$$
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                                                                                                                                                                                                                                                                                                                         of the Kappa light chain of catalytic antibodies which are able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 2AlO antibody (AAW39809 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoseter transition state analogue. Antibody 2AlO has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can
                                                                                                                                                                                                                                                                                                          AAW39801-05 represent the amino acid sequences of the variable domain
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                                                                                                                                                                 New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimeric mouse human antibodies - used in treatment, diagnosis prophylaxis of HIV infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 77; DB 19; L
Pred. No. 2.1e-05;
L; Mismatches 0;
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                                                                                                                                                                                                                                                                  Claim 16; Pages 73-74; 147pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse MAb 2E12 L chain V region
                                                  (UYCO ) UNIV COLUMBIA NEW YORK,
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            96US-0672345.
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N-PSDB; AAQ12012.
                                                                                                                              WPI; 1998-077166/07.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV-1; chimera.
                                                                                                                                                                                                                              simply binding
25-JUN-1996;
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                                                                                          Landry DW;
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SXTTXBBXTXBXBXBXBXBXBXBXBX

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AAW39924-26 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 12H1, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified using TSA2, and has a per minute Kcat of 0.16. The antibody particularly for the treatment of an overdose. They are also used for treatment of an overdose. They are also used for treatming addiction (by reducing the in vivo concentration that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Variable domain; lambda light chain, catalytic antibody; degradation, cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction
                                        Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue, TSA, benzoic acid; phenyl cocaine, immunogenic conjugate, reduction, cocaine, treatment; overdose; addiction.
                                                                                                                                                                                                                                                                                                                                                                   New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.6%; Score 75; DB 19; Length 16
87.5%; Pred. No. 5.2e-06;
ive 2; Mismatches 0; Indels
               Light chain CDR1 of catalytic antibody 12H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Light chain of the catalytic antibody 6A12.
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                                                                                                                                                                                                                                                                              (UYCO ) UNIV COLUMBIA NEW YORK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                              Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue, TSA, benzoic acid, phenyl cocaine, immunogenic conjugate, reduction, cocaine, treatment, overdose, addiction.
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87.5%; Pred. No. 5.2e-06;
ive 2; Mismatches 0; Indels
                                                                                                                                                                                   Light chain CDR1 of catalytic antibody 3B9.
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                                                                                           AAW39815 standard; peptide; 16 AA.
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1 RSSKSLLYKDGKTYLN 16
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AAW39824
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AC AAW39
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Length 16;

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AMW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade occaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-bhenyl cocaine. The JBS antibody (AMW39806 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can
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New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 113;
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87.5%; Pred. No. 4.6e-05;
ive 2; Mismatches 0; Indels
                                                                                                             Claim 12; Pages 71-72; 147pp; English.
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les 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              113 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents the light chain of a catalytic antibody which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be
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Pred. No. 4.6e-05;
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                                                                                                                                                                                                                        WPI; 1998-077166/07.
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Best Local Similarity
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                                                         25-JUN-1997;
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    31-DEC-1997
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were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 6A12 antibody (AAW39807 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 6A12 has a per minute Kcat of 0.072. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
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les 14; Conserv
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Query Match 92.6%; Score 75; DB 19; Length 113;
Best Local Similarity 87.5%; Pred. No. 4.6e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSRSLLYRDGKTYLN 39
Search completed: April 22, 2003, 12:51:11
Job time: 41.5714 sece
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113 AA

Sequence

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Sequence 32, Appl Sequence 55, Appl Sequence 51, Appl Sequence 75, Appl Sequence 76, Appl Sequence 24, Appl Sequence 66, Appl Sequence 66, Appl Sequence 11, Appl Sequence 12, Appl Sequence 12, Appl Sequence 1364, Appl Sequence 1964, Appl Sequence 22, Appl 22, Appl
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Sequence 13, A
Sequence 11, A
                                                                                                                April 22, 2003, 12:53:59 ; Search time 16.8571 Seconds (without alignments) 76.055 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/NSO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

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6: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/NSO7_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-09-840-459-55
US-09-840-459-55
US-10-194-975-75
US-10-194-975-76
US-09-840-459-23
US-09-840-459-56
US-09-840-459-56
US-09-479-64-20
US-09-479-64-20
US-09-479-64-20
US-09-479-64-20
US-09-840-459-62
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 RSSKSLLYKDGKTYLN 16
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Maximum DB seq length: 200000000
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Sequence 59, Appli
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Patent No. US2002015057611

GENERAL INPORMATION.

APPLICANT: LAGORS, Gregory J.

APPLICANT: Newman, Walter

APPLICANT: Newman, Walter

APPLICANT: O'Erien, Siobhan H.

TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REPRERENCE: 1855.1022-01

CURRENT APPLICATION NUMBER: PCT/USO1/03537

PRIOR PELING DATE: 2001-02-02

PRIOR PEPLICATION NUMBER: 09/497,625

PRIOR PELING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/359,193

PRIOR PLING DATE: 1998-07-22

PRIOR PLING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-23

NUMBER OF SEQ ID NOS: 107

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 107
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100.0%; Score 81; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 16; Conservative 0; Mismatches 0;
                                    US-09-840-459-54
US-09-840-459-53
US-09-840-459-63
US-09-880-748-1991
US-09-96-851-38
US-09-96-851-38
US-09-96-459-60
US-09-98-0-459-60
US-09-98-0-459-67
US-09-840-459-67
US-09-840-459-67
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US-09-835-087-3
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US-09-809-739-14
US-09-809-739-15
US-09-809-739-16
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    CRGANISM: Mus musculus US-09-840-459-32
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US-10-194-975-76
US-10-194-975-76
US-10-194-975-76
US-10-194-975-76
Sequence 76, Application US/10194975
Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: POCLE, Jefferson
TITLE REPERRENCE: 501231-01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOUTWARE: Patentin version 3.1
SEQ ID NO 76
LENGTH: 100
                                                                                2; Mismatches
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US-09-840-459-23
Sequence 23, Application US/09840459
Factor No. US20020150576A1
GENERAL INFORMATION:
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APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0
Matches 12; Conservative
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    24 RSSQSLVHSDGKTYLN 39
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-76
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US-09-840-459-55

5 Sequence 55, Application US/09840459

Fatent No. US20020150576A1

GENERAL INFORMATION:

APPLICANT: LAROSA, Gregory J.

APPLICANT: Ones, S. Tarran

APPLICANT: Ones, S. Tarran

APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

TITLE OF INVENTION: WUMBER: US/09/840,459

CURRENT FILING DATE: 2001-02-02

FRIOR APPLICATION NUMBER: 09/497,625

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR PILING DATE: 1999-07-23

PRIOR PILING DATE: 1999-07-23

NUMBER OF SEQ ID NOS: 107

SOFTWARE FEASESC for Windows Version 3.0

LENGTH: 112
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US-09-905-243-61

Sequence 61, Application US/09905243

Sequence 61, Application US/09905243

Sequence 61, Application US/09905243

Sequence 61, Application US/09905243

GENERAL INFORMATION:

TITLE OF INVENTION: Immunogenicity

TILE OF INVENTION: Immunogenicity

TILE REFERENCE: PS0770

CURRENT APPLICATION NUMBER: US/09/905,243

CURRENT FILING DATE: 2001-07-16

PRIOR PILING DATE: 2001-07-16

NUMBER OF SEQ ID NOS: 97

SOFTWARE: FARSERE FOR Windows Version 3.0

SEQ ID NO 61

LENGTH: 93
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ORGANISM: Macaca cynomolgus
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Matches 12, Conservative
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COCATION: (54)...(61)
COTHER INFORMATION: CDRII
US-09-905-243-61
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OTHER INFORMATION: CDRI
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COGGANISM: Homo sapiens
US-09-840-459-55
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NAME/KEY: DOMAIN
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1 RSSKSLLYKDGKTYLN 16

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IS-09-840-459-56
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Pred. No. 0.0017;
3; Mismatches 1; Indels
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Pred. No. 0.0017;
3; Mismatches 1; Indels
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Sequence 24, Application US/09840459
Patent No. US20020150576A1
GENERAL INFORMATION:
APPLICANT: LAGGA, Gregory J.
APPLICANT: Newman, Walter
APPLICANT: O'Erien, Siobhan H.
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT PILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-03
PRIOR PLING DATE: 2000-02-03
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE PARENCE PARENCE IN NUMBER: 09/121,781
PRIOR FILING DATE: 1999-07-23
SOFTWARE PARENCE PARENCE FARENCE PARENCE PAREN
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND TITLE OF INVENTION: METHODS OF USE THEREFOR FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: DET/US01/03537
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1998-07-23
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CHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-24
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Best Local Similarity 75.0%;
Matches 12; Conservative
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Best Local Similarity 75.0%;
Matches 12; Conservative
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24 KSSQSLLYSNGKTYLN 39

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Sequence 8(a, publication 18/09840459)

Sequence 8(a, publication 18/09840459)

Sequence 8(a, publication 18/09840459)

Sequence 8(a, publication 18/09840459)

Septicant Sequence 8(a, publication 18/09840459)

Sequence 18(a, publication 18/09840459)

Title 8(a) Fundament 18(a) Fundamen
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Publication No. US20030013183A1

Publication No. US20030013183A1

APPLICANT: McCall, Catherine

APPLICANT: Weber, Exic

TITLE OF INVENTION: Feline Immunoglobulin B Molecules and Related Methods

FILE REPREMEE: P-1047

CURRENT APPLICATION NUMBER: US/09/479,614

CURRENT FILING DATE: 2000-01-07

EARLIER FILING DATE: 1999-01-07

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 20

LENGTH: 242
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Sequence 1964, Application US/09880748

Publication No. US2003065937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 05/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0
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Pred. No. 0.0044;
2; Migmatches 2; Indels
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Pred. No. 0.0047;
2; Mismatches 2; Indels
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Patent No. US2/0201555/6Al
GENERAL INFORMATION:
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Ones, S. Tarran
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Best Local Similarity 75.0%
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Best Local Similarity 75.0
Marches 12, Conservative
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ORGANISM: Homo sapiens
US-09-880-748-1964
                                                                                                                                                                                                                                                                                       ; TYPE: PRT; ORGANISM: Felis catus
US-09-479-614-20
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US-09-880-748-1964
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US-09-840-459-70
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US-10-006-773-11
Sequence 11, Application US/10006773
Sequence 11, Application US/10006773
Sequence 11, Application US/10006773
Sequence 11, Application US/10006773
Fatent No. US20020132983A1
FAPLICANT: VUNDARATION:
TILE REPERENCE: 003
CURRENT APPLICATION NUMBER: US/10/006,773
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/250,089
FRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
SEQ ID NO 11
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US-09-479-614-26

i Sequence 26, Application US/09479614

publication No. US20030013183A1

GENERAL INFORMATION:

APPLICANT: Weber, Exic

TILE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

FILE REFREENCE: P-1047

CURRENT APLICATION NUMBER: US/09/479,614

CURRENT PILING DATE: 1000-01-07

EARLIER APLICATION NUMBER: 60/115,033

SEALIER PILING DATE: 1999-01-07

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 26

LENGTH: 222
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                                            Score 64; DB 10; Length 112;
Pred. No. 0.0019;
2; Mismatches 2; Indels
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79.0%; Score 64; DB 9; Length 222;
Best Local Similarity 75:0%; Pred. No. 0:004;
Matches 12; Conservative 2; Mismatches 2; Indels
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US-09-479-614-20
; Sequence 20°, Application US/09479614
                                              Query Match
Best Local Similarity 75.0%;
Matches 12; Conservative
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Best Local Similarity
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; ORGANISM: Mus sp.
US-10-006-773-11
        US-09-840-459-66
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Search completed: April 22, 2003, 13:11:11 Job time : 17.8571 secs

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74.1%; Score 60; DB 10; Length 112;
Best Local Similarity 68.8%; Pred. No. 0.0087;
Matches 11; Conservative 3; Mismatches 2; Indels
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Pred. No. 0.006;
3; Mismatches 2; Indels
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Sequence 62, Application US/09840459

Patent No. US20020150576A1

GENERAL INFORMATION:
APPLICANT: LARGAGA, Gregory J.
APPLICANT: Newman, Walter
APPLICANT: O'Brien, Siohan H.
APPLICANT: O'Reie, Theresa
APPLICANTON: NUMBER: US/09/840, 459
PRIOR FILING DATE: 2000-02-03
PRIOR PLING DATE: 2000-02-03
PRIOR PLING DATE: 1999-07-22
PRIOR PLING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SEQ ID NO 62
BENGTH: 112
APPLICATION: NUMBER: US/121, 781
PRIOR PLING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SEQ ID NO 62
BENGTH: 112
APPLICÂNT: O'Brien, Siobhan H.
APPLICANT: O'Reefe, Theresa
ITILE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TILLE OF INVENTION: HUMANIZED OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/121,791
PRIOR PILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SEQ ID NO 70
LENGTH: 112
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Best Local Similarity 68.8%;
Matches 11; Conservative
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CORGANISM: Homo sapiens
US-09-840-459-62
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CORGANISM: Homo sapiens
US-09-840-459-70
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24 RSSQSLVFSDGNTYLN 39

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                                                                                                                                                                          April 22, 2003, 12:46:53 ; Search time 3.5 Seconds (without alignments) 82.953 Million cell updates/sec
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GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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1 LMSTRAS 7
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RA WEDLINE=19000273; PubMed=99160;
RAT "Kappa Chain variable region from M167, a phosphorylcholine binding
RT "Kappa Chain variable region from M167, a phosphorylcholine binding
RT "Rappa Chain variable region from M167, a phosphorylcholine binding
RT "Rappa Chain variable region from M167, a phosphorylcholine."

RIC "Biochemistry 1": 2703-2707 (1978).

C -1. MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOWA FROTEIN THAT
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CC THAIN HAS ALSO BEEN DETERMINED.

RESP. PRO1052; INTU.

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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1989 (Rel. 03, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Kappa chain V-II region MOPC 167.
16 Kappa chain V-II region MOPC 167.
17 Mus musculus (Mouse).
18 Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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COMPLEMENTARITY-DETERMINING-1.
PRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%; Score 31; DB 1; Length 112; Local Similarity 100.0%; Pred. No. 0.29; es 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12349 MW; A58EDFD6404B9726 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 AA
                                                                                                                                                                                                                                                                                                     PRT; 112 AA.
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                                                                                                                                                                                                                       ALIGNMENTS
                            CA13 RAT
METE YEAST
ALRI YEAST
YAGI RHISN
YBK4 YEAST
STHI YEAST
HRP1 SCHPO
HRP3 SCHPO
                                                                                                                                                      APX XENLA
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548
6364
766
909
909
11359
11359
11420
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Gaps

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SEQUENCE

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X MEDLINE=80040403; PUDMEGG938437;
XX MEDLINE=80040403; PUDMEGG938437;
XA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA BOUTISE R., Bursen, C.V., Caldwell B., Capusno V., Carter N.M.,
Chois S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniell R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari B., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Coris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Xiein C.,
Kabayashi Y., Koetter P., Roningstein G., Krogh S., Kumano M.,
Kobayashi Y., Koetter P., Roningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mallado R.P., Mizuno M., Mosetl D., Nakai S., Noback M.,
RA Presecan B., Pulic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Schleich S., Schroeter R., Sator P., Skoweka A., Servor S.J., Sarror P., Shin B. S., Soldo B.,
RA Fosecan V., Uchiyama S., Vandelbr H., Waitzenegger T.,
Tosauco V., Uchiyama S., Vandelbr H., Waitzenegger T.,
Yuari A., Wambutt R., Wedler E., Waeler E., Waeler F., Yasasuctti A.,
Valari A., Wainbutt R., Wedler E., Waeler F., Yasasuctti A.,
Valari A., Wainbutt R., Yamamoto H., Yamane K., Yasuwoto K., Yata K.,
                                                                                                                                                                                IG KAPPA CHAIN V-II REGION VKAPPA167.
                                                                                                                                                                                                 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                         FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 1; Length 120;
Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Noback M.A., Terpstra P., Holsappel S., Venema G., Bron Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
63BB571F0B4DE3E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1994 (Rel. 30, Created)
15-JTL-1998 (Rel. 36, Last sequence update)
15-JTN-2002 (Rel. 41, Last annotation update)
YHGB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                  FRAMEWORK-3
PRT;
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MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                     113 B
                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                        120 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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75 LMSTRAS 81
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P38048;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                               MEDLINE=81052016; PubMed=6776396;

A Appella E.;

"Amino acid sequence of the light chain variable region of M511, a phosphorylcholine-binding murine myeloma protein.";

If mod I mmunol. 17:711-718 (1980).

- I MISCELLANECOUS: THIS CHAIN WAS ISOLATED FROM A WYELOWA PROTEIN THAT BINDS PHOSPHORYLCHOLINE.

RINDS PHOSPHORYLCHOLINE.

RINGSP; PRO03006; Ig.MHC.

RINGEPRO: IPRO03006; Ig.MHC.

RINGEPRO: IPRO03596; Ig.V.

REMARY: SMO0406; IG; I.

REMARY: SMO0406; IG; I.

REMINOGATION V region.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                            Mus musculus (Mouse).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-82002223; PubMed=6791832; Selaing E., Storb U.; "Somatic mutation of immunoglobulin light-chain variable-region "Somatic mutation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 31; DB 1; Length 113; 100.0%; Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY - DETERMINING - 1.
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12496 MW; EFB0DC4DA2BD3450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 18, Last annotation update)
1g kappa chain V-II region VKAPPA167 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AA.
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EMBL; K02415; AAA39051.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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HSSP; P80362; 1WTL.
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55
62
94 1
103 1
23
113 AA;
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es 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 LMSTRAS 61
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RESULT 3
KV2B MOUSE
ID KV2B MOUSE

DISULFID NON TER

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SEQUENCE Query Match

Best Loca Matches

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RESULT 6
MCM7_SCHPO
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Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
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Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M. Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yellon M., Botstein D., Davis R.W.; Subth C. Ubb. C., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                  Popham D.L., Setiow P.;
"Cloning, nucleotide sequence, and regulation of the Bacillus subtilis paper gene, which codes for a putative class A high-molecular-weight penicillin-binding protein.";
J. Bacteriol. 175:4870-4876 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 25.6 kDa protein in NTF2-SRP1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.1%; Score 27; DB 1; Length 104;
85.7%; Pred. No. 3.1;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete proteome.
SEQUENCE 104 AA; 11998 MW; 6B44CD77B52FD968 CRC64;
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                                                                                                                                                                                                                                             MEDLINE=93328693; PubMed=8335642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y14083; CAA74515.1; -. EMBL; Z99109; CAB12849.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L10630; AAA71940.2; -. PIR; C40614; C40614. SubtiList; BG10426; yhgB.
                                                                                                                                                                          SEQUENCE OF 1-67 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                      Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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01-FEB-1995 (
01-OCT-1996 (
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P40011;
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YEKO YEAST
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EMBL; U18778; AAB64543.1; -.

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Gaps
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A globular complex formation by Ndal and the other five members of
the MCM protein family in fission yeast.";
Genes Cells 2:467-479(1997).
                                                                                                                                                                                                                                                                                         STRAIN=011;
Liang D.T., Forsburg S.L.;
"Fission yeast mcm7+ is an essential gene required for normal DNA
                                                                                                                                           MCM7_SCHPO STANDARD; PRI; 760 AA.
075001; P87302;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 41, Last sequence update)
15-JUM-2002 (Rel. 41, Last annotation update)
DNA replication licensing factor mcm7 (Minichromosome maintenance
                                                        ö
                                     Length 234;
                                                        0; Indels
                                                                                                                                                                                                                                                                                                                            Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
SGD; S0000812; YER010C.
Hypothetical protein.
SEQUENCE 234 AA; 25563 MW; EC109F224240F980 CRC64;
                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Pungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                    87.1%; Score 27; DB 1;
100.0%; Pred. No. 7.8;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 415:871-880(2002).
                                                         6; Conservative
                                                                                                                                                                                                             MCM7 OR SPBC25D12.03C.
                                                                                                                                                                                                                                                     Schizosaccharomyces.
                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              NCBI_TaxID=4896;
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102 LMSTRA 107
                                                                                                                                                                                                                                                                                                                      replication.";
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Local Similarity 100.
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NCBI TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                      2 MSTRAS 7
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WIS4_SCHPO
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                                    This SWISS-PROT entry is copyright. If is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1994 (Rel. 30, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA replication licensing factor CDC47 (Cell division control protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDC47 OR YBR202W OR YBR1441.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                 EMBL; AF070481; AAC23693.1; --
EMBL; AL031158; CAA20099.1; --
EMBL; AL031158; CAA20099.1; --
EMBL; AL001065; CAA03898.1; --
InterPro; IPRO01209; MCM.
Pfam; PF00493; MCM; 1.
ProDom; PF001041; MCM; 1.
PROSITE; PS00847; MCM 1; 1.
PROSITE; PS00847; MCM 1; 1.
PROSITE; PS00847; MCM 1; 1.
PROSITE; PS00847; MCM 2; 1.
Transcription requiration; DNA-binding; Nuclear protein; DNA replication; Cell cycle; ATP-binding.
DOMAIN
PEND 403 410 ATP-binding.
CONFLICT 457 457 V -> I (IN REF. 3).
SEQUENCE 760 AA; 85622 MW; 2141F8F9CB0BAA34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                87.1%; Score 27; DB 1; Length 760; 100.0%; Pred. No. 29; o; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dalton S.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
 -!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE MCM FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           845 AA
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                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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P38132;
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RESULT 9
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ID RS3A_S
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Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galllardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sapachez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Grrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shapakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE 17. Shiozaki M., Russell P.;
Shiozaki K., Shiozaki M., Russell P.;
Shiozaki K., Shiozaki M., Russell P.;
Mosaki K., Shiozaki M., Russell P.;
Molozaki K., Shiozaki M., Russell P.;
Molozaki K., Shiozaki M., Russell P.;
Molozaki M., Russell P.;
Molozaki M., Russell M., Signal M., Molozaki M., Molozaki M., Russell M., Rassell M., Molozaki M., Rassell M., Molozaki M., Molozaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The Mcs4 response regulator coordinately controls the stress-activated Wak1-Wis1-Sty1 MAP kinase pathway and fission yeast cell
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( Interpro), | Inter
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Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                            Shieh J.C., Wilkinson M., Buck V., Morgan B., Makino K., Millar J.B.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              529A989D2B627F3D CRC64,
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RL -> SP (IN REF. 3).

D -> V (IN REF. 1).
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EMBL; Y07750; CAA65030.1; ALT_INIT.
EMBL; Y11989; CAA72718.1; -.
EMBL; U61521; AAB39762.1; -.
HSSP; P24941; 1CKP.
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97282620; PubMed=9136929;
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Genes Dev. 11:1008-1022(1997).
                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 96-1401 FROM N.A.
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85.7%;
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1066 106
1161 116
484 48
1346 134
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Burppean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                             Archaea, Crenarchaeota, Thermoprotei, Sulfolobales, Sulfolobaceae, Sulfolobus.
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1-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
30S ribosomal protein $3Ae.
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InterPro; IPR001593; Ribosomal S3AE.
Profon; PF001015; Ribosomal S3Ae; 1.
PROSTIE; P0003035; Ribosomal S3Ae; 1.
PROSTIE; P801191; RIBOSOWAL S3AE; PALSE NEG.
Ribosomal protein; Complete proteome.
193 AA.
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Lewis D.L., Farr C.L., Kaguni L.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 71.4%;
5; Conservative
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STANDARD;
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                                                                                                                                                                                                                                                                                                    Sulfolobus tokodaii
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=111955;
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NU2M_DROME
ID _NU2M_DROME
SULTO
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0; Mismatches

Conservative

Local Similarity

Matches

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                                                                                                                                                                                                                              SEQUENCE OF 1-56 FROM N.A.
SEQUENCE OF 1-56 FROM N.A.
MEDLINE=88011348; PubMed=3116271;
Clary D.O., Wolstenholme D.R.;
"Drosophila mitochondrial DNA: conserved sequences in the A + T-rich region and supporting evidence for a secondary structure model of the small ribosomal RNA.";

    J. Mol. Evol. 25:116-125(1987).
    CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
    SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial

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P11087, 060635,
01-ULJ-1989 (Rel. 11, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UTM-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(1) chain precursor.
Collagen alpha 1(1) chain precursor.
Evaryota; Meusealus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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EMBL; X05915; CAA29342.1; -.
PIR; A00418; QXFP2Y.
PIR; A25797; A25797; Dayk\mt:ND2.
FlyBase; FBgn0013184; Dyak\mt:ND2.
InterPro; IPR001750; Oxidored_q1.
Prime PF00361; O
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MEDLINE=86137403; PubMed=3841523;
French B.T., Lee W.-H., Maul G.G.;
"Nucleotide sequence of a cDNA clone for mouse pro alpha 1(I) collagen protein.";
Gene 39:311-312(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.9%; Score 26; DB 1; Length 341;
85.7%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
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                                        Clary D.O., Goddard J.M., Martin S.C., Fauron C.M.-R., Wolstenholme D.R.; "Drosophila mitochondrial DNA: a novel gene order.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                     Nucleic Acids Res. 10:6619-6637(1982)
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     MEDLINE=83090428; PubMed=6294611;
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Matrix Biol. 14:593-595(1995).
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                                                                                                                                                                                                                                                                                                                                   "Drosophila melanogaster mitochondrial DNA, a novel organization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDUINE=84041489; PubMed=6314262;
Clary D.O., Wolgtenholme D.R.;
"Genes for cytochrome c oxidase subunit I, URF2, and three tRNAs in prosophila mitochondrial DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                               Januare 304:234-241(1983).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=2117.6 I vory Coast;
STRAIN=2117.6 I vory Coast;
MEDLINE-86089137; Pubmed=3001325;
Clary D.O., Wolstenholme D.R.;
"The mitochondrial DNA molecular of Drosophila yakuba: nucleotide sequence, gene organization, and genetic code.";
J. Mol. Evol. 22:252-271(1985).
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EMBL, J01404; AAB59238.1; -.
PIR; A00419; QXFP2M.
PIYBase, FBGn0013680; mt.ND2.
InterPro; IPR001750; Oxidored_q1.
Pfam, PF00561; oxidored_q1.
Pfam, PF00561; oxidored_q1.
SEQUENCE 341 AA; 39773 WW; 2B8E9528C28007D8 CRC64;
"Drosophila melanogaster mitochondrial DNA: completion of the nucleotide sequence and evolutionary Gomparisons."; Insect Mol. Biol. 4:263-278(1995).
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85.7%; Pred. No. 22;
ive 0; Mismatches 1; Indels
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1-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
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                                                                                                                                                                                          SEQUENCE OF 56-341 FROM N.A.
MEDLINE=83245048; PubMed=6408489;
de Bruijn M.H.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila yakuba (Fruit fly).
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SEQUENCE OF 1-56 FROM N.A.
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                                                                                                                                  -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. -!- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
                  MEDLINE=83141374; PubMed=6298597; Monson J.W., Friedman J., McCartby B.J.; Monson J.W. procollagen gene: "DNA sequence analysis of a mouse pro alpha 1 (I) procollagen gene: evidence for a mouse B1 element within the gene.";
                                                                       MEDLINE-83157109; PubMed-6219867; MOSDLINE-83157109; PubMed-6219867; Monson J.M., McCarthy B.J.; "Identification of a Balb/c mouse pro alpha 1(I) procollagen gene: evidence for insertions or deletions in gene coding sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSO1208; VWFC; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Signal.
SIGNAL 1 22
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COLLAGEN ALPHA 1(I) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
VWFC.
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Probom, PD002078; Fib collagen_C; 1.
SMART; SM00038; COLFI; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000087; Collagen.
InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                          Mol. Cell. Biol. 2:1362-1371(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; K03033; AAA37332.1; JOINED.
EMBL; K03034; AAA37332.1; JOINED.
BML; K03035; AAA37332.1; JOINED.
PIR; A23982; A23982.
MGD; MGI:88467; COllal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF01391, Collagen, 18.
Pfam, PF01410, COLFI; 1.
          SEQUENCE OF 735-1130 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               EMBL; U08020; AAA88912.1; -.
EMBL; X15896; CAA33904.1; -.
EMBL; M14423; AAA37333.1; -.
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1207
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eulheria, Carnivora, Fissipedia, Canidae, Canis.
1182 1207 NONHELICAL REGION (C-TERMINAL).
56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
734 736 CELL ATTACHMENT SITE (POTENTIAL).
1082 1084 CELL ATTACHMENT SITE (POTENTIAL).
11450 1450 A -> V (IN REF. 5).
1453 AA; 137944 MW; 3B802E535DF81808 CRC64;
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InterPro; IPR000865; Fib collagen_C.
InterPro; IPR000865; Fib collagen_C.
InterPro; IPR0001007; VWF_C.
Pfam; PF01391; Collagen; 1.
Propom; PF001410; COLFT; 1.
Probom; PF00107; Collagen; 1.
SMART; SM00184; VMC; 1.
SMART; SM00184; VMC; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
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TRIPIDE-HELICAL REGION
NONHELICAL REGION (C-TERMINAL).
CELL ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                         Score 26; DB 1; Length 1453;
Pred. No. 1.1e+02;
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COLLAGEN ALPHA 1(1) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Collagen alpha 1(1) chain precursor.
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85.7%;
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                                                                                                                                           Query Match
Best Local Similarity 85.77
Conservative 6;
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157
1214
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TISSUE=Skin;
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SIGNAL
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Q9XSJ7;
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CARBOHYD
CARBOHYD
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Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.;
M. Comparative study of glycopeptides derived from selected
vertebrate collagens. A possible role of the carbohydrate in fibril
formation.";
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BEDLINES BA270697. PubMedes62220;
Chu M.-L., de Wet W.J., Bernard M.P., Ding J.-F., Morabito M.,
Myers J., Williams C., Ramirez P.;
Myers J., Williams C., Isamirez P.;
Human pro alpha 1(1) collagen gene structure reveals evolutionary
conservation of a pattern of introns and exons.";
Nature 310:337-340(1984).
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MEDLINE-84080385; PubMed=6689127;
Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry E.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=8002564; PubMed=3178743;

MEDLINE=8002564; PubMed=3178743;

Jacomp G., Kuivanieni H., Stacey A., Shikata H., Baldwin C.T.,

Jacomp G., Kuivanieni H., Stacey A., Shikata H., Baldwin C.T.,

Jacomp G., Kuivanieni H., Etacek C., Stacek J., Shikata H., Baldwin C.T.,

Jacomp G., All-length cDNA clone for the prepro alpha 1(1)

Chain of human type I procollagen.";

Biochem. J. 253:919-922(1988).
1089 1091 CELL ATTACHMENT SITE (POTENTIAL).
1361 1361 N-LINKED (GLCNAC. . .) (POTENTIAL)
1460 Aa; 138762 MW; 5883674D28570697 CRC64;
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                                                                                                                   Length 1460;
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                                                                                                                   Score 26, DB 1; I Pred. No. 1.1e+02; 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88124208; PubMed-3340531;
Maekeloc J.K., Raassina M., Virta A., Vuorio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ļ
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Click E.M., Bornstein P.;
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VARIANT OI-II CYS-926.
MEDLINE=88033031; PubMed=3667599;
VOGGI B.E., Minor R.R., Freund M., Prockop D.J.;
VAGOI mutation in a type I procollagen gene converts glycine 748 of the alpha I chain to cysteine and destabilizes the triple helix in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91184577; PubMed=2010058; Kuivaniemi H., Tromp G., Prockop D.J.; "Mutations in collagen genes: causes of rare and some common diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuivaniemi H., Tromp G., Prockop D.J.;
"Mutations in fibrillar collagens (types I, II, III, and XI), fibrilassociated collagen (type IX), and network-forming collagen (type X) cause a spectrum of disease of bone, cartilage, and blood vessels.";
Hum. Mutat. 9:300-315(1997).
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MEDLINE-88033098; PubMed=2822714;
ROBBOUW C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=86287390; PubMed=3016737;
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change in one human pro alpha 1(1) collagen allele.";
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Byers P. H., Wallis G.A., Willing M.C.;
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MEDLINE-85130970; PubMed=2857713;
Chu M.-L., de Wet W.J., Bernard M.P., Ramirez F.;
"Rine structural analysis of the human pro-alpha 1 (1) collagen of Promoter structure, Alul repeats, and polymorphic transcripts.";
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Nucleic Acids Res. 25:181-187(1997).
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MEDLINE=88097389; PubMed=3480516;
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MEDLINE=87222295; PubMed=3108247;
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MEDLINE=97255959; PubMed=9101290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FASEB J. 5:2052-2060(1991).
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MEDIANE=90062068; PubMed=2511192;
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MEDLINE-89255493; PubMed-2470760;
Patterson E., Smiley E., Bonadio J.;
"RNA sequence analysis of a perinatal lethal osteogenesis imperfecta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89109573; PubMed=2913053; Constantinou C.D., Nielsen K.B., Prockop D.J.; Constantinou C.D., Nielsen K.B., Prockop D.J.; a tethal variant of osteogenesis imperfecta has a single base mutation that substitutes cysteine for glycine 904 of the alpha 1(I) chain of type I procollagen. The asymptomatic mother has an unidentified mutation producing an overmodified and unstable type I
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lethal variant of osteogenesis imperfecta.";
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MEDLINE=90009313; PubMed=2794057;
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                      Biol. Chem. 262:14737-14744(1987)
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                                                          VARIANT OI-II ARG-842.
MEDLINE=88298828; PubMed=3403550;
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MEDLINE=89308591; PubMed=2745420;
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1 83.9%; Score 26; DB 1; Length 1464; Similarity 85.7%; Pred. No. 1.1e+02; 6; Conservative 0; Mismatches 1; Indels

Best Local Similarity Matches 6; Conserv

Query Match

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Triticeae; Triticum.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

BEDLINES-91370843, bubmed=2491677;
Smith J. G. Raikhel N.V.;
"Nucleotide sequences of cDNA clones encoding wheat germ agglutinin"
                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                        e wheat germ agglutinin isolectins:
   polyploid wheat.";
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                                                                                                                   01-JUL-1989 (Rel. 11, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Agglutinin isolectin 1 precursor (WGA1) (Isolectin A)
                                                                                           PRT; 212 AA
                                                                                                                                                                                                                                                                                                                                                                                                Wright C.S., Raikhel N.V.,
"Sequence variability in three wheat
products of multiple genes in polyplo
J. Mol. Evol. 28:327-336(1989).
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MEDLINE=91039324; PubMed=2231724;
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Plant Mol. Biol. 13:601-603(1989)
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S07289; S07289.
7WGA; 15-OCT-90.
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                        1357 LMSTEAS 1363
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1 LMSTRAS
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Query Match
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Search completed: April 22, 2003, 12:51:47 Job time : 5.5 secs

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GenCore version 5.1.4 p5_4578

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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:48:24 ; Search time 6.875 Seconds (without alignments)
97.882 Million cell updates/sec

Title: US-09-674-716B-5
Sequence: 1 LMSTRAS 7
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283224 segs, 9613422 residues
Total number of hits satisfying chosen parameters: 283224
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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database: PIR 73:*
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RESULT 1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C;Accession: E69832; C40614
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C;Accession: B59832; C40614
C;Bron, S;Brouiller, S;Bruschi, C;V;Caddwell, B;Capuano, V;Carter, N.M.; Cho A;Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, X.; Fuma, S.; Galizzi, A.; Galler Scheter, J.; Harwood, C.R.; Henaut, A.; Hilbert, H; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krosqi, S.; Kumano, M.; Kuitta, K.; Lapidus, A.; Canlon, A; Authors: Schleich, A.; Yamano, A.; V.; Sachor, A.; V.; Vala, A.; Vala, 
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CySpecies: Saccharomyces cerevisiae
CySpecies: Saccharomyces cerevisiae
CyBecies: Saccharomyces cerevisiae
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R;Dietrich, F.S.
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R;Dietrich, F.S.
Shoeription: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda A;Reference number: S5043
A;Reference number: S5043
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A;Ression: RMBL;U18778; NID:g603592; PID:g603602; GSPDB:GN00005; MIPS:YER010c
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J. Bacteriol. 175, 4870-4876, 1993
A;Title: Cloning, nucleotide sequence, and regulation of the Bacillus subtilis pbpF gene A;Title: A40614; MUID:93328693; PMID:8335642
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Pred. No. 11;
0; Mismatches 1; Indels
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85.7%;
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A;Map position: 5R
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Best Local Similarity 85...
Fra 6; Conservative
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A;Residues: 1-67 <POP>
A;Cross-references: GB:L10630
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Best Local Similarity
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A,Gene: MIPS:YER010c
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C;Species: Mus musculus (house mouse)

R;Sclaing, E; Storb, U.

C;Species: Musculus (house mouse: Signature)

A;Title: Somatic mutation of immunoglobulin light-chain variable-region genes.

A;Title: Somatic musber: A01909; MuID:82002223; PMID:6791832

A;Accession: A01909

A;Molecule type: DNA

A;Rocestion: An immunoglobulin heterotetramer subunit consists of two identical light (kap aline disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer

F;1-20/Domain: signal sequence #status predicted <AMT>
F;31-110/Product: Ig Kappa achain V region (VKI67) #status predicted <AMT>
F;31-115/Domain: immunoglobulin homology <AMMT>
F;43-115/Domain: immunoglobulin homology <AMT>
F;43-115/Domain: immunoglobulin homology <
                                                                                                                                                                                                                                                                Systems chain V region (W511) - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A01910
R;Appella, E.
Mol. Immunol. 17, 711-718, 1980
Mol. Immunol. 17, 711-718, 1980
A;Reference number: A01910; MUID:81052016; PMID:6776396
A;Reference number: A01910; MUID:81052016; PMID:6776396
A;Recession: A01910
A;Residues: 1-113 cAPP>
C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as 194 and 19M, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
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100.0%; Score 3.7; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels
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F;16-95/Domain: immunoglobulin homology <IMM>
F;23-93/Disulfide bonds: #status predicted
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Best Local Similarity 100.0
Matches 7; Conservative
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LMSTRAS 81
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A,Map position: 2
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ses 6; Conserv
A; Residues: 1-409 < HAY>
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Matches 6
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R. Parkilli, J.; Wren, B. W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Bacham, D.; Chillin R. Parkilli, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Bacham, D.; Chillin Nature 403, 665-668, 2000

Nature 403, 665-668, 2000

A. Paritice: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. Reference number: A01250; MUD:20150912; PMID:10688204

A. Recession: C81451

A. Accession: C81451

A. Accession: C81451

A. Residues: 1-342 < PAR>
A. Residues: 1-
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A;Residues: 1-409 <STO>
A;Residues: 1-409 <STO>
A;Cross-references: GB:AE005174; NID:g12518154; PIDN:AAG58601.1; GSPDB:GN00145; UWGP:Z48
A;Experimental source: strain 0157:H7; substrain EDL933
C;Genetics:
A;Gene: Z4866
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew liler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                              flagellar motor switch protein Cj0319 [imported] - Campylobacter jejuni (strain NCTC 111 C;Species: Campylobacter jejuni
C;Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
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A; Status: preliminary
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A;Gene: fliG; Cj0319
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minichromosome maintenance protein mcm7p [imported] - fission yeast (Schizosaccharomyces N;Alternate names: cell division control protein 47 homolog
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession: T39991; T45282
R;Lyne, M; Rajandream, M.A.; Barrell, B.G.; Whithead, S.; Chillingworth, T.; Churcher, Submitted to the EMBL Data Library, July 1998
A;Reference number: Z21897
A;Accession: T39991
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-760 <a href="https://docume.com/d/">LYNA</a>
A;Residues: 1-760 <a href="https://docume.com/d/"
A,Cross-references: GB:BA000007; PIDN:BAB37764.1; PID:g13363815; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC84341
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
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C:Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Aug-2000
C;Accession: T16198
R;Leimbach, D.
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A,Description: The sequence of C. elegans cosmid F28B4.
A,Reference number: Z18475
A,Accession: T16198
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A;Molecule type: DNA
A;Residues: 1-760 <LIA>
A;Cross-references: EMBL:AF070481; PIDN:AAC23693.1
A;Experimental source: strain Sp.011
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A;Molecule type: DNA
A;Residues: 1-842 <LEI>
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100.0%; Pred. No. 85;
tive 0; Mismatches
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A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-112 < CRUN;
CXC48909:1; PID:g15140382; GSPDB:GN00167
A; Experimental source: gtrain 1021, wegaplasmid pSymB
A; Cross-references: GB:AL591985; PIDN:CAC48909:1; PID:g15140382; GSPDB:GN00167
A; Experimental source: gtrain 1021, wegaplasmid pSymB
A; Catinberr, F: Finan, T.M.; Long, S.R.; Puhlerr, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Dela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones
T.; Hyman, R.W.; Jones
T.; Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Hebault, P.; Vandenbol, M.; Vorholter, P.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A; Feference number: A96039; MUID:21360234; PMID:11474104
A; Contents: annotation
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C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: E95905
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics: SPDB:SPAC9G1.02 A; Gene: SPDB:SPAC9G1.02 A; Map position: 1 C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
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CiSpecies: Schizosaccharomyces pombe
CiSpecies: Schizosaccharomyces pombe
CiSpecies: Schizosaccharomyces pombe
CiDate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
CiDatession: 139225
Rychurcher, C.M.; Gentles, S.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
A.Reference number: 221837
A.References: EMBI: 298763; PIDN:CAB11500.1; GSPDB:GN00066; SPDB:SPAC9GI.02
A.References: EMBI: 298763; PIDN:CAB11500.1; GSPDB:GN00066; SPDB:SPAC9GI.02
A.References: EMBI: 298763; PIDN:CAB11500.1; GSPDB:GN00066; SPDB:SPAC9GI.02
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Pred. No. 22;
2; Mismatches (
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Similarity 71.4%;
5; Conservative
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Matches 5; Conserv
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5 IMSTRSS 11
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81 LMSTRTS 87
                                            300 MSTRAS 305
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A;Genome: plasmid
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A,Molecule type: DNA
A,Residues: 1-645.
A,Bussereau, F.; Mallet, L.; Gaillon, L.; Jacquet, M.
A;Residues: 1-645.
A,Forose-references: EMBL:236071; NID:g536576; PIDN:CAA85166.1; PID:g536577; GSPDB:GN0000
R;Bussereau, F.; Mallet, L.; Gaillon, L.; Jacquet, M.
Yeast 9, 797-806, 1993
A,Title: Yeast Sequencing Reports. A 12.8 kb segment, on the right arm of chromosome II
A;Reference number: S34925; MUID:93377417; PMID:8368014
A;Accession: S34925
A,Molecule type: DNA
A;Residues: 407-620 < 8U2.
A;Cross-references: EMBL:221487
R;Dalton, S.
Submitted to the EMBL Data Library, September 1994
A;Reference number: S56049
A;Reference number: S56049
A;Reference number: S56049
A;Reference number: BMBL:14730; NID:9608169; PIDN:AAA86309.1; PID:9608169
A;Residues: 1-551, G',553-555, TLN',559-573, Y',575-845 < DAL.
A;Residues: 1-551, G',553-555, TLN',559-573, Y',575-845 < DAL.
A;Residues: 1-551, G',553-555, TLN',559-573, Y',575-845 < DAL.
A;Residues: 1-551, G',553-555, TLN',559-573, TLN',575-845 < DAL.
A;Residues: 1-551, G',553-555, TLN',559-573, TLN',575-
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NyAlternate names: cell division control protein CDC47; protein YBR2024
C;Specias: Saccharomyces cerevisiae
C;Date: 13-Aug-1999 #sequence revision
C;Accession: S34027; S46074; S34925; S56049
gubmitted to the EMBL Data Library, January 1993
A;Reference number: S34022
A;Reference number: S34022
A;Resaduas: 1-845 a.OAC>
A;Rossaron: S14027
A;Rossaron: S14027
A;Rossaron: S14027
A;Resaduas: 1-845 a.OAC>
A;Resaduas: 1-
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A;Cross-references: EMBL:U42834; NID:g1125756; PID:g1125758; PIDN:AAA83583.1; CESP:F28B4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 2R
C; Complex: The predominant form is a hererohexamer of MCM2 (PIR:S45757), MCM3 (PIR:A3637
component of replication licensing factor.
                                                                                                                       A;Gene: CESP:F28B4.2
A;Introns: 17/3; 59/3; 93/2; 116/2; 229/3; 333/2; 510/2; 659/3; 738/3; 803/2
C;Superfamily: CDC25-type guanine nucleotide exchange activator homology
F;212-481/Domain: CDC25-type guanine nucleotide exchange activator homology <80S>
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                                                                                                                                                                                                                                                                                                                                                                  87.1%; Score 27; DB 2; Length 842; ilarity 100.0%; Pred. No. 94; Conservative 0; Mismatches 0; Indels
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A;Gene: SGD:CDC47; MIPS:YBR202w
A;Cross-references: SGD:S0000406; MIPS:YBR202w
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                                                                                                                                        A; Gene: pcaQ; SMb20580
A; Genome: plasmid
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Search completed: April 22, 2003, 12:54:47 Job time : 8.875 secs

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XX MEDLINE=20150112; PubMed=10688204;

MEDLINE=20150112; PubMed=10688204;

Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,

Jagels K., Xarlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

And Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Mitchead S., Barrell B.G.;

Whitchead S., Barrell B.G.;

Whitchead S., Barrell B.G.;

I'm genome sequence of the food-borne pathogen Campylobacter jejuni

reveals hypervariable sequences.";

Nature 403:665-668(2000).

RASSP, O3WY63; 10C7.

RASSP, O3WY63; 10C7.

RASSP, O3WY63; 10C7.

RASSP, CAB12786.1;

RASSP, CAB12706; Flg_Motor_Flig.

RASSP, RANOFOSP, Flig.Notor_Flig.

RASSP, TIGROOSP, Flig.1.

RASSP, TIGROOSP, Flig.1.
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Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
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SEQUENCE 342 AA; 38429 MW; ED4D214417C1524C CRC64;
                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Flagellar motor switch protein.
FLIG OR CU0319.
                                                                                                                                                                                                                                                                                                                                             342 AA
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                  Q9MGN7
Q9MGN2
Q9MGL3
Q90YJ1
Q99LL6
Q69650
Q9GY27
                                                                                                                Q8WA98
Q9LF68
Q8VKC3
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Q9F3E2
Q9XWW6
Q9UT39
Q8UX77
Q9UT77
Q9UT77
Q9TXN8
Q9LUQ7
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Q8ZAR5
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NCBI_TaxID=197;
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 Q9PII0
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           GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
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Q8X5US
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Q9XBP6
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Q16050
Q95ND8
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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STRAIN=BALB/C; Mynyair. ... yamashita T., Okuda K., Mishina M., Kawamoto S.; "Delphilin: A novel PDZ-containing protein associates with the GluRdelta? subunit.";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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100.0%; Pred. No. 1.6e+02;
ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-ERISTOL N2;
Leimbach D.;
"The Bequence of C. elegans cosmid F28B4.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Direct Submission.";
Submitted (UN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: 1042834; AA83583.2; -.
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
GLUGL2D philtc-protein.
GRID2IP OR DELPHILIN.
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MGD; MG1:2176.13; Grid2ip.
InterPro; IPR001104; FH2.
InterPro; IPR001478; PDZ.
InterPro; IPR002965; P_rich_extensn.
                                             STRAIN=BRISTOL N2;
MEDLINE=99069613; Pubmed=9851916;
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Pfam; PF00595; PDZ; 1.
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Q9ESJS
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                                                                                                                                                                                                                                                                                                                        PERFAINATION OF THE TRUE OF SECTION OF SECTI
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019852;
01-NOV-1996 (TEMBLrel. 01, Created)
01-OCT-2001 (TEMBLrel. 18, Last sequence update)
01-OTV-2002 (TEMBLrel. 21, Last annotation update)
Hypothetical 96.1 kDa protein.
F2884.2.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Chabditidae; Peloderinae; Caenorhabditis.
[1]
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SEQUENCE FROM N.A.
MEDINE=21074933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunket G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Melch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
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81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000794; Ketoacyl-synt.
Pfam; PF00109; ketoacyl-synt; 1.
Pfam; PF02801; ketoacyl-synt; 1.
PROSITE; PS000606; B_KETOACYL_SYNTHABE; UNKNOWN 1.
COMPLECE PROCEOME.
SEQUENCE 409 AA; 44148 MW; A4DABOAFAIIED883 CI
                                                                                                                                                                                                                                                         409 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.1%; Score 27; DB 3 100.0%; Pred. No. 81; ative 0; Mismatches
                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 8:11-22(2001).
EMBL; AE005571; AAG58601.1; -.
EMBL; AP002565; BAB37764.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
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289 MSTRAS 294
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01985:
AC 01986:
AC 01986:
DT 01-00
DT 01-00
DT 01-00
DF 7288
GN 7288
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O9XBP6; Q9XBP6

RESULT 5 09XBP6

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Matches

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Finan T.M., Weldner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Golding B., Puchler A.;

Golding B., Puchler A.;

Fine complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium mellioti.";

Proc. Natl. Acad. Sci. U. S.A. 98:9889-9894 (2001).

EMBL; ALG013643; CAC48909-1; Complete proteome.

Plasmid; Hypothetical protein; Complete proteome.

SEQUENCE 112 AA; 11488 MW; 95FD54B0FC5CA90E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91138770; PubMed=1995349;

MEDLINE-91138770; PubMed=1995349;

A Mattra A., Bornstein P., Pentrinen R.P.;

A Mattra A., Bornstein P., Pentrinen R.P.;

"Highly conserved sequences in the 3'-untranslated region of the Col.Al gene bind cell-specific nuclear proteins.";

FEBS Lett. 279:9-13(1991).

REMBL; 864596; AAA57049.1; -.

REMBL; MS5998; AAA52049.1; -.

REMBL; MS5998; AAA52049.1; -.

REMBL; MS5998; AAA52049.1; -.

REMBL; MS5998; ACAF2040.1; -.
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MEDILINE-9332646; PubMed=8349697;
MEDILINE-9332646; PubMed=8349697;
MEDILINE-93325646; PubMed=8349697;
MILLINE-93325646; PubMed=8349697;
"Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I)
chain of type I collagen result in defective chain association and
produce lethal osteogenesis imperfecta.";
J. Biol. Chem. 268:18218-18225(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90110490; PubMed=2295701;
Willing M.C., Cohn D.H., Byers P.H.;
Willing M.C., Cohn D.H., Byers P.H.;
Willing M.C., Cohn D.H., Byers P.H.;
"Frameshift mutation near the 3' end of the COLIA1 gene of type I collagen predicts an elongated Pro alpha 1(1) chain and results in osteogeneats imperfecte type 1.";
J. Clin. Invest. 85:282-290(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 1.1e+02;
0; Mismatches 1; Indel8
                                                                                                                                                                                                                                         Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
Type I collagen PRO alpha 1(I) chain propeptide (Fragment).
                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 AA; 31452 MW; A233E40D8545AA7B CRC64;
                                                                                                                                                                                                                                    Score 26; DB 16;
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 AA.
                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
MEDLINE=21396508; PubMed=11481431;
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85.7%;
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                                                                                                                                                                                                                                           83.9%;
ilarity 71.4%;
Conservative
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Best Local Similarity 85...
6; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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5 IMSTRSS 11
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SEQUENCE
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Inouye S., Jain R., Ucki T., Nariya H., Xu C., Hsu M.,
Inouye S., Jain R., Terez-Vidal E., Inouye M.;
Whunoz-Dorado J., Farez-Vidal E., Inouye M.;
"Sequence Analysis of 13 Eukaryotic-like Protein Ser/Thr Kinases of
Myxococous xanthus, a Developmental Bacterium and Significance of
Myxococous xanthus, protein His Kinases.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFISOSO1, AAD42856.1;
InterPro; IPR00019; Euk pkinase.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein RB0509.
RB0509 OR SMB20530.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2).
Bacteria, Proteobacteria, alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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                                                                                         Score 27; DB 11; Length 1024;
Pred. No. 1.9e+02;
1; Mismatches 0; Indels 0
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Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, delta subdivision, Myxobacteria;
Myxococcales, Cystobacterineae, Myxococcaceae, Myxococcus.
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Pfam; PF000515; TPR; 5.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00028; TPR; 3.
PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 1049 AA; 114313 MW; 7752862DAA25338C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
         SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
SEQUENCE 1024 AA; 112578 MW; E318AFDEE02F846A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
serine/threonine kinase PKN8.
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85.7%;
                                                                                            h 87.1%;
Similarity 85.7%;
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myxococcus xanthus.
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Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                   Query Match
Best Local Similarity
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NCBI_TaxID=382;
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53 LVSTRAS 59
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Q92W36; Q92W36

RESULT 6 Q92W36

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KW Plasmid, Hypothetical protein, Complete proteome.
SQ SEQUENCE 313 AA, 33832 MW, 4787BC1BE5476709 CRC64;
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                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                  199 LMPTRAS 205
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                                                                                         1 LMSTRAS 7
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                                       Query Match
Best Local 8
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WREDLINE=11395608; PubMed=11481431;

REDLINE=11395608; PubMed=11481431;

Rinan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,

RA Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,

RA Golding B., Puehler A.;

The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-

RI The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-

RI Taing endosymbiont Sinorhizobium meliloti.",

RE PROL. Acad. Sci. U.S.A. 98:9889-9894(2001).

RE PROL. Acad. Sci. U.S.A. 98:9889-9894(2001).

B. InterPro: IPR005119; LysR.

DR InterPro: IPR005119; LysR.

DR PROLISE: LysR. Substrate; 1.

PROMISE: LysR. Substrate; 1.

PROMISE: LysR. Substrate; 1.
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                                                                                                                                        Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovine; Bos.

NCBI_TAXID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative transcriptional activator of the pca operon, LysR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid DsymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Grosse-Hovest L., Brem G.;

Grosse-Hovest L., Brem G.;

"Bos taurus pro alpha 1(1) collagen gene, exon 49.";

"Bos taurus pro alpha 1(1) collagen gene, exon 49.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ312110; CAC38832.1;

EMBL; AJ312112; CAC38832.1; JOINED.

InterPro; IPRO00087; Collagen.

InterPro; IPRO00087; Collagen.

InterPro; IPRO00085; Fib_collagen_C.
                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 83.9%; Score 26; DB 6; Length 287; Local Similarity 85.7%; Pred. No. 1.16+02; nes 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 287 AA; 31698 MW; A9122CAEB7DC3DAE CRC64;
                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Pro alpha 1(1) collagen (Fragment).
                                                    287 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 AA.
                                                                                                                                                                                                                                                                                                                                                             ProDom; PD002078; Fib_collagen_C; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCAQ OR RB1492 OR SMB20580.
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                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 LMSTEAS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=382;
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                                                                                                                                                                                                                                                                                                                                                                         Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                    Q95ND8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q92TL9
                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                         RESULT 8
Q95ND8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Cochliomyia.
NCBI_TaxID=115425;
                                                                          Gaps
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MEDLINE=20485491; PubMed=11028671;
MEDLINE=20485491; Autins Junqueira A.C., Lemos T.A., Kemper B.L.,
da Silva F.R., Vettore A.L., Arruda P., Azeredo-Espin A.M.;
"The mitochondrial genome of the primary screwworm fly Cochliomyia hominivorax (Diptera: Calliphoridae).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEQUENCE FROM N.A.

A Lu Z., Laptev A.V., Prockop D.J.;

Lu Z., Laptev A.V., Prockop D.J.;

Lu Z., Laptev A.V., Prockop D.J.;

Lu mithe nutleoided sequence of conk for the last 5 exons and 3'-

untranalated region of murine type I(1) procollagen.";

Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.

R MGDJ MG188467; Collag.

R MGDJ MG188467; Collagen.

R InterPro; IFR000885; Fib_collagen_C.

R Pfam, PF01410; Collagen; 1.

R Pfam, PF01410; Collagen; 1.

R ProDom; PD002078; Fib_collagen_C; 1.

R SMART; SM0038; COLFI; 1.
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       Length 313;
                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQÜENCE 325 AA; 35229 MW; A5A21E74DFDE3EF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Alpha-1 type I procollagen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0RR-2002 (TrEMBLrel. 20, Last annotation update)
NADH subunit 2.
/ Match 83.9%; Score 26; DB 16; Local Similarity 85.7%; Pred. No. 1.2e+02; Local 6; Congervative 0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cochliomyia hominivorax (Primary screw-worm). Mitochondrion.
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Gaps

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341 AA

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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7240;
                                                                 MEDLINE=20225575; PubMed=10762421; Spanos L., Koutroumbas G., Kotsyfakis M., Louis C.; Spanos L., Koutroumbas G., Kotsyfakis M., Louis C.; Spanos L., Koutroumbas G., Kotsyfakis M., Louis C.; The complete sequence of the mitochondrial genome of the Medfly, Caratitis capitata."; Insect Mol. Biol. 9:139-144(2000).

Insect Mol. Biol. 9:139-144(2000).

EMBL; AJ242872; CAB45088.1; -
InterPro; IPR001750; Oxidored_q1.

Effan; PF00361; oxidored_q1.

Mitochondrion; NAD; Oxidored_q1; 1.

Mitochondrion; NAD; Oxidoreduses; Ubiquinone.

SEQUENCE 340 AA; 39231 MW; F4C646EICE5E3F4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                               83.9%; Score 26; DB 8; Length 340; ilarity 85.7%; Pred. No. 1.38+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.9%; Score 26; DB 8; Length 341
85.7%; Pred. No. 1.38+02;
cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00361; oxidored g1; 1.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SEQUENCE 341 AA; 39734 MW; 8C42C96FF977A173 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=RU35, C167, DSW, DSR, MD106, MD225, AND SC00;
Ballard J.W.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
NADH dehydrogenase subunit 2.
Drosophila simulans (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Tephritoidea, Tephritidae, Ceratitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase, FBgn0012880; Dsim/mt:ND2.
InterPro; IPR001750; Oxidored_q1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF200840; AAF77382.1;
EMBL; AF200841; AAF77395.1;
EMBL; AF200843; AAF77408.1;
EMBL; AF200843; AAF77421.1;
EMBL; AF200844; AAF77434.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF200845; AAF77447.1; -. EMBL; AF200839; AAF77369.1; -.
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Q9MD83;
01-0CT-2000 (TEMBLrel. 15,
01-0CT-2000 (TEMBLrel. 15,
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Best Local Similarity
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                                                       SEQUENCE FROM N.A.
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                         NCBI_TaxID=7213;
                                                                                                                                                                                                                                                                                                                                                                                                              50 LMSTEAS 56
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Chrysomya.
NCBI_TaxID=142978;
                                                                                                                                                                                                                                                                                         Gaps
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Junqueira A.C.M.;
"The complete mitochondrial genome of the Chrysomya putoria.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
                                                                                                                                                                                                                                                                                         ô
                                         SEQUENCE FROM N.A.
Lessinger A.C., Junqueira A.C.M., Lemos T.A., Kemper E.L.,
Letsinger A.C., Junqueira A.C.M., Lemos T.A., Kemper E.L.,
submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
-I.-CATTVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
EMBL, AF260826; AAF76613.1; -.
InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361, oxidored_q1, I.
Mitochondrion; NAD; Oxidored_q1, I.
Mitochondrion; NAD; Oxidored_q1, I.
Mitochondrion; NAD; Oxidored_q1, I.
SEQUENCE 338 AA, 39337 MW; E6901A86D02439D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.9%; Score 26; DB 8; Length 338;
85.7%; Pred. No. 1.2e+02;
.ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                Similarity 85.7%; Pred. No. 1.2e+02; 6; Conservative 0; Mismatches 1; Indels
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InterPro, IPR003917; NADHub_oxred2.
InterPro, IPR001750, Oxidored_q1.
Pfam, PF00361; oxidored_q1, 1.
PRINTS; PR01436; NADHDHGNASE2.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SEQUENCE 338 AA; 39228 MW; ABD581B5A5A46A23 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAV-2002 (TrEMBLrel. 20, Last annotation update)
NADH dehydrogensse (ubiquinone) chain 2 (EC 1.6.5.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ceratitis capitata (Mediterranean fruit fly). Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
         Insect Mol. Biol. 9:521-529(2000)
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2002 (TrEMBLrel. 20,
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                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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Q9XMP1;
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Q9XMP1
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Gaps

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Length 341;

Title: Perfect score: Sequence: Scoring table:

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Total number Searched:

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Light chain CDR2 o Variable domain of Single chain Fv re Light chain CDR2 o

Propionibacterium Propionibacterium Mouse MAD 2E12 L C Light (kappa) chai Human reproductive Bscherichia coli p Propionibacterium Human peptide #557 encod Protein #545 encod Human bone marrow Peptide #567 encod Peptide #57 encod Collagen type I al Collagen type I al Amino acid sequenc Human preproalpha

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Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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AAR12354
AAM95756
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AAM53875
AAM66263
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AAW12845
AAW12845
AAG475593
AAB43439
AAG81232
AAG81232
AAG96122
AAR71701
AAR96122
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AAR96122
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AAM26539
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ABG35910
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                                                                                                                                                                                                                                                                                                ABB27906
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  97WO-US10965
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identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW39824-26 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 12H1, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified using TSA2, and has a per minute Kcat of 0.16. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                     Gaps
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Best Local Similarity 100.0%; Pred, No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0;
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Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain CDR2 of catalytic antibody 12H1.
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                                                                                                                   AAW39818-20 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 6Al2, which is able to degrade cocarine. A series of cocarine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 6Al2 antibody was identified using TSAl, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 6Al2 has a per minute Kcat of 0.072. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW39821-23 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 2A10, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction
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in far smaller doses than antibodies that antagonise cocaine by simply binding
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                                                                             Claim 13; Page 81; 147pp; English.
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cution sequence temptreminators described in the sequence compression anti-CD23 (FCERII) monoclonal antibody CI1 (see also AAY3262). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of CI1 light and heavy chain CDRs (see AAY3254-59) to render them capable of binding to the CD23 (type II molecule expressed on haematopoietic cells. The antibodies of type II molecule expressed on haematopoietic cells. The antibodies of sea used to block soluble CD23 formation for treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic colitis, crohn's disease, sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhintis, eczema, graft-versus-host disease, COPD, insulitis, bronchitis conditises, promothitis or diabetes), and B-cell malignancies (Claimed). They are also useful for studying interactions between CD23 and various ligands and cetermining the binding agents.
                                                                                                                                                                                    Light chain CDR L2 of mouse anti-CD23 MAb C11.
                                                                                                 AAY32255 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 40; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                                  B-cell malignancy; therapy.
                                                                                                                                                         (first entry)
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LMSTRAS 7
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LMSTRAS 7
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Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasis; Ksppa light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O'Brien S, O'Keefe T;
                                                                                                                                  Mouse germline kappa light chain variable (VK) region, 167/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 151; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Larosa GJ, Horvath C, Newman W,
                                 AAE06969 standard; Protein; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-2001; 2001WO-US03537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-FEB-2000; 2000US-0497625.
                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                               WO200157226-A1.
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                                                                                                        16-OCT-2001
                                                                   AAE06969;
                                                                                                                                                                                                                                                                                                                                                              Mus sp.
RESULT 5
                    AAE06969
                                   Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                               CD23; FCBRII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; lupus erythematosus; multiple sclerosis; urticaria; nephrotic syndrome; glomerulonephritis; psoriasis; inflammatory bowel disease; ulcerative collitis; Crohn's disease; sjogren's syndrome; allergy, asthma; thinitis; eczema; insulitis; graft-vergus-host disease; COPD; bronchitis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents complementarity determinating region 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crowe SJ, Ellis JH, Rapson NT, Shearin J;
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The patent discloses a humanised antibody or its antigen-binding CC fragment, having binding specificity for CC-chemokine receptor 2 and at least a portion of an immunoslobulin of human origin. The and at least a portion of an immunoslobulin of human origin. The chumanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating CCC a leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatory disorder, autoimmune disorders such as rheumatorid or and for inhibiting restenosis. They are useful in therapy or disquence, and in the manufacture of a medicament for treating alleray, anaphylaxis, anaphylax

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Gaps

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100.0%; Score 31; DB 21; Length 7; 100.0%; Pred. No. 7.8e+05; tive 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 7; Conservative

Query Match

Sequence Query Match

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Matches

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The present sequence represents the light chain of a catalytic antibody which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to o immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treatment of an overdose. They are also used for treatment of an overdose. They are also used for the actual section (by reducing the in vivo concentration that can be
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                                                                                                                                                                                                                                 Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction
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                                                                                                                                                                            Light chain of the catalytic antibody 2A10.
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AAW39882 standard, Protein, 113 AA.
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N-PSDB; AAV09789.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue; TSA, benzoic acid; phenyl cocaine, immunogenic conjugate, reduction; cocaine, treatment;
                                                                                                                   Gaps
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                                                    DB 22; Length 100; 5.8;
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                                                                                                                                                                                                                                                                                                                                                                                         AAW39886 standard; Protein; 113 AA.
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tes 7; Conserv
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100 AA;
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31-DEC-1997.

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Landry DW;

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Query Match

Matches

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RESULT 7 AAW39882

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New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
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                                                                                                                                                                                                                                              AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 6Al2 antibody (AAW39807 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 6Al2 has a per minute Kcat of 0.072. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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                                                                                                                                                                        New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
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                                                                                                          (UYCO ) UNIV COLUMBIA NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SXEXEXEXEXEXEXERREPRESENTATIONS
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AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW39808 represents the heavy chain) was identified using TSA2, and has a per minute Kcat of 0.016. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variable domain of the Kappa light chain of catalytic antibody 2A10.
                                                                                                                                                                                            New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h Similarity 100.0%; Score 31; DB 19; Length 113; Similarity 100.0%; Pred. No. 6.6; 7; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vivo concentration that can be achieved)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW39804 standard; protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                      Claim 18; Page 73; 147pp; English.
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(UYCO ) UNIV COLUMBIA NEW YORK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             overdose; addiction.
                                                                                                                        WPI; 1998-077166/07.
P-PSDB; AAV09802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LMSTRAS 7
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                                                             Landry DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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98GB-0009839.

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This sequence represents the light chain variable region (VL) of humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human framework (HSIGNVII) and the light chain complementarity determining regions (see AAV3254-56) of murine antibody C11. The DNA was constructed by splice overlap FCR. The invention provides attered antibodies, wuch as chimneric or humanised antibodies, which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on hamanatopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematobus, Hashimoto's thyroiditis, multiple sclerosis, clabetes, uveitis, dermatitis, inflammatory bowel disease, ulcerative syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogram's syndrome, allergies allergies asthma, intrinais asthma, acte asthmatic exacerbation, rhinitis, estema, intrinais asthma, acte asthmatic exacerbation, rhinitis, cathmia and B-cell malignancies (Claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                            Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                              Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  determining the binding agents.
                                                                                                                                                                                            Claim 9; Fig 3; 81pp; English.
                                (GLAX ) GLAXO GROUP LTD.
                                                                                               WPI; 2000-053101/04.
                                                                                                                N-PSDB; AAZ34747.
 09-MAY-1998;
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                         AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade occaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. 3H-benzoic acid from 3H-phenyl cocaine. The ZAIO antibody (AAW39809 represents the heavy chain) was identified using TSAI, which is an immunogenic conjugate of a phosphate monoseter transition state analogue. Antibody ZAIO has a per minute Kcat of 0.01. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomernlonephritis; inflammatory bowel disease; ulcerative collitis; Crohn's disease; sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graff.versus-host disease; COPD; bronchitis; diabetes;
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                                                                                                                                                                                                                                                                                      100.0%; Score 31; DB 19; Length 113; 100.0%; Pred. No. 6.6; 1ve 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised anti-CD23 MAb C11 light chain variable region.
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/note= "framework region 4"
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/note= "framework region 3"
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Claim 16; Pages 73-74; 147pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY32262 standard; Protein; 116 AA.
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94..102
..= "CDR 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                         Seguence 113 AA;
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55 LMSTRAS 61
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                                                                                                                                                                                                                            be achieved).
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY32262;
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Region
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                                                 100.0%; Score 31; DB 21; Length 116; 100.0%; Pred. No. 6.8;
                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse anti-CD23 MAb C11 light chain variable region.
                                                                                                         ö
                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                     AAY32261 standard; Protein; 145 AA.
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/note= "CDR L1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-FEB-2000 (first entry)
                                                                      Best Local Similarity 100.
Matches 7, Conservative
Sequence 116 AA;
                                                                                                                                                                                                             55 LMSTRAS 61
                                                                                                                                                           1 LMSTRAS 7
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                                                    Query Match
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                                                                                                                                                                                                                                                                                                      RESULT 12
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WO9749800-A1

Region Region

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determining regions (CDRs) of the catalytic antibody 3B9, which is able to degrade cocaine. A series of cocaine transition state analogues to degrade cocaine. A series of cocaine transition state analogues (TSRs) were preparted and used to immunise mice for production of thybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the 1n vivo concentration that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
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                                                                                                                                                                                                                                                                              New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.3%; Score 28; DB 19;
85.7%; Pred. No. 7.8e+05;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW39801 standard; protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 80; 147pp; English.
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                                                                                                                                                            (UYCO ) UNIV COLUMBIA NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overdose; addiction
                                                                                                                                                                                                                                             WPI; 1998-077166/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can be achieved)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LMSTRAS 7
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                                                                                                                                                                                                                                                                                                                                                 simply binding
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                                                                              25-JUN-1997;
                                                                                                                       25-JUN-1996;
                                       31-DEC-1997
                                                                                                                                                                                                        Landry DW;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the light chain variable region (VL) of murine anti-CD23 (FCERII) monoclonal antibody Cll. The invention provides altered antibodies, such as chimerioc rhumanised antibodies (see AAY22262 and AAY32265), which comprises sufficient of the amino acid sequences of the Cll light and heavy chain complementarity determining regions (see AAY32254-99) to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble, CD23 formation in human therapy, for the treatment of arthritis, liquid servhematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Solgren's syndrome, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, crohn's disease, Solgren's syndrome, allergic stathmatic tricularly chronic bronchitis) or diabetes (DD2) insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignanches (Claimed). They are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Variable domain; lambda light chain; Catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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                                                                                                                                                                                                                                                                                                                                                                                                                Cell receptor specific antibodies useful for treating e.g. arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 31; DB 21; Length 145; 100.0%; Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                 Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                 Ellis JH, Rapson NT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        diabetes, multiple sclerosis and psoriasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       determining the binding agents.
                     /note= "CDR L2"
                                                                 "CDR L3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Fig 2; 81pp; English.
                                                                                                                                                                                         99WO-GB01434.
                                                                                                                                                                                                                                98GB-0009839
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                                             125..134
/note= "C
                                                                                                                                                                                                                                                                                                                 Crowe SJ,
                                                                                                                                                                                                                                                                       (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-053101/04.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ34746
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86 LMSTRAS 92
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                                                                                                                                                                                                                                                                                                                   Bonnefoy JMP,
                                                                                                                                                                                                                                  09-MAY-1998;
                                                                                                          W09958679-A1
                                                                                                                                                                                           07-MAY-1999;
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Matches

RESULT 13 AAW39816

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Gaps

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Length 7; 0; Indels

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Search completed: April 22, 2003, 12:51:12 Job time : 18.75 secs
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                                                                                                                                                                                           AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl occaine. The 3B9 antibody (AAW39806 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "complementarity determining region 2 of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "complementarity determining region 3 of the
                                                                     New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /notes "complementarity determining region 1 of 119ht chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single chain Fv region of the catalytic antibody 3B9.
                                                                                                                                                             Claim 12; Pages 71-72; 147pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW39899 standard; Protein; 274 AA.
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           WPI; 1998-077166/07.
P-PSDB; AAV09791.
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Best Local Similarity
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55 LMSTRSS
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1 LMSTRAS 7

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The present sequence represents the single chain Fv region of the monoclonal catalytic antibody 3B9, which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAB) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
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85.7%; Pred. No. 91;
iive 1; Mismatches 0; Indels
                             259..263 _
/note= "Flag epitope sequence"
light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 27; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                    (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                            96US-0672345.
                                                                                                                                                                                                                                                97WO-US10965.
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nes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      simply binding
                                                                                                                                                                                                                                                25-JUN-1997;
                                                                                                                                                                                                                                                                                                        25-JUN-1996;
                                                                                                                          WO9749800-A1
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Sequence 32, Appl Sequence 33844, A Sequence 884, App Sequence 281, App Sequence 1708, App Sequence 1708, App Sequence 336, App Sequence 31, Appl Sequence 5, Appl Sequence 5, Appl Sequence 61, Appl Sequence 61, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 18, Appl Sequence 318, Appl Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                    (without alignments)
76.055 Million cell updates/sec
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                                                                                                                                                                                                April 22, 2003, 12:53:59 ; Search time 7.375 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications AA:*

1. /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
2. /cgn2_6/ptodata/1/pubpaa/PCT NEW_PUB.pep:*
3. /cgn2_6/ptodata/1/pubpaa/PCT NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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10 US-09-864-761-33844

10 US-09-55-301-884

9 US-10-060-38-159

10 US-09-712-363-159

10 US-09-764-877-1708

9 US-10-060-38-159

10 US-09-864-776-144

9 US-09-866-050-336

9 US-09-862-936A-31

9 US-09-829-936A-31

9 US-09-829-936A-31

9 US-09-829-936A-31

10 US-09-138-626-4088

10 US-09-138-626-4088

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10 US-09-936A-16

9 US-09-936A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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29

ALIGNMENTS

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US-09-840-459-32

i Sequence 32, Application US/09840459

patent No. US20020150576A1

GENERAL INFORMATION:
APPLICANT: Horvath, Christopher
APPLICANT: Horvath, Christopher
APPLICANT: Horvath, Christopher
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: METHODS OF USE THEREFOR
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE PERERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: 05/09/840,459
CURRENT APPLICATION NUMBER: 00/00-20-2

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

NUMBER OF SEQ ID NOS: 107

SEC ID NO 32

LENGTHER PRESENCE: 1998-07-23

CORENTSH: 100

TYPE: PRI
CORGANISM: Mus musculus
US-09-840-459-32

QUELY MATCH

DO 014; Pred No. 24; Pred No. 24;

Dest Local Similarity 100.0%; Pred No. 24;

Matches 7; Corservative 0; Mismatches 0; Indels 0;
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Gaps

RESULT 2

us-09-674-716b-5.open.rapb

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                                                                                                                                                                                                                             Sequence 844, Application US/09925301
Sequence 844, Application US/09925301
Sequence 82020020052308A1
GENERAL INFORMATION: Nucleic Acids, Proteins and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT APPLICATION NUMBER: DCT/USO0/05882
PRIOR FILING DATE: 2000-03-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PARENTIN Ver. 2.0
SEQ ID NO 884
INNOR 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 83.9%; Score 26; DB 10; Length 449; Best Local Similarity 85.7%; Pred. No. 1.8e+02; Matches 6; Conservative 0; Mismatches 1; Indels
  2; Mismatches
5; Conservative
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ORGANISM: Homo sapiens
US-09-925-301-884
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US-09-925-301-884
Matches
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                                                 PREMERIAL INFORMATION:

PAPPLICANT: Perm, Sharron G.

APPLICANT: Henrel, David R.

APPLICANT: Chen, Wencheng C.

FILE REPRESENCE: Acent Car. A. Inc. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INPORMATION: MAP TO ACOO7786.1

OTHER INPORMATION: EXPRESSED IN HELLOD, SIGNAL = 1.8

OTHER INPORMATION: EXPRESSED IN HELLOD, SIGNAL = 1.7

OTHER INPORMATION: EXPRESSED IN HEART, SIGNAL = 1.7

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OTHER INPORMATION: EXPRESSED IN HEART, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.96

OTHER INFORMATION: SYPRESSED IN LUNG, SIGNAL = 0.96

OTHER INFORMATION: SYPRESSED IN LUNG, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.96

OTHER INFORMATION: BST HUMAN HIT: AA306055.1, EVALUE 6.60e-01

US-09-864-761-33844
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Pred. No. 42;
                    Sequence 33844, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.9%;
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
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, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-877-1708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Sequence 1708, Application US/09764877

Patent No. US20020147140A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION Nucleic Acids, Proteins, and Antibodies

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

CURRENT FILING DATE: 2001-01-17

SPIOR APPLICATION OF SEQ 1D NOS: 4031

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1708

TENNETH. 100

SEG ID NOS: 4031
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.45

OTHER INFORMATION: EST_HUMAN HIT: AU121127.1, EVALUE 1.50e-02
US-09-864-761-45487
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77.4%; Score 24; DB 10; Length 32;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 0; Indels
                                        PRIOR FULLING DATE: 2001-01-30
PRIOR FULLING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PELICATION NUMBER: PCT/USO1/00668
PRIOR PELICATION NUMBER: PCT/USO1/00668
PRIOR PELICATION NUMBER: PCT/USO1/00663
PRIOR PELICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PELICATION NUMBER: PCT/USO1/00661
PRIOR PELICATION NUMBER: PCT/USO1/00661
PRIOR PELICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2000-06-31
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 45487
LENGTH: 32
                      APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
LOCATION: (107)
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: HUMBER: US/09/664,761
CURRENT FILING DATE: 2000-05-23
FRIOR PELING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: US 60/180,312
FRIOR APPLICATION NUMBER: US 60/207,456
FRIOR APPLICATION NUMBER: US 60/236,356
FRIOR APPLICATION NUMBER: US 60/236,356
FRIOR PILING DATE: 2000-08-03
FRIOR PILING DATE: 2000-08-03
FRIOR PELING DATE: 2000-08-03
FRIOR PILING DATE: 2000-08-03
FRIOR PELING DATE: 2000-09-07
FRIOR APPLICATION NUMBER: US 60/236,359
FRIOR APPLICATION NUMBER: PCT/US01/00666
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US-10-60-036-159
i Sequence 159, Application US/10060036
j Publication No. US20030073144A1
i GENERAL INFORMATION:
i APPLICANT: Benson, Darin R.
i APPLICANT: Enemon, Darin R.
i APPLICANT: Hepler, Michael D.
i APPLICANT: Hepler, William T.
i APPLICANT: Hepler, William T.
i APPLICANT: Howevilon: Compositions and MEFHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND MEFHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER TILE REFERENCE: 210121.566
i CURRENT FILING DATE: 2002-01-30
i SOFTWARE: FESTESC FOR WINDOWS VERSION 4.0
i SOFTWARE: FESTESC FOR WINDOWS VERSION 4.0
i SEQ ID NO 159
i LENGTH: 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 83.9%; Score 26; DB 9; Length 1464; Best Local Similarity 85.7%; Pred. No. 6e+02; Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                           Query Match
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
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Patent No. US20020048763A1

    i TYPE: PRT
    i ORGANISM: Mycobacterium tuberculosis
    US-09-712-363-281

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CORGANISM: Homo sapiens
US-10-060-036-159
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US-09-864-761-45487
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RESULT 11
US-09-829-936A-31
US-09-829-936A-31
Sequence 31, Application US/09829936A
Publication No. US20030048699A1
GENERAL INFORMATION:
TITLE OF INVENTION: P63 Protein
TITLE OF INVENTION: P53 Protein
TITLE REFERENCE: S198033
FILLE REFERENCE: S198033
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: F89812754
NUMBER OF SEQ ID NOS: 33
*SOFTE NOS: 34
*SOFTE NOS: 35
*SOFTE 
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CURRENT MYMBER: US/10/005,057A
CURRENT FILING DATE: 2011-12-04
PRIOR APPLICATION NUMBER: 60/251,555
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Post Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
PATURE INFORMATION: Fragment C-term MBP1 murine
US-09-829-936A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Human fragment C-term MBP1
US-09-829-936A-31
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Sequence 5, Application US/10005057A
Sequence 6, Application US/10005057A
Parent On US30020170087A1
APPLICANT: Tao, Yumin, Malliam J. APPLICANT: Gordon-Kamm, Milliam J. APPLICANT: Chow, Kealth S. APPLICANT: Danilevskaya, Olga APPLICANT: Danilevskaya, Olga APPLICANT: Rafalski, Antoni J. APPLICANT: Sakai, Haime
APPLICANT: Sakai, Haime
APPLICANT: Sakai, Haime
APPLICANT: Sakai, Haime
PRIOR APPLICATION NUMBER: FR9812754
PRIOR FILING DATE: 1998-10-12
NUMBER OF SEQ ID NOS: 33
SSOFWARE: Patentin version 3.1
SSO ID NO 9
LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85...
G; Conservative
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Publication No. US20030049699A1
GENERAL INFORMATION:
APPLICANT: Aventis Pharma, S.A.
ITILE OF INVENTION: Polyopeptide (MBP1) Capable Of Interacting With Oncogenic Mutante
TITLE OF INVENTION: PS3 Protein
FILE REFERENCE: ST98033
CORRENT APPLICATION NUMBER: US/09/829,936A
CURRENT FILING DATE: 2001-04-11
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US-09-866-050A-336
| Sequence 336, Application US/09866050A
| Sequence 316, Application US/09866050A
| Publication No. US20030040471A1
| GENERAL INFORMATION:
| APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna
| APPLICANT: Sleeman, Matthew APPLICANT: Onrust, Rene G. APPLICANT: Kumble, Krishnand D. APPLICANT: Kumble, Krishnand D. TITLE OF INVENTION: Compositions Isolated From Skin Cells TITLE OF INVENTION: and Methods for Their Use FILE REFERENCE: 11000.1011cd US/09/866,050A
| CURRENT APPLICANT: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24; DB 9; Length 114;
Pred. No. 1.3e+02;
1; Mismatches 1; Indels
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                                                                                              RESULT 8

US-10-083-357-784

Sequence 784, Application US/10083357

Publication No. US20030054370A1

GENERAL INFORMATION:

APPLICAM: Glandong Zeng et al.

TITLE OF INVENTION: Systemic Discovery of New Genes

FILE REPRENCE: 032796-090

CURRENT PELLAGTION NUMBER: US/10/083,357

CURRENT FILING DATE: 2002-02-27

SEQ ID NO 784
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-083-357-784
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Similarity 71.4%;
5; Conservative
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Best Local Similarity
Matches 5; Conserv
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19 LMTTRGS 25
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          67 LPSTRAS 73
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; ORGANISM: Human
US-09-866-050A-336
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US-09-829-936A-9
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CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US01/01340
PRIOR PELICATION NUMBER: US01/01344
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: US01/01344
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: US01/01345
PRIOR PELICATION NUMBER: US01/01345
PRIOR PELICATION NUMBER: US01/01345
PRIOR PELICATION NUMBER: US01/01329
PRIOR PELICATION NUMBER: US01/01329
PRIOR PELICATION NUMBER: US01/01329
PRIOR PELICATION NUMBER: US01/01340
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 20
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OR APPLICATION NUMBER: 09/764,896

OR FILING DATE: 2001-01-17

OR APPLICATION NUMBER: 09/764,864

OR FILING DATE: 2001-01-17

OR PELING DATE: 2001-01-17

OR APPLICATION NUMBER: 09/764,864

OR FILING DATE: 2001-01-17

OR APPLICATION NUMBER: 09/764,866

OR FILING DATE: 2001-01-17

OR APPLICATION NUMBER: 09/764,866

OR FILING DATE: 2001-01-17

OR APPLICATION NUMBER: 09/764,868

OR FILING DATE: 2001-01-17

OR APPLICATION NUMBER: 09/764,868

OR FILING DATE: 2001-01-17

OR APPLICATION NUMBER: 09/764,868

OR PILING DATE: 2001-01-17

OR APPLICATION NUMBER: 09/764,868

OR PILING DATE: 2001-01-17

OR APPLICATION NUMBER: 06/109,065

OR FILING DATE: 2000-01-31

OR APPLICATION NUMBER: 06/109,628

OR PILING DATE: 2000-02-04

OR APPLICATION NUMBER: 60/109,628

OR PILING DATE: 2000-02-04
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Sequence 78, Application US/09908711
Sequence 78, Application US/09908711
SECUENCE No. US20020045230A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAL28
CURRENT APPLICATION NUMBER: US/09/908,711
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77.4%; Score 24; DB 9; Length 297;
Best Local Similarity 83.3%; Pred. No. 3.46+02;
Matches 5; Conservative 1; MismaÆches 0; Indels
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77.4%; Score 24; DB 9; Length 30:
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels
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US-09-738-626-4088
1 Sequence 4088, Application US/09738626
2 Publication No. US20020197605A1
2 GENERAL INFORMATION:
APPLICANT: NRKAGANA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MADO, SEIKO
APPLICANT: TATEISHI, MIKEO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, MAKAO
APPLICANT: TATEISHI, MAKAO
APPLICANT: TATEISHI, MASATO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AMINISO
APPLICANT: SENOH, AMINISO
APPLICANT: SENOH, AMINISO
APPLICANT: OZAKI, AKIO
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PALGATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-08-03
NUMBER: PALGATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-08-03
NUMBER: PALGATION NUMBER: JP 00/159162
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PRIOR FILING DATE: 2000-08-03
NUMBER: PALGATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-08-03
NUMBER: PALGATION NUMBER: JP 00/159162
PRIOR PLING DATE: 2000-08-03
                    PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 297
TYPE: PRT
ORGANISM: Zea may8
                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: VARIANT
LOCATION: (1) ... (425)
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-005-057A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Corynebacterium glutamicum US-09-738-626-4088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||:|||
246 VMSSRAS 252
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66 LLSTRA 71
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WARTERS OF SEO ID NOS: 167

SOFTWARE OF SECULATION (1967)

SOFTWARE OF SECULATION (1967)

SOFTWARE OF SECULATION (1967)

OTHER IMPORMATION: Xaa equals any of the naturally occurring L-amino acids (1968)

OTHER IMPORMATION: Xaa equals any of the naturally occurring L-amino acids (1969)

OTHER IMPORMATION: Xaa equals any of the naturally occurring L-amino acids (1969)

OTHER IMPORMATION: Xaa equals any of the naturally occurring L-amino acids (1969)

OTHER IMPORMATION: Xaa equals any of the naturally occurring L-amino acids (1969)

OTHER IMPORMATION: Xaa equals any of the naturally occurring L-amino acids (1969)

OTHER IMPORMATION: Xaa equals any of the naturally occurring L-amino acids (1969)

DE COMMENTALION: Xaa equals any of the naturally occurring L-amino acids (1969)

ON 1 LASTRAS 7

MASTRAS 7

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Search completed: April 22, 2003, 13:11:12 Job time : 8.375 secs

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GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

April 22, 2003, 12:48:24; Search time 8.83929 Seconds (without alignments) 97.882 Million cell updates/sec Run on:

US-09-674-716B-7 48 Title:

1 QQLVEYPFT 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results fredicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ubiquinol-cytochro	Ig kappa chain V r	Ig kappa chain V r	Ig kappa chain V r	Ig kappa chain pre	probable calmoduli	Ig lambda chain V	phosphatidyl synth	Ig kappa chain pre	hypothetical prote						Ig kappa chain V r	lysozyme (EC 3.2.1	hypothetical prote	glycerol-1-phospha	ubiquinol-cytochro	B. subtilis YxiO p	B. subtilis Yxio p	3',5'-cyclic-nucle	long-chain-fatty-a	long-chain-fatty-a	long-chain-fatty-a		glycine-tRNA ligas	
SUMMARIES	ΙD	C42622	G30538	KVMS16	KVMS51	KVMS67	A85363	836277	T38148	B29775	A86371	D82100	D89903	876367	T01906	126317	D26317	AD3322	D83163	D90527	841834	AG1614	AI1251	A25346	S41589	B90943	F85791	AC0725	F70483	T21138
	DB	2	N	7	~	7	ď	N	~	~	~	N	N	N	N	N	N	~	N	~	٦	~	N	N	~4	~	~	24	~	~
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de	Query	89.6		87.5	87.5	77.1	77.1	75.0	75.0	72.9	72.9	70.8	70.8	70.8	70.8	68.8	68.8	68.8	68.8	68.8	æ	æ	68.8	Ф	68.8	æ	68.8	œ,	68.8	68.8
	Score	43	42	42	42	37	37	36	36	35	35	34	34	34		33		33		33			33				33			33
	Result No.	-	7	c	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	56	27	28	29

Ig Rappa chain V region (253.15E2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Sate: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C;Accession: G30538
R;Claflin, J.L.; Berry, J.

:||:||||| 341 KQLIEYPFT 349 1 QQLVEYPFT 9

ð 셤 RESULT 2 G30538

ataxin-1 - human	hypothetical prote	hemoglobin delta c		Ig kappa chain pre	Ig kappa chain - h	unknown protein, 7	hypothetical prote	probable 2-hydroxy	probable dicarboxy	biliverdin reducta	biliverdin reducta	biliverdin reducta	hypothetical prote	conserved hypothet	probable bHLH DNA-
846268	T15138	165317	B49060	A29775	S40334	G96705	AF2397	T45421	T49628	A42268	G02066	S62624	T01948	F69999	A85019
N	N	4	N	N	N	~	N	N	N	N	C)	N	N	-	N
816	817	19	112	120	132	151	180	242	282	295	296	296	298	313	315
68.8	68.89	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7
33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - honeybee mitochondrion C;Species: mitochondrion Apis mellifera (honeybee)
A;Variety: 1iguatica
C;Date: 09-Sep-1994 #sequence revision 09-Sep-1994 #text_change 03-Jun-2002
C;Date: 09-Sep-1994 #sequence revision 09-Sep-1994 #text_change 03-Jun-2002
C;Accession: C42622; S52971
A;Title: The cytochrome b and AIPase genes of honeybee mitochondrial DNA.
A;Reference number: A42622; MUID:92261310; PMID:1533894
A;Accession: C42622
A;Attle: The cytochrome b and AIPase genes of honeybee mitochondrial DNA.
A;Reference number: A42622; MUID:92261310; PMID:1533894
A;Reference number: A72622; MUID:92261310; PMID:1533894
A;Reference number: A72622; MUID:92261310; PMID:1533894
A;Reference number: By 7.17, 1993
A;Accession: C42622
A;Accession: A72622; MUID:93114603; PMID:8417993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Genome: mitochondrion
A; Genome: code: SGC4
C; Superfamily: cytochrome b, cytochrome b homology; cytochrome b6 homology; plastoquinol.
C; Superfamily: cytochrome b; cytochrome transfer; heme; iron; metalloprotein; mitochondrion,...
F;14-340/Domain: cytochrome b homology <CBH>
F;14-340/Domain: cytochrome b6 homology <CBH>
F;23-340/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>
F;85,184/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted F;99,198/Binding site: heme iron (His) (axial ligands) (high potential) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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A;Moleovile type: DNA
A;Residues: 1-383 <CR2>
A;Cross-references: EMBL:L06178; NID:g336279; PIDN:AAB96809.1; PID:g552449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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89.6%; Score 43; DB 2; Length 383;
Best Local Similarity 77.8%; Pred. No. 0.55;
Matches 7; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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C;Species: Arabidopsis thallana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: A65363
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thallana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: A85363
A;Status: preliminary
A;Molecule type: DNA
A;Reference number: A85003
A;Cross-references: GB:NC_001268; NID:97270002; FIDN:CAB79818.1; GSPDB:GN00140
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A) Introne: 17/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-120/Pondouct: Ig kappa chain V region (VK167) #status predicted <MAT>

F;36-115/Domain: immunoglobulin homology <IMM>

F;34-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                          Till Rappa chain precursor V region (VK167) - mouse Cispecies Mus musculus (house mouse)
Cispecies Solution Allo Musculus Mus
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C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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2.8;
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Similarity 75.0%;
6; Conservative
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Best Local Similarity
Matches 6; Conserv
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A,Map position: 4
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C;Species: Mus musculus (house mouse)
C;Accesion: A01910
R;Appella, E.
Mol. Immunol. 1. 8.
Mol. Immunol. 1. 711-718, 1980
A;Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcho
A;Accession: A01910
A;Accession: A01910
A;Accession: A01910
A;Residues: 1-113 -AAPP
C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C;Complex: An immunoglobulin heteroteroteramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as Igh and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMMN
F;23-93/Domain: immunoglobulin predicted
F;23-93/Domain: immunoglobulin predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Noveled the second of the seco
J. Immunol. 141, 4012-4019, 1988
A/ittle: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu
A/Accession: Gabiliary
A/Accession: Gabiliary
A/Accession: Gabiliary
A/Accession: Gabiliary
A/Accession: Ordinary; nucleic acid sequence not shown; not compared with conceptual tra
A/Residues: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A/Residues: 1-74 cCLA>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Superfamily: immunoglobulin betweence tramer; Ammunoglobulin page and a preliminary conceptual tra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 87.5%; Score 42; DB 2; Length 74; Best Local Similarity 88.9%; Pred. No. 0.16; Matches 8; Conservative 0; Mismatches 1; Indels
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F,36-115/Domain: immunoglobulin homology <IMM>
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Matches 6; Conserv
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                                                         Query Match
Best Local Similarity
Matches 6; Conserv
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A; Status: preliminary
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114 QQIVEYP 120
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           C; Accession: S36277

K; Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993

A; Title: Human anti-self antibodies with high specificity from phage display libraries. A; Reference number: S3625; MUID:93178448; PMID:7679990

A; Reference number: S3625; MUID:93178448; PMID:779990

A; Status: preliminary; nucleic acid sequence not shown
A; Scatus: mRNA
A; Residues: 1-108 < GRI>
A; Cross-references: EMBL:218829; NID:933417; PIDN:CAA79281.1; PID:9939910
C; Superfamily: immunoglobulin immunoglobulin homology
C; Keywords: heteroctetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CyAccession: T38148

Ryperation, D; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

Ryperation, D; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

ByReference number: Z21774

A;Reference number: Z21774

A;Status: T38148

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-570 - PEBA>

A;Cross-references: EMBL:Z99295; PIDN:CAB16578.1; GSPDB:GN00066; SPDB:SPAC22A12.08c

A;Experimental source: strain 972h-; cosmid c22A12
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C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C;Accession: B29775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Schizosaccharomyces pombe
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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R;Jouvin-Marche, B.; Rudikoff, S.
R;Jouvin-Marche, B.; Rudikoff, S.
Immunogenetics 24, 191-201, 1986
A;Title: Evolution of a V-kappa gene family.
A;Reference number: A91781; MUID:87006895; PMID:3093373
A;Accession: B29775
A;Molecule type: DNA
A;Residues: 1-120 <-700
A;Cross-references: GB:M15553; NID:9197470; PIDN:AAA39037.1; PID:9197471
A;Note: this sequence was determined from the germline gene
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A; nurons: 17/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-20/Product: Ig kappa chain V region 24.1 #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                      75.0%; Score 36; DB 2; Length 108;
66.7%; Pred. No. 4;
tive 1; Mismatches 2; Indels
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A;Gene: SPDB:SPAC22A12.08c
A;Map Dosfition: 1
A;Introns: 43/2; 62/2; 227/2; 483/1
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.77
Best Local Similarity 67.77
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547 KQLVEYSFT 555
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mesu protein VC2242 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: B32100

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

chardelberg, J.F.; Basen, J.A.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301
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A;Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F508.25 - Arabidopsis thaliana
(Species: Arabidopsis thaliana (mouse-ear cress)
(Species: Arabidopsis thaliana (mouse-ear cress)
(Species: Arabidopsis thaliana (mouse-ear cress)
(Spacession: A86371
(Spacession: Ar.) Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Khan, S.; Khaykin, E.; Kim, C.
(A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marziali, R.; Alathors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.A., Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.A., Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Fitle: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
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A;Status: preliminary
A;Nolecule type: DNS
A;Reaiduee: 1-480 <STO>
A;Reaiduee: 1-480 <STO>
A;COBS-references: GB:AE005172; NID:g4056452; PIDN:AAC98025.1; GSPDB:GN00141
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llarity 75.0%; Pred. No. 46;
Conservative 0; Mismatches 2; Indels
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   Length 120;
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Score 35; DB 2;
Pred. No. 7.2;
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                                                                        1; Mismatches
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85.7%;
   th 72.9%;
Similarity 85.7%;
6; Conservative
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Gaps

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Cypecies: Mus musculus (H158-89H4) - mouse
CySpecies: Mus musculus (house mouse)
CyDate: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
CyAccession: 126317
RyCaton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
AyTitle: Structural and functional implications of a restricted antibody response to a d
AyReference number: A91043; MUID:86300658; PMID:2427335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Wolecule type: DNA
A; Residues: 1-12 < CAT-
A; Note: this sequence was determined from the germline gene
C; Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C; Superfamily: immunoglobulin, immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1074;
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A; Description: The sequence of A. thaliana T12H20.
A;Reference number: 214453
A;Recession: T01906
A;Status: translated from GB/EMBL/DDBJ
A;Residuse: 1-1074 <CCC>
A;Experimental translates EMBL;RP080119; NID:g3600029; PID:g3600033
A;Experimental source: cultivar Columbia
A;Map position: 4
A;Note: T12H20.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.8%; Score 34; DB 2; Length 107
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels
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853 ELIEYPF 859
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A) Accession: S76367
A) Status: preliminary
A; Molecule type: DNA
A; Residues: 1-722 < KAN>
A; Residues: 1-722 < KAN>
A; Cross-references: BMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA10219.1; PID:g100159
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Superfamily: glycine-tRNA ligase beta chain
                                                                                                                                                                                                                                                                                                               C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: D89903
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein - Synechocystis sp. (strain PCC 6803)
[Speciae: Synechocystis sp.
[Speciae: Synechocystis sp.
[Avariety: PCC 6803]
[Spate: 25-Apr-1997]
[Spate: 25-Apr-1967]
[Spate: 25-Apr-1997]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: SA1131
C;Superfamily: Halobacterium halobium 2-oxoacid ferredoxin oxidoreductase; 2-oxoacid fer
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-586 «KUR»
A;Cross-references: GB:BA000018; PID:g13701089; PIDN:BAB42384.1; GSPDB:GN00149
                                                                                                                                                                                                                                                                               hypothetical protein SA1131 [imported] - Staphylococcus aureus (strain N315)
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85.7%; Pred. No. 78;
ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.8%; Score 34; DB 2; Length 586;
Best Local Similarity 75.0%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 1; Indels
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Best Local Similarity 85.77
6, Conservative
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109 QLIELPFT 116
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EWBL; L06178; AAB96809.1; -.
EWBL; M87052; -; NOT_ANNOTATED_CDS.
EMBL; (42622; C42622; InterPro; IPR00179; Cyt. b. b6.
Ffam; PP00032; Cytochrome_D_C; 1.
Ffam; PP00033; Cytochrome_D_C; 1.
FROSITE; PS00192; CYTOCHROME_B HENB; 1.
FROSITE; PS00193; CYTOCHROME_B HENB; 1.
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                                                                                                                    April 22, 2003, 12:46:53; Search time 4.5 Seconds (without alignments) 82.953 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                         112892 segs, 41476328 residues
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KV2A MOUSE
KV2E MOUSE
KV2B MOUSE
CYP AKOJE
CYB AKOJE
CYB SIGHI
CYB
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BIEA_RAT
YOO BORBU
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CYB BOLAM
MSRS CYACA
YPZ BACLI
TYSY MSTAT
HNLS SORBI
HNLS SORBI
CYB ALCAA
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Maximum Match 100%
Listing first 45 summaries
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CAPPY
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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48
1 QQLVEYPFT 9
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BOUND TO THE PROTEIN.

-I - SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME CI AND THE RIESKE PROTEIN.

-I - SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

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09tf32 eutamias do 048372 glaucomys s 04730 hydropotes 03530 saimiri sci 035895 sciurus nig 09tf51 spermophilu P4041 spermophilu P4041 spermophilu P00156 homo sapien 03372 microtus ar P56731 microtus ar
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"The mitochondrial genome of the honeybee Apis mellifera: complete sequence and genome organization.";

sequence and genome organization.";

elementics 133:97-17(1993).

-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX II OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS.

-!- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
Aculeata; Apoidea; Apidae; Apis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Thorax; Madel=1533894; Madel=1533894; Crozier R.H., Crozier Y.C.; Crozier R.H., Crozier Y.C.; "The cytochrome b and Arpase genes of honeybee mitochondrial DNA."; Mol. Biol. Evol. 9:474-482(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apis mellifera ligustica (Common honeybee). Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                     CYB_HYDIN
CYB_SAISC
CYB_SCINI
CYB_SPEAN
CYB_SPEAN
CYB_SPERI
CYB_HUMAN
CYB_HUMAN
CYB_HUMAN
CYB_HUCLO
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MEDLINE=93114603; PubMed=8417993;
          CYB
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                                                                                                              Appella E.;
"Amino acid sequence of the light chain variable region of M511, a
"Maino acid sequence of the light chain variable region of M511, a
bhosphoryLcholine-binding murine myeloma protein.";
Mol. Imminol. 17:11-718 (1980).

--- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS PHOSPHORYLCHOLINE.
PIR; A0191; KWMS1.
HSSP; P80362; 1WTL.
TherePro; IPR003566; Ig_W.
FRAN, FR00406; Ig_MHC.
InterPro; IPR003566; Ig_W.
FRAN, SM00406; IGY.
Imminoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
Ig kappa chain V-II region MOPC 511.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=82002223; PubMed=6791832;
Selsing E., Storb U.;
"Somatic mutation of immunoglobulin light-chain variable-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                   COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
Local Similarity 88.9%; Pred. No. 0.15;
Local Similarity 88.9%; Pred. No. 0.15;
Local Similarity 0; Mismatches 1; Indels
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12496 MW; EFBODC4DA2BD3450 CRC64;
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21-JUJ-1986 (Rel. 01, Last sequence update)
15-JUJ-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 AA.
                                                                                 SEQUENCE.
MEDLINE=81052016; PubMed=6776396;
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EMBL; K02415; AAA39051.1; -.
PIR; A01909; KVMS67.
HSSP; P80362; IWTL.
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                                                    NCBI_TaxID=10090;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myeloma protein.";
Blochmistry 17:2703-2707(1978).
Blochmistry 17:2703-2707(1978).
-1- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN HAS ALSO BEEN DETERMINED.
PIR; A01908; KWAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                       Gaps
    Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=79000273; PubMed=99160;
Rudikoff S., Potter M.;
"Kappa Chain variable region from M167, a phosphorylcholine binding
                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1989 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-II region MOPC 167.
Mus musculus (Mouse).
Pukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musil
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                         95 IRON 1 (HEME B562 AXIAL LIGAND).
99 IRON 2 (HEME B566 AXIAL LIGAND).
1184 IRON 2 (HEME B562 AXIAL LIGAND).
128 IRON 1 (HEME B566 AXIAL LIGAND).
45256 MW, A140A05E6053C2D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEMENTARITY-DETERMINING-2.
PRAMENORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMENORK-4.
                                                                                                           / Match 89.6%; Score 43; DB 1; Length 383; Local Similarity 77.8%; Pred. No. 0.32; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.5%; Score 42; DB 1; Length 112;
88.9%; Pred. No. 0.15;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12349 MW; A58EDFD6404B9726 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                               112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAMEWORK-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P80362; IWTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM0406; IGv; 1.
Immunoglobulin V region.
23 F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 88.9%;
es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                               STANDARD;
                              85
99
184
198
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39
54
61
102
112
                              85
99
184
198
383 AA;
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                                                                                                                                                                                   341 KQLIEYPFT 349
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                                                                                                                                                                 QQLVEYPFT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QQLVEYPFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986
21-JUL-1986
15-JUL-1999
                                                                                                                                                                                                                                                          KV2A MOUSE
P01626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KV2C MOUSE
P01628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULPID
NON TER
SEQUENCE
                                                                     METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                  RESULT 3
KV2C_MOUSE
ID KV2C_MC
AC P01628;
DT 21-JUL-
DT 21-JUL-
DT 15-JUL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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Matches
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Matches
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    SHIFFE
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Gaps

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AKOTO
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METAL
METAL
VARIANT
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METAL
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CYB AKOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=WOZ Catalog 173074, 173083, and 173084; TISSUE=Liver;
STRAIN=WOZ Catalog 173074, 173083, and 173084; TISSUE=Liver;
XX MEDLINE=9163325; PubMed=2002767;
A Smith M.F., Patton J.L.;
"Variation in mitochondrial cytochrome b sequence in natural populations of South American akodontine rodents (Muridae:
Typoulations of South American akodontine rodents (Muridae:
Typoulations)
Typoulations of Typoulations
Typ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith M.F., Patton J.L.; Trhe diversification of South American murid rodents: evidence from mitochondrial DNA sequence data for the akodontine tribe."; Biol. J. Linn. Soc. Lond. 50:149-177(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                              IG KAPPA CHAIN V-II REGION VKAPPA167. FRAMEWORK-1.
                                                                                                                                                                                                                                                                                              ö
                                                                                                                         COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
                                                                                                                                                                                              COMPLEMENTARITY-DETERMINING-3.
BY SIMILARITY.
                                                                                                                                                               COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                            77.1%; Score 37; DB 1; Length 120; 100.0%; Pred. No. 1.6; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                               63BB571F0E4DE3E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1991 (Rel. 18, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                379 AA
                                                                                                                                                                                  FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; l.
SMART; SM00406; IGv; l.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                  13280 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-133 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-267 FROM N.A.
                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytochrome B.
MTCYB OR COB OR CYTB.
Akodon jelskii.
                                                                                                                                                                                                                                  120 AA;
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10079;
                                                                                                                                                                                                                                                                                                                                                   114 QQLVEYP 120
                                                                                                                                                                                                                                                                                                                                 1 QQLVEYP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                CYB AKOJE
P21715;
                                                                                                                                                                                                                 DISULFID
                                                                                                                    DOMAIN
                                                                                                                                                     DOMAIN
                                                                                     SIGNAL
                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
CYB AKOJE
                                                                                                                                                                                                                                                                                                  Matches
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                   EMBL; M35114; AAA16998.2; ALT_TERM.
EMBL; M35715; AAA31629.1; -.
EMBL; M35715; AAA31629.1; -.
EMBL; M35715; AAA31629.1; -.
EMBL; M35715; AAA31629.1; -.
EMBL; M35715; C41824; C41829.1; -.
EMBL; M35715; C41800.1; -.
EMBL; M35715; C41800.1; -.
EMBL; M500032; C41800.1; C4180.1; C4180.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith M.F., Patton J.L.;
"The diversification of South American murid rodents: evidence from mitochondrial DNA sequence data for the akodontine tribe.";
Biol. J. Linn. Soc. Lond. 50:149-177(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 IRON 1 (HEWE B562 AXIAL LIGAND).
97 IRON 2 (HEME B566 AXIAL LIGAND).
182 IRON 2 (HEWE B562 AXIAL LIGAND).
196 IRON 1 (HEME B566 AXIAL LIGAND).
118 V -> I (IN STRAINS 173083 AND 173084).
122 T -> A (IN STRAINS 173083 AND 173084).
42559 MW; F9F012A46671D59A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith M.F.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1991 (Rel. 18, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-267 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytochrome B.
MTCYB OR COB OR CYTB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10078;
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Heme.
METAL
METAL
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                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Phylogenetic relationships and the radiation of sigmodontine rodents
"Phylogenetic relationships and the radiation of sigmodontine rodents
in South America: evidence from cytochrome b.";
J. Mammal. Evol. 6:89-128 (1999).

-1- FUNCTION: COMPLOX TO THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS.

-1- COPACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
COUPLED TO ATP SYNTHESIS.
-!- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.
-!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIBEKE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M35700; AAA18897.2; -.
EMBL; M35701; AAA31624.1; -.
EMBL; M35702; AAA31625.1; -.
EMBL; M35702; AAA31625.1; -.
EMBL; M35702; AAA31625.1; -.
EMBL; M5000372; G2725.
InterPro; IPR000179; Cyt.b.b6.
Pfam; PF00032; Cytochrome D.C; 1.
PROSITE; PS00193; CYTOCHROME D.Q; 1.
PROSITE; PS00192; CYTOCHROME B.Q; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
IRON 1 (HEME B562 AXIAL LIGAND).
IRON 1 (HEME B562 AXIAL LIGAND).
V -> A (IN STRAINS 174053 AND 174054).
4C94CPRA92CCC34F CRC64).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOUND TO THE PROTEIN.
SUBBUNIT: THE MAIN SUBBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 1; Length 379; Pred. No. 8; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytochrome B.
MTCYB OR COB OR CYTB.
Sigmodon hispidus (Hispid cotton rat).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 IRC
97 IRC
182 IRC
196 IRC
108 V
115 V
42611 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
97
182
196
108
115
379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 QPVEYPFT 348
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Q9XNU6;
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055690;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
01-NOY-1897 Aynchetase beta chain (EC 6.1.1.14) (Glycine--tRNA ligase GLYS OR SLR0220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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-i- SIMILARITY: BELONGS TO CLASS-11 AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                              EMBL, AF108702; AAD45484.1; -.
InterPro; IPR000179; Cyt b b6.
Pfam; PF00032; cytochrome b C; 1.
PROSITE; PS00193; cytochrome b N; 1.
PROSITE; PS00193; cyTOCHROME B HEME; 1.
PROSITE; PS00193; CYTOCHROME B LOO; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRON 2 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
IRON 2 (HEME B562 AXIAL LIGAND).
IRON 1 (HEME B566 AXIAL LIGAND).
0472259421B38284 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.0%; Score 36; DB 1; Length 381; 87.5%; Pred. No. 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            + glycyl-trna(gly).
-!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Pfam; PF02092; tRNA synt_2f; 1.
PRINTS; PR01045; TRNASYNTHGB.
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97 97 IRC
182 182 IRC
196 196 IRC
381 AA, 42965 MW, C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 87.5
hes 7; Conservative
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Gaps

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-!- SIMILARITY: BELONGS TO THE CAMP PHOSPHODIESTERASE CLASS-II FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87010528; PubMed=3020155; Podgorski G.J., Franke J., Kessin R.H.; Pisolation of a cDNA encoding a portion of the cyclic nucleotide phosphodienterase of Dictyostellum discoideum."; J. Gen. Microbiol. 132:1043-1050 (1986).

-I- FUNCTION: TO MAINTAIN THE RESPONSIVENESS OF CELLS TO THE CHEMONTRACTANT CAMP DURING THE AGGREGATION PHASE OF DEVELOPMENT.
TIGRFAMS; TIGR00211; glyS; 1.
PROSITE; PS50861; AA TRNA LIGASE II GLYAB; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1989 (Rel. 12, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
3',5'-cyclic-nucleotide phosphodiesterase precursor (EC 3.1.4.17)
(PDEase) (3':5'-CNP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lacombe M.-L., Podgorski G.J., Franke J., Kessin R.H.; "Molecular cloning and developmental expression of the cyclic nucleotide phosphodiesterase gene of Dictyostelium discoideum."; J. Biol. Chem. 261:16811-16817(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=89384621; PubMed=2779573;
MEDLINE=89384622; PubMed=2779573;
Podgorski G.J., Franke J., Faure M., Kessin R.H.;
Prde cyclic nucleotide phosphodiesterase gene of Dictyostellium alteorate promoters and splicing for the synthesis of multiple mRNAs.";
Mol. Cell. Biol. 9:3938-3950(1989).
                                                                                                                                                                                                  70.8%; Score 34; DB 1; Length 722;
85.7%; Pred. No. 38;
:ive 1; Mismatches 0; Indels
                                                                                                                                     722 AA; 80051 MW; F7085BA5A23436D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostelium discoideum (Slime mold),
Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452 AA
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InterPro; IPR000396; Pdlesterase2.
Pfam; PF02112; PDEase II; 1.
PRINTS; PR00388; PDIESTERASE2.
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SEQUENCE OF 1-69 FROM N.A.
                                                                                                                                                                                                                                                                                 6; Conservative
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PIR; A32573; A32573.
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Best Local Similarity
                                                                                                           Complete proteome
SEQUENCE 722 AA
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254 EQLVEYP 260
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Black P.N., Dirusso C.C., Metzger A.K., Heimert T.L.; 
"Cloning, sequencing, and expression of the fadb gene of Bscherichia coli encoding acyl coenzyme A synthetase."; 
J. Biol. Chem. 267:25513-25520(1992).
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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SEQUENCE FROM N.A.
MEDILINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) (Long-chain acyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fulda M., Heinz E., Wolter F.P.;
"The fadD gene of Escherichia coli K12 is located close to rnd at 39.6 min of the chromosomal map and is a new member of the AMP-binding protein family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILINE=97251358; PubMed=9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
Isono K., Kasai H., Kimura S., Kitekawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horluchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                           N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
NN -> LT (IN REF. 3).
A8F3C19OD4603BD1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 452; 38;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                3', 5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE.
                      PROSITE; PS00607; PDEASE II; 1.
Glycoprotein; Hydrolase; CAMP; Zinc; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          561 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          1, Mismatches
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                                                                                                                                                                                                                                                                                                                                                      Score 33;
Pred. No.
                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Gen. Genet. 242:241-249(1994).
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MEDLINE=93094273; PubMed=1460045;
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Pdiesterase2; 2.
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51093 MW;
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83.3%;
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141
277
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FADD OR OLDD OR B1805.
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452 AA;
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  ProDom; PD010003;
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CARBOHYD
CARBOHYD
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complete genome of the hyperthermophilic bacterium Aquifex
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SEQUENCE 664 AA
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P54254,
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                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Ree. 3:379-392(1996).

-I. FUNCTION: ESTERIFICATION, CONCOMITANT WITH TRANSPORT, OF EXOGENOUS LONG-CHAIN FATTY ACIDS INTO METABOLICALLY ACTIVE COA THIOSEFIERS
FOR SUBSEQUENT DEGRADATION OR INCORPORATION INTO PHOSPHOLIPIDS.

-I. CATALYTIC ACTIVIT: ATP + a long-chain carboxylic acid + CoA = AMP + dibhosphate + an acyl-CoA.

-I. COPACTOR: MAGNESIUM.

-I. SUBUNIT: HOMODIMER (PROBABLE).

-I. SUBUNIT: HOMODIMER (PROBABLE).

-I. SUBUNIT: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EcoGene; EG11530; rauw.
InterPro; IRR008033; AMP-bind.
Pfam; PR00501; AMP-binding; 1.
Pro51TE; PS00455; AMP_BINDING; 1.
Ligase; Fatty acid metabolism; Magnesium; Membrane; Complete proteome.
CONFLICT 34 51 ARADOPAFVAMGEWATF -> GALRRSTCVCEYGGGNDL
(IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40)
16-
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TRLKMSSCSMVAYRKSRLLAYLP (IN REF. G. IN REF. 2).
A -> G (IN REF. 2).
Z49B0AAS-4B3DBFAS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.8%; Score 33; DB 1; Length 561;
llarity 55.6%; Pred. No. 47;
Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X70994; CAA50321.1; -.
EMBL; L02649; AAA23752.1; -.
EMBL; BO00275; AAC74875.1; -.
EMBL; D90824; BAA15600.1; -.
EMBL; D90824; BAA15609.1; -.
EMBL; D90825; BAA15614.1; -.
FIR; A45062; A45062.
HSSP; P08659; 1LCI.
ECGENE; EGI1530; fadD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62332 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496
555
561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 5, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::| :||||
293 KELAKYPFT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QOLVEYPFT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYGB AQUAE
067898;
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Matches
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6 X CBA, TISSUE=Brain, Thymus, and Retina;

XX MEDLINE=63814424; Dubmde48189437;

Banfil S., Servadio A., Chung M.-Y., Capozzoli F., Duvick L.A.,

Elde R., Zoghbi H.Y., Orr H.T.;

A. Cloning and developmental expression analysis of the murine homolog

of the spinocerebellar ataxia type 1 gene (Scal).";

thum. Mol. Genet. 5:33-40(1996).

C. -! TISSUE SPECIFICITY: WIDELY EXPRESSED. IN BRAIN, THE PATTERN OF

DISTRIBUTION IS LIMITED TO NEURONS POPULATIONS.

C. -! DEVELOPMENTAL STAGE: TRANSIENT EXPRESSION BURST IN PURKINDE CELLS

AS THE CEREBELLAR CORTEX BECOMES FUNCTIONAL (POSTNATAL DAY 14),

AND IN MESSENCHYMAL CELLS OF THE DEVELOPING INTERVERTEBRAL DISCS OF

THE SPINAL COLUMN:

C. -! POLYMORPHISM: THE MURINE POLY-GLN REGION IS VERY LIMITED IN

C. -! POLYMORPHISM: THE HUMAN SCAI AND IS NOT POLYMORPHIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license afterement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Nature 392:353-358(1998).
-!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate
                                                                                           + glycyl-trna(gly).
-!- SUBINIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS
(EN SIMILARITY).
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000775; AAC07870.1; -.
InterPro; IRP00231; tRNA synt 2f.
Prfam; PR01045; TRNA synt 2f. 1.
PRINTS; PR01045; TRNASNWTHGB.
TIGREMB; TIGR0021; A TRNASNWTHGB.
PROSTER: PS50661; A TRNA LIGASE II GLYAB; 1.
Aminoacyl-tRNA synthētase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.8%; Score 33; DB 1; Length 664; 100.0%; Pred. No. 56; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               664 AA; 77523 MW; 7FFEF7A8F552E3DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0cr.1996 (Rel. 34, Created)
01-0cr.1996 (Rel. 34, Last sequence update)
30-MXY-2000 (Rel. 39, Last annotation update)
Ataxin-1 (Spinocerebellar ataxia type 1 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                792 AA.
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DB 1; Length 816; 68;

Pred. No.

100.08;

68.8%; Score 33;

87051 MW; D49BA5DB423D0777 CRC64;

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InterPro; IPR003652; Atax_HMG.
SWART; SM00536; AXH; 1.
Polymorphism; Triplet repeat expansion; Alternative splicing.
DOMAIN 197 226 POIY-GLN.
                                                                                                             SEQUENCE 816 AA;
                                                                                                                                                                Best Local Similarity
                   MIM; 164400; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reductase)
                                                                                                                                                                                                                                                                                                                                                             BIEA RAT
                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                           P4684;
                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                      RESULT 14
BIEA_RAT
   SHRRRRS
                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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 agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE 1; ALSO KNOWN AS OLIVOPONTOCEREBELLAR ATROPHY I (OPCA I).

SCAL IS AN AUTOSOMAL DOMINANT NEUGODEGENERATIVE DISORDER
CHARACTERIZED BY PROGRESSIVE NEUGONAL LOSS IN THE CEREBELLUM,
BRAIN STEM AND SPINOCEREBELLAR TRACTS. CLINICAL FEATURES ARE
CREBELLAR ATAXAL, DYSARTHRIA, OPHTALMOPARESIS, MUSCLE WASTING AND
NEUROPATHY. ONSET OF THE DISEASE USUALLY OCCURS IN THE THIRD OR
POURTH DECADE OF LIFE AND DEATH OCCURS IN THE THIRD OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Banfi S., Servadio A., Chung M.-Ÿ., Kwiatkowski T.J. Jr., McCall A.E., Duviok L.A., Shen Y., Roth E.J., Orr H.T., Zoghbi H.Y.; "Identification and characterization of the gene causing type 1 spinocerebellar ataxia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tubby B.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS ARE PRODUCED BY
ALTERNATIVE SPLICING.

-!- TASSUE SPECIFICITY: WIDELY EXPRESSED THROUGHOUT THE BODY.

-!- TASSUE SPECIFICITY: WIDELY EXPRESSED THROUGHOUT THE BODY.

-!- TASSUE SPECIFICITY: WIDELY EXPROSO THE BODY.

-!- TASSUE SPECIFICITY: WIDELY EXPROSOD TO SOUTH OF 39 REPEATS) IN THE NORMAL POPULATION AND IS EXPANDED TO ABOUT 40-81 REPEATS IN SCA1 PATIENTS. LONGER EXPANSIONS RESULT IN EARLIER ONSET AND MORE SEVERE CLINICAL MANIFESTATIONS OF THE DISEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISEASE: DEFECTS IN SCA1 ARE THE CAUSE OF SPINOCEREBELLAR ATAXIA
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                            ö
                                                                                                                                                                                   68.8%; Score 33; DB 1; Length 792;
                                                                                                                                                                                                                            0; Indels
                                                                                                                                                792 AA; 84052 MW; CASF59C0013499DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          P54251 (QNUG2;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Ataxin-1 (Spinocerebellar ataxia type 1 protein).
SCAI OR ATXI.
                                                                                                                                                                                                                                                                                                                                                                                              816 AA
                                                                                                                                                                                                                            0; Mismatches
entities requires a license agreement (sor send an email to license@isb-sib.ch)
                                                                                                                                POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Cerebellum, and Brain;
MEDLINE=95038838; PubMed=7951322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X79204; CAA55793.1; -. EMBL; AL009031; CAA15622.1; -.
                                                                        MGD; MGI:104783; Scal.
InterPro; IPR003652; Atax_HMG.
SMART; SM00536; AXH; 1.
DOMAIN 214 217 Pt
                                       EMBL; X83542; CAA58533.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat. Genet. 7:513-519(1994).
                                                                                                                                                                    Query Match
Best Local Similarity 10v..
---- 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:10548; SCA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                 621 LVEYPF 626
                                                                                                                                                                                                                                                               3 LVEYPF 8
                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCCOURTEY W.K. Jr., Maines M.D.;

T. Site-directed mutagenesis of cysteine residues in biliverdin
"Site-directed mutagenesis of cysteine residues in biliverdin
reductase. Roles in substrate and cofactor binding.";

Eur. J. Biochem. 222.597-603(1994).

-!- FUNCTION: CONVERTS BILIVERDIN TO BILIRUBIN, DISPLAYS TWO DISTINCT
PH OPTIMA USING A DIFFRENT COPACTOR AT EACH PH: NADH AT THE LOWER
PH 6.7-6.9 RANGE AND NADH AT PH 8.5-8.7. NADPH, HOWEVER, IS THE
PROBABLE COPACTOR IN BIOLOGICAL SYSTEMS.

-!- CATALYTIC ACTIVITY: Bilirubin + NAD(P) (+) = biliverdin + NAD(P) H.

-!- PATHWAY: FIRAL STRP IN HEME METABOLISM.

-!- SUBUNIT: MONOMER (BY SIMILARITY).

-!- SUBUNIT: MONOMER (BY SIMILARITY).

-!- SUBUNITY: TO E.COLI YHHX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license attement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  ö
                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fakhrai H., Maines M.D.; "Expression and characterization of a cDNA for rat kidney biliverdin reductase. Evidence suggesting the liver and kidney enzymes are the same transcript product.", J. Biol. Chem. 267:4023-4029(1992).
Gaps
                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Biliverdin reductase A precursor (EC 1.3.1.24) (Biliverdin-IX alpha-
;
0
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BILIVERDIN REDUCTASE A. POLY-VAL.
                                                                                                                                                                               295 AA.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; PR000683; GFO IDH MocA. Pfam; PF01408; GFO IDH MocA; I. Oxidoreductase; NAD; NADP; Zinc. PROPEP
                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94291657; PubMed=8020496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92156147; PubMed=1371282;
6; Conservative
                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                          646 LVEYPF 651
                                                                                                                                                                                                                                                                                                                    BLVRA OR BLVR.
                                       3 LVEYPF 8
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-1- SIMILARITY: TO E.COLI YHHX.
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CONFLICT
CONFLICT
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METAL
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X MEDLINE=95014177; PubWed=7929092;

X MEDLINE=95014177; PubWed=7929092;

Y amaguchi T., Komoda Y., Nakajima H.;

Y amaguchi T., Komoda Y., Nakajima H.;

Y amaguchi T., Komoda Y., Nakajima H.;

Biliverdin-IX alpha reductase and biliverdin-IX beta reductase from the profile of the profile of
                                                                                                                                                                                                               ö
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Biliverdin reductase A precursor (BC 1.3.1.24) (Biliverdin-IX alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maines M.D., Trakshel G.M.; "Purification and characterization of human biliverdin reductase."; Arch. Biochem. Biophys. 300:320-326(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Placenta;
MEDLINE=96202961; PubMed=8631357;
Maines M.D., Polevoda B.V., Huang T.-J., McCoubrey W.K. Jr.;
"Human biliverdin IXalpha reductase is a zinc-metalloprotein.
Characterization of purified and Escherichia coli expressed
                                                                                                                                                                    Score 32; DB 1; Length 295; Pred. No. 39; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-117 FROM N.A.
Cordes M., Wollam C., Carter T.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Komuro A., Tobe T., Nakano Y., Yamaguchi T., Tomita M.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                 219C8EA96C150588 CRC64;
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
C->A: LOSS OF ACTIVITY.
C->A: REDUCED ACTIVITY.
C->A: REDUCED ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                            296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 3-36; 48-74 AND 228-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Biochem. 235:372-381 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Liver;
MEDLINE=93143333; PubMed=8424666;
                                                                                                                                 33565 MW;
                                                                                                                                                                    66.7%;
                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
279
280
291
292
73
280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLVRA OR BLVR OR BVR.
279
280
291
292
73
73
280
291
295 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                 ||||| |
94 LVEYPMT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 3-22.
                                                                                                                                                                                                                                           3 LVEYPFT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reductase).
                                                                                                                                                                                                                                                                                                                                                                        BIEA HUMAN
                                                                      MUTAGEN
MUTAGEN
MUTAGEN
SEQUENCE
                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                              POLY-VAL.
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
A -> T (IN REF. 2).
B -> AG (IN REF. 2).
D -> B (IN REF. 2).
W, ODFD3B386F4DFCOA CRC64;
                                                                                                                                                                                                                                                                                                                                                                               BILIVERDIN REDUCTASE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 1
Pred. No. 39;
0; Mismatches
                                                                                                                                                                            EMBL; X93086; CAA63635.1; -.
EMBL; J04877; AAC35588.1; -.
EMBL; AC005189; AAC25526.1; -.
Genew; HGNC:1062; BLVRA.
MIM; 109750; -.
InterPro; IPR000683; GFO_IDH_MOCA.
Pfam; PF01408; GFO_IDH_MOCA.
CAIGORECTASE; NAD; NADP; Zinc.
CAIGORECTASE; ACTAIN.
3 296 BILIVERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33488 MW;
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            281
292
293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 AA;
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95 LVEYPMT 101
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280
281
292
293
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Search completed: April 22, 2003, 12:51:48 Job time : 5.5 secs

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GenCore version 5.1.4 p5_4578

Copyright (c) 1993 - 2003 Compugen_Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2003, 12:47:43 ; Search time 18 Seconds

(without alignments)
103.024 Million cell updates/sec

Title: US-09-674-716B-7
Perfect score: 48
Sequence: 1 QQLVEYPFT 9
Scoring table: BLOSUM62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5
Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 200000000

Maximum Match 100*
Post-processing: Minimum Match 100*
Listing first 45 summaries
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| SPTREMBL_21:*
| Sp archea!*
| Sp bacreria:*
| Sp phuman:*
| Sp phuman:*
| Sp phage:*
| Sp

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	OBW454 arabidopsis 065550 arabidopsis 099313 neoceratodu 099m934 bothriomyrm 09xnv8 delomys dor 09xnv6 scapteromys 09xnv7 oreithrodon 09tg14 cervus elap 09tf12 spermophilu 09tf12 spermophilu 09tf11 spermophilu 09tf11 spermophilu 09tf108 spermophi
SUMMARIES	Q8W454 O65550 Q9B313 Q9M34 Q9XNV8 Q9XNV0 Q9XNV0 Q9TE14 Q9TE12 Q9TF11 Q9TF08 Q33887 Q33887 Q3387 Q3387 Q3387 Q3387
DB	011000000000000000000000000000000000000
* Query Match Length DB	278 874 874 874 874 874 874 874 874 874 8
* Query Match	7.1.1 7.5.0 7.0 7.0 7.0 7.0 7.0 7.0 7.0 7.0 7.0 7
Score	
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	17	9	Š.	380	œ	9XNX60		69xnx6	blarinomys
	18	ø	'n	380	œ	O3XNX60		O3xux0	thomasomys
	19		75.0	380	ø	6MNX60		6MUX60	thomasomys
	20		'n	380	æ	O9XNW8		O9xnw8	thomasomys
	21		ď	380	α	CWNX90		09xnw7	thomasomys
	22			380	00	9MNX60		9wux60	thomasomys
	23			380	0	O9XNW3		09xnw3	rhipidomys
	24			380	ω	CVNX V		Cynx60	delomys sub
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	26		75.0	380	8	035970		035970	thomasomys
	27		75.0	380	œ	Q34853		034853	lenoxus api
	28		75.0	380	æ	CINIM60		Q9mnt7	andinomys e
	29		75.0	380	œ	O9MNTS		Q9mnt5	andalgalomy
	30		75.0	380	æ	Q9MNT4		Q9mnt4	tapecomys p
	31		75.0	380	œ	Q9MNT3		Q9mnt3	
	32		75.0	380	8	Q9MNT2		Q9mnt2	eligmodonti
	33		75.0	380	8	Q9MNT1		Q9mnt1	graomys gri
•	34		75.0	380	œ	OTMW60		Q9mnt0	
	35		75.0	380	8	98MM60		Q9mns8	calomys cal
	36	9	75.0	380	œ	CSMMS0		09mns7	calomys lep
	37	9	75.0	380	80	Q9T7L7		Q9t717	œ
	38	9	75.0	380	œ	Q9MHF9		O9mhf9	microtus lo
	39	9	75.0	380	8	Q94WP7		Q94wp7	calomys mus
	40	9	75.0	380	8	Q94V01		094v01	microtus oa
	41	9	75.0	380	80	Q94UZ9		Q94uz9	microtus gu
	42	36	75.0	380	œ	095602		Q956q2	acomys igni
	43	36	S	381	œ	Q9TGS0		09tg80	abrothrix o
	44	36	•	381	œ	Q9B1W5		09b1w5	abrothrix o
	45	36	75.0	381	œ	Q9B1W4		Q9b1w4	abrothrix s
						ALIGNMENTS	MENTS		
RES	RESULT 1								
08W454	454								
qi	Q8W454		PRELIMINARY	INARY;		PRT;	278 AA.		
AC	Q8W454;	•-							
던	01-MAR-2002	-2002	(TrEMBLrel.		20,	Creat			
Τđ	01-MAR	-2002	(TrEMBLrel.		20,	Last	sequence update)		
Б	01-JUN-2002	-2002	(TrEMBLrel.	Lrel.	21,	Last	annotation update)		
DE	Putatin	ve cal	Putative calmodulin-binding	n-bind	1,10	protein.			
N5	AT4G31000, F6118.90 OR AT4G31000	300, F	6118.9	O OR A	T4G	31000.			
SO	Arabidopsis thaliana (Mouse-ear	spais	thalia	na (Mo	use	-ear cress)	в).		
ပ	Eukaryo	ota; V	'iridip	lantae	 S	Eukaryota; Viridiplantae; Streptophyta;	ta; Embryophyta; Tracheophyta;	Tracheo	phyta;
S O	Spermat	cophyt	a; Mag	noliop	hyt	a; eudico	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	udicots;	Rosidae;
ဗ	eurosids	de II;	Brass	Brassicales;	E	Brassicaceae;	ae; Arabidopsis.		
XO	NCBI TaxID=3702;	axID=3	702;						
ě	-	í	•						

77.1%; Score 37; DB 10; Length 278;

Query Match

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Gaps
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Petrygota, Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata,
Formicidae, Dolichoderinae, Bothriomyrmex.
NCBI_TAXID=121499;
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                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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SEQÜENCE 247 AA; 29263 MW; CC68F8BAOD065B1A CRC64;
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Last annotation update)
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(TrEMBLrel. 15, I
(TrEMBLrel. 19, I
                                                                                                                                                                                                                                                                                                                                                                      75.0%;
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Best Local Similarity
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01-0CT-2000
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"Augratian lungfish (Neoceratodus forsteri) have low genetic
diversity at allozyme and mitochondrial loci: A conservation alert for
a living fossil?",
Conserv. Genet. 0.0-0(2001).
-!** FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
                                                                                                                                                                                                                                                                                                                01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last senctation update)
Putative calmodulin-binding protein.
FGIB-90 OR AT4G31000.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicocyledons; core eudicots; Rosidae;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Benes V., Rechmann S., Borkova D., Ansorge W., Mewes H.W., Lemcke K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                       Gaps
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Bevan M., Benea V., Rechmann S., Borkova D., Ansorge W., Hoheisel
Mewes H.M., Mayer K., Schueller C.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion.
Bukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Dipnoi; Ceratodontiformes; Ceratodontidae; Neoceratodus.
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                                       1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neoceratodus forsteri (Australian lungfish).
                                                                                                                                                                                                                                                                   467 AA.
           Pred. No. 14;
1; Mismatches
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        Best Local Similarity 75.0%;
Matches 6; Conservative
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145 QHLIEYPF 152
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AC Q98313
DT Q98313;
DT Q1-JUN-1
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06556
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RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

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à
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Smith M.F., Patton J.L.;

Smith M.F., Patton J.L.;

Smith M.F., Patton J.L.;

"Phylogenetic relationships and the radiation of sigmodontine rodents
"Phylogenetic Estationships and the radiation of sigmodontine rodents
"The South America: Evidence from cytochrome b.";

J. Mammal. Evol. 6:89-128(1999).

-I-FUNCTION: COMPLEX III OR CYTOCHROWE B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO AFP SYMMIESIS (BY SIMILARITY).

-I-SUBUND TO THE PROTEIN (BY SIMILARITY).

-I-SUBUND TO THE PROTEIN (BY SIMILARITY).

-I-SUBUND TO THE PROTEIN (BY SIMILARITY).

-I-SUBULARITY: BELONGS TO THE CYTOCHROME B FAMILY.

-I-SUBULARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL. AP108686; AAD454681.

-I-SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL. AP108033; CYTOCHROME B B. DO; UNROWN 1.

PÉAM; PRO0133; CYTOCHROME B. DO; UNROWN 1.

PROSITE; PS00193; CYTOCHROME B. DO; UNROWN 1.
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Smith M.F., Patton J.L.;

"Phylogenetic relationships and the radiation of sigmodontine rodents in South America: Exidence from cytochrome b.";

J. Mammal. Bvol. 6:89-1281(1999).

-I- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
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Pred. No. 29;
0; Mismatches 1; Indels
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SEQUENCE 352 AA; 39631 MW; AA408DB627140D6C CRC64;
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Last annotation update)
                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                       Delomys dorsalis (striped Atlantic forest rat).
                                        352 AA.
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                                                                       01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
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                                                                                                                          Cytochrome B (Fragment).
                                      PRELIMINARY;
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NCBI_TaxID=89126;
                                                                                                                                                                                                                                                                NCBI_TaxID=89119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 OPVEYPFT 348
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                                    9VNX69
                                                         9VNX60
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RESULT 5
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                      9XNX60
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Smith M.F., Patton J.L.;

Smith M.F., Patton J.L.;

In Phylogenetic relationships and the radiation of sigmodontine rodents in South America: Bvidence from cytochrome b.";

J. Mammal. Evol. 6:89-128(1999).

-!- FUNCTION: COMPLEX III OR CYTOCHROME B.-CI COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERALES AN ELECTROCHEMICAL POTENTIAL.

C. COUPLED TO ATP SYNTHESTS (BY SIMILARITY).

-!- COPACTOR: TWO HEME GROUPS (BSCS AND BSCS), WHICH ARE NOT COVALENTLY. BOUND TO THE PROTEIN (BY SIMILARITY).

-!- SUBBINIT: THE MAIN SUBBNITS OF COMPLEX B.-CI ARE: CYTOCHROME B.

C. CYTOCHROME CI AND THE RISKE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

REMBL; AF108694; AAD45476.1; --
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            COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-!-CORACYON: TWO HEMBE GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).

-!-SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-!-SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL; AF108669; AAD45451.1; -
INTERPO: IPRO0019; CYT be.

Ffam; PRO0031; CYTOCHROME B C3.

PFam; PRO0032; CYTOCHROME B L BINE; 1.

PROSITE; PRO0193; CYTOCHROME B HEME; 1.

PROSITE; PRO0193; CYTOCHROME B D3: UNKNOWN 1.

ERGETRON LYANGROME B D4: UNKNOWN 1.
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                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Mammalla, Butheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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Pfam; PF00032; cytochrome_D_C; 1.

Pfam; PF00033; cytochrome_D N; 1.

PROSITE; PS00192; CYTOCHROME_B HEME; 1.

PROSITE; PS00193; CYTOCHROME_B QO; UNKNOWN 1.

Electron transport; Heme; MiTochondrion; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 75.0%; Score 36; DB 8; Length 377; Local Similarity 87.5%; Pred. No. 31; Local Similarity 60; Mismatches 1; Indels 1988.
                                                                                                                                                                                                                                                                                                                                             75.0%; Score 36; DB 8; Length 377; 87.5%; Pred. No. 31; 2.1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                     NON TER 1 1 1 SEQUENCE 377 AA, 42392 MW; 692D67AE20B6F3BB CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cytochrome B (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reithrodon auritus (bunny rat).
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ses 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=56234;
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Transmembrane.
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Matches
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2 QLVEYPFT 9

Q9TGL4

RESULT 8 Q9TGL4

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A molecular phylogeny of ground squirrels and prairie dogs.";

"A molecular phylogeny of ground squirrels and prairie dogs.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: COMPONENT OF THE UBIOUTNOL.—CYTOCHROWE C REDUCTASE

COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A
RESEPRATORY CALAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-!- COPACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY

BOUND TO THE PROTEIN (BY SIMILARITY).

-!- SUBMIT: THE MAIN SUBMITS OF COMPLEX B-CI ARE: CYTOCHROME B,

CYTOCHROME CI AND THE RIESKE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELEVORG TO THE CYTOCHROME B FAMILY.

EMBL: AF157946; AAD50230.1; --

INTERPO: IPRO00179; CYTOCHROME B C:

PEAM: PF00033; CYTOCHROME B C:

PEAM: PF00033; CYTOCHROME B O: UNKNOWN 1.

PROSITE: PS00192; CYTOCHROME B PERME; 1.
                  Mitochondrion.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae; Spermophilus.

NCBI_TaxID=99842;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 75.0%; Score 36; DB 8; Length 379; Best Local Similarity 87.5%; Pred. No. 31; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    379 AA; 43024 MW; 1F115AE16850F5AA CRC64;
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  Harrison R.G., Sherman P.W., Yensen E., Hoffmann R.S.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
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SEQUENCE 37
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SEQUENCE 37
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REDLINE-2022950. Pubmed=10764539;

KREDLINE-2022950. Pubmed=10764539;

KREDLINE-2022950. Pubmed=10764539;

KREDLINE-2022950. Pubmed=10764539;

RT "Phylogenetic relationships among european red deer, wapiti, and sika deer inferred from mitochondrial DNA sequences.";

RL "And. Phylogenetic relationships among european red deer, wapiti, and sika deer inferred from mitochondrial DNA sequences.";

RL "Phylogenetic relationships among european red deer, wapiti, and sika deer inferred from mitochondrial DNA sequences.";

RL "Phylogenetic relationships among european red deer, wapiti, and sika deer inferred from mitochondrial DNA sequences.";

ROWDLEX (COMPLEX III) R CYTOCHROME D-CYTOCHROME CREDUCTASE COMPLEX THE RESTRE ROYDLEX NELCYCHROME B, CYTOCHROME D-CYTOCHROME B, CYTOCHROME B, CATOCHROME D-CYTOCHROME B, DNA SIBLONGS TO THE CYTOCHROME B FAMILY.

RESELOTION TO THE PROTEIN (BY SIMILARITY).

CYTOCHROME CATOCHROME D-CYTOCHROME B FAMILY.

BRIATY PRODUCTS; LER CYTOCHROME D-CYTOCHROME B, CYTOCHROME D-CYTOCHROME D-CYTOCH
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
Cervidae, Cervinae, Cervus.
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Mammalia; Eutheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
Spermophilus.
NCBI_TaxID=100390,
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75.0%; Score 36, DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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Mitochondrion.
                                                                                                                                                                                                                                                                                                                   Cervus elaphus (Red deer).
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338 QPVEYPFT 345
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RESULT 9
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ID 097F64
DT 01-M
DT 01-M
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DG 07F6
COFF66
COFF66
COFF66
COFF666
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MCBI_TaxID=100390;
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Lubmitted (UTN-1999) to the EMBL/GenBank/DDBJ databases.

Lubmitted (UTN-1999) to the EMBL/GenBank/DDBJ databases.

LECOMPLEX (COMPLEX II OR CYTOCHROWE B-CI COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

COUPLED TWO HEME GROUPS (BS62 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).

CTOCARCTOR: TWO HEME GROUPS (BS62 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).

CTOCARCTOR: TWO THE RIESES PROTEIN (BY SIMILARITY).

REMBL, AR157941, AADS02011.1.

BERL, AR157941, AADS02011.1.

BREAL, AR157941, AADS02011.1.

PREMBL, PROSITE; PROSO013; CYTOCHROWE B HEME; 1.

PROSITE; PROSO13; CYTOCHROWE B HEME; 1.

PROSITE; PROSO13; CYTOCHROME B DO, UNKNOWN 1.

REMBL PROSITE; PROSO193; CYTOCHROME B DO, UNKNOWN 1.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae, Spermophilus.
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae;
Spermophilus.
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  8; Length 379,
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                         1; Indels
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                                                                                                                                                                                                               Spermophilus madrensis (Sierra Madre ground squirrel).
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Last annotation update).
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Last sequence update)
Last annotation update)
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  Score 36; DB 8
Pred. No. 31;
0; Mismatches
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  75.0%;
87.5%;
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Matches 7; Conservative
Query Match 75.0
Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                             341 QPVEYPFT 348
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Q9TF08
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Q9TF11
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                                                                                                   "A molecular phylogeny of ground squirrels and prairie dogs.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
-!- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
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STRAIN=UMMZ CATALOG # 133965; TISSUE=LIVER;
Smith M.F., Patton J.L.;
"Phylogenetic relationships and the radiation of sigmodontine rodents in South America: Evidence from cytochrome b.";
J. Mammal. Evol. 6:89-128(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                             Smith M.F.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
- COMPLEX (COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-267 FROM N.A.
STRAIN=UMMZ CATALOG # 133965, TISSUE=LIVER;
Smith M.F., Patton J.L.;
"Diversification of South American murid rodents: Evidence from mitochondrial DNA sequence data for the akodontine tribe.";
Biol. J. Linn. Soc. 50:149-177(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.0%; Score 36; DB 8; Length 379; 87.5%; Pred. No. 31; tive 0; Mismatches 1; Indels
                          STRAIN-SEY1069;
Harrison R.G., Sherman P.W., Yensen E., Hoffmann R.S.,
Bogdanowicz S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42994 MW; 767009AD223C18AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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STRAIN=UMMZ CATALOG # 133965; TISSUE=LIVER;
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les 7; Conservative
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SEQUENCE FROM N.A.
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PROSITE, PS00193, CYTOCHROME B QO, UNKNOWN 1.
Electron transport; Heme; Mitochondrion; Respiratory chain;
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                                                                           Transmembrane.
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19940CB
AC 09440C
AC 09440C
BD 01-DB
DT 01-DB
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COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

COPACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY

BOUND TO THE PROTEIN (BY SIMILARITY).

CI SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,

CI SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

CI SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

REMBL: U03527; AAD12554.2; - 1.

Rems.; PRO0013; CYTOCHROME D C; 1.

Rems.; PRO0013; CYTOCHROME D C; 1.

Rems.; PRO013; CYTOCHROME D C; 1.

REMS.; PROSITE; PS00193; CYTOCHROME D C; 1.

RESCRIPE; PS00193; CYTOCHROME D C; 1.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
COMPLEX (COMPLEX II OR CYTOCHROME B.C.1 COMPLEX), WHICH IS A REPERATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL.
COMPLEX IO ATP SYNTHERSIS (BY SIMILARITY).
C. -- COFACTOR: TWO HEME GROUPS (BS52 AND B566) WHICH ARE NOT COVALENTLY COUPLED TO ATP SIMILARITY).
C. -- SUBUNIT: THE MAIN SUBMITS OF COMPLEX B.C.1 ARE: CYTOCHROME B, C.T.OCHROME CI AND THE RIESE PROTEIN (BY SIMILARITY).
C. -- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
C. -- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR FEMEL, 1003649; AADL2575.2, -..
DR FEMEL, 1003649; AADL2575.2, -..
DR FEMEL, 1003649; AADL2575.2, -..
DR FEMEL; PRO00179; CYTOCHROME B. FAMILY.
DR PFÉM: PF00031; CYTOCHROME B. HEME; 1.
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STRAIN=USNM CATALOG # 560661; TISSUE=LIVER;
Smith M.F., Patton J.L.;
"Phylogenetic relationships and the radiation of sigmodontine rodents in South America: Evidence from cytochrome b.";
J. Mammal. Evol. 6:89-128(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-267 FROM N.A.
STRAIN=USNW CATALOG # 560661; TISSUE=LIVER;
Smith M.F., Patton J.L.;
"Diversification of South American murid rodents: Evidence from mitochondrial DNA sequence data for the akodontine tribe.";
Biol. J. Linn. Soc. 50:149-177(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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Last annotation update)
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87.5%; Pred. No. 31;
iive 0; Mismatches
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STRAIN=USNM CATALOG # 560661; TISSUE=LIVER;
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(TrEMBLrel. 12,
(TrEMBLrel. 19,
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hes 7; Conservative
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01-NOV-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Mitochondrion.
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Q33940;
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Matches
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A Ludt C.J., Kuehn R., Schroeder W., Rottmann O.;

AT Phylogeny of Cervidae based on mitochondrial genes.";

Bubhitted (SER-2010) to the EmBL/GenBank/DBU databases.

COMPLEX COMPONENT OF THE UBIQUINOL-CYTOCHROME C.

COMPLEX (COMPLEX III OR CYTOCHROME B.C.1 COMPLEX), WHICH IS A

RESPIRATORY CHAIN THAT GENERALES AN ELECTROCHEMICAL POTENTIAL

COUPLED TO ATP SYNTHESIS (BY SIMILARITY)

C. -I CORACTOR: TWO HEME GROUPS (BS62 AND Bs66) WHICH ARE NOT COVALENTLY)

C. -I COPACTOR: TWO HEME GROUPS (BS62 AND Bs66) WHICH ARE NOT COVALENTLY)

C. -I SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B.C.1 ARE: CYTOCHROME B,

CTTOCHROME C.1 AND THE RIESER PROTEIN (BY SIMILARITY).

C. -I SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C. -I SIMILARITY: AL17842.11 -

C. -I SIMILARITY: AL17842.11 -

C. -I STANICARONE C.1 AND THE RIESER PROTEIN (BY SIMILARITY).

C. -I SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C. -I SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C. -I STANICARONE C.1 AND THE RIESER PROTEIN.

REMBL: AF423200; AAL17842.11 -

C. -I STANICARONE C. AND THE RIESER PROTEIN.

REMBL: AF423200; AAL17842.11 -

C. -I STANICARONE C.1 AND THE RIESER PROTEIN.

REMBL: AF423200; AAL17842.11 -

C. -I STANICARONE C.1 AND THE RIESER PROTEIN.

REMBL: AF423200; AAL17842.11 -

C. -I STANICARONE C.1 AND THE RIESER PROTEIN.

REMBL: AF423200; AAL17842.11 -

C. -I STANICARONE C.1 AND THE RIESER PROTEIN.

REMBL: AF423200; AAL17842.11 -

C. -I STANICARONE C.1 AND THE RIESER PROTEIN.

REMBL: AF423200; AAL17842.11 -

C. -I STANICARONE C.1 AND THE RIESER PROTEIN.

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C. -I STANICARONE C.1 AND THE RIESER PROTEIN.

REMBL: AF423200; AAL17842.11 -

C. -I STANICARONE C.1 AND THE RIESER PROTEIN.

REMBL: AF423200; AAL17842.11 -

C. -I STANICARONE C.1 AND THE RIESER PROTEIN.

REMBL: AF423200; AAL17842.11 -

C. -I STANICARONE C.1 AND THE RIESER PROTEIN.

REMBL: AF423200; AAL17842.11 -

C. -I STANICARONE C.1 AND THE RIESER PROTEIN.

REMBL: AF423200; AAL17842.11 -

C. -I STANICARONE C.1 AND THE RIESER PROTEIN.

REMBL: AF423200; AAL1
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
Cervidae, Cervinae, Cervus.
NCBI_TaxID=173988,
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                                                                                                                                                                                1; Indels
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379 AA; 42766 MW; 8B74E09004D8E663 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                        Score 36; DB 8;
Pred. No. 31;
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                                                                                                                                                                           0; Mismatches
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                                                                              75.0%;
87.5%;
                                Query Match
Best Local Similarity 87.59,
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                  341 OPVEYPFT 348
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Insulin/insulin-li Human BLyS binding Human BLyS binding Single chain Fv re S11-VEGF2 construc S11-sevEGF2 construc 2G3 hybridoma VL d Protein involved i

Light chain CDR3 o Variable domain of Variable domain of Human WSX receptor Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Murine 13410 light Murine 13410 light

Amino acid sequenc Staphylococcus epi S. epidermidis ope C242:11 MAb kappa Peptide #4456 enco Human anti-Rh(D) c BW 435 VK. Synthe Sequence of the ma 260F9 hybridoma VL

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Searched:

Minimum DB Maximum DB

Database

Scoring table:

Perfect score:

Sequence:

OM protein

Run on:

gil variable domai CTMO1 VL. Synthet Sequence of the li Sequence of the li CDR grafted humani MAD CT.-MO1 light gil2 variable domai Human polypeptide

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CD23; FCERII; IgB receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimerac antibody; humanised antibody; commonoclonal antibody; chimeracic antibody; unumanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; lashlunco's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; inflammatory bosel disease; asthma; rhinitis; eczema; insultis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Light chain CDR L3 of mouse anti-CD23 MAb C11.
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                                                                                                   AAB10863
AAB10864
AAY90813
AAY36951
AAG27700
AAG27699
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AAR59513
AAY90819
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AAR33951
AAR59509
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AAY92164
AAW28154
ABP40069
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AAG93597
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AAW29754
AAY56874
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  99WO-GB01434.
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                                                                                                                                                                                                                                                     07-MAY-1999;
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AAY32256;
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  Light chain CDR L3
Humanised anti-CD2
Mouse anti-PAb-42
Murine anti-PAb-42
Mouse MAb 2E12 L
Light (kappa) Chai
Light chain CDR3 o
Light chain CDR3 o
Light chain CDR3 o
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                                                                           April 22, 2003, 12:45:19 ; Search time 22.8214 Seconds (without alignments) 52.550 Million cell updates/sec
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| SIDSS/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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| SIDSZ/gcgdata/geneseqg/geneseqp-embl/AA1985.DAT:*
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            GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                             hits satisfying chosen parameters:
                                                                                                                                                                                                         908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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AAY32262
AAY32261
AAY70790
AAY70790
AAX12232
AAX12354
AAW398823
AAW39882
                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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WPI; 2000-053101/04.
N-PSDB; AAZ34747.
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Matches 9; Conserv
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                                                                                                                                                                            This sequence represents complementarity determinating region 3 (CDR L3) of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11 (see also AAY3262). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY32264-59) to render them capable of binding to the CO23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus exprhematosus, Hashimoto's thyroidatis, multiple sclerosis, diabetes, uveltis, dermatifis, psoriasis, unlitiple sclerosis, diabetes, uveltis, dermatifis, psoriasis, unlitiple sclerosis, csyndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, 5jogren's syndrome, allergies, allergie cathma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, CO9D, insulitis, bronchitis (particularly tronic bronchitis) or diabetes (particularly type I for studying interactions between CD23 and various ligands and cermining the binding agents.
                                                                                       Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Shearin J;
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0; Indels
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 Bonnefoy JMP, Crowe SJ, Ellis JH, Kapson NT,
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55..61
/note= "CDR 2"
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/note= "framework region 1"
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                                                                                                                                              Claim 1; Page 40; 81pp; English
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                                   2000-053101/04.
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1 QQLVEYPFT 9
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Synthetic.
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Matches

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%XGCCCCCCCCCCCCX%X47X88X1

AAY32262 ID AAY3 RESULT 2

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this sequence represents the light chain variable region (VL) of humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human framework (HSTGKVII) and the light chain complementarity determining regions (HSTGKVII) and the light chain complementarity determining regions (HSTGKVII) and the light chain complementarity and was constructed by splice overlap PCR. The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on the capable of binding to the CD23 type II molecule expressed on the capable of binding to the CD23 type II molecule expressed on the capable of binding to the CD23 type II molecule expressed on the capable of binding to the CD23 type II multiple sclerosis, diabetes, uveatis, defamatitis, psoriasis, multiple sclerosis, diabetes, uveatis, defamatitis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies, allergie asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, COPD, insulitis, bronchitis continion the color of the color of
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      "framework region 3"
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/note= "framewor
94..102
/note= "CDR 3"
103..113
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Region

Region Region Region

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This sequence represents the light chain variable region (VL) of murine anti-CD23 (FCBRII) monoclonal antibody C11. The invention provides altered antibodies, such as chimeric or humanised antibodies (see AAY22262 and AAY32263), which comprises sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions (see AAY32254-59) to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble, CD23 formation in human therapy, for the treatment of arthritis, couple expressed on habences. Washimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, cromn's disease, Sjogren's syndrome, allergies allergic asthma, articularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful convenient the binding and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell receptor specific antibodies useful for treating e.g. arthritis
inflammation, arthritis, lupus erythematosus, multiple sclerosis; Habilmoto's thyroiditis, diabetes; uveitis; benatitis, psoriasis; urticaria, nephrotic syndrome; glomerulomephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; inflammatory bowel disease; asthmatory asthma; rhinitis; czema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                    cocation/Qualifiers
                                                                                                                                                                                                                                   83..92
/note= "CDR L2"
125..134
/note= "CDR L3"
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AAY70790 standard; Protein; 122 AA.
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19 AA;
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Sequence
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Matches
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AAY70804 standard; peptide; 19 AA.

RESULT 4
AAY70804
ID AAY7

Conservative

9

Matches

125 QQLVEYPFT 133

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1 QQLVEYPFT 9

Best Local Similarity

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                                                                                                       Murine, p53 protein, monoclonal antibody, mAb, PAb-421, IDI-1; IDI-1 Li3; light chain variable region, VL; complementarity determining region, CDR, dermatological, immunosuppressive, antiinflammatory; autoimmune responee, SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erythematosus (SLE) by down-regulating the autoimmune response to th C-terminal DNA-binding domain of p53 protein by an active compound. The present sequence is a IDI-1 L3 peptide which comprises the complementarity determining region (CDR) of the light chain of IDI-1 monoclonal antibody (MAb). The IDI-1 mAb is an anti-idiotypic antibody/AD2 mAb specific for PAb-421 which is an Ab1 mAb specific to the C-terminal DNA-binding domain of murine p53 protein. The peptide corresponds to residues 92-110 of IDI-1 light chain variable region. It is an example of the active compound useful in the diagnosis, prevention and treatment of SLE in humans.
                                                                    Murine anti-PAb-421 IDI-1 mAb light chain CDR based peptide IDI-1 L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       patent discloses a method for the treatment of systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treatment of systemic lupus erythematosus by down-regulating the autoimmune response to the C-terminal DNA-binding domain of the protein by an active compound comprising of antibodies to p53 or
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88.9%; Pred. No. 0.031;
ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herkel J;
                                                                                                                                                                                    DNA-binding domain; anti-idiotypic antibody.
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                                   31-JUL-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragments of p53
                                                                                                                                                                                                                                                               WO200023082-A1.
                                                                                                                                                                                                                                                                                                                                       19-OCT-1999;
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 AAY70804;
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Mus sp. Region Region

Region

19-OCT-1999; .9-OCT-1998;

27-APR-2000

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The mouse VI gene product may be used to produce chimeric mouse-
human Abs against HIV-1 comprising human Ig constant regions and
murine variable regions. These novel sequence are useful in
treatment, diagnosis and prophylaxis of HIV infections, and may be
produced by a bacterial, yeast or mammalian expression system.
                                                                                                                                                                                                                             New chimeric mouse human antibodies - used in treatment, diagnosis and prophylaxis of HIV infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New chimeric mouse-human antibodies - used to detect, kill and remove HIV-1 antigen from sample
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88.9%; Pred. No. 0.24;
cive 1; Mismatches 0; Indels
                                                                                                                                         Ghosh-Dastidar P, Robinson RR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chain variable region of murine 2E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric antibodies; immunoconjugates; HIV; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR12354 standard; Protein; 132 AA.
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                                                                                                                                                                                                                                                                                       Disclosure; Fig 1; 108pp; English.
                                  90WO-US06627.
                                                                     89US-0433703.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 88.9
hes 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (XOMA-) XOMA CORP. (GREC ) GREEN CROSS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Better MD, Horwitz AH,
                                                                                                                                           Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-178044/24.
                                                                                                                                                                              WPI; 1991-178106/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 QQLVEYPYT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 131 AA;
                                                                                                        (XOMA-) XOMA CORP
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                                                                                                                                                                                              N-PSDB; AAQ12012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Light (kappa) c
immunoglobulin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                  13-NOV-1990;
                                                                     13-NOV-1989;
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                                                                                                                                           Better MD,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses a method for the treatment of systemic lupus erythematosus (SLE) by down-regulating the autoimmune response to the cetrefainal DNA-binding domain of Ep3 protein by an active compound. The present sequence is a light chain variable region of IDI-1 an anti-diotypic antibody/Ab2 monoclonal antibody (mAb) specific for PAb-421 which is an Ab1 mAb specific to the C-terminal DNA-binding domain of murine p53 protein. The Ab1 and Ab2 mAbs and peptides based on complementarity determining regions of light and heavy chain variable regions of these antibodies, are examples of active compounds useful in the diagnosis, prevention and treatment of SLE in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treatment of systemic lupus erythematosus by down-regulating the autoimmune response to the C-terminal DNA-binding domain of the p53 protein by an active compound comprising of antibodies to p53 or
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                                                                                                                      58.64
[Jabel= CDR]
/note= "Complementarity determining region"
/1abel= CDR
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/note= "Complementarity determining region"
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                                                                                                     "Complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Herkel J;
                                                  ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 78; Fig 9; 87pp; English.
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/label= CDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ragments of p53
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19-AUG-1991

AAR12232;

Sequence

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Mus sp.

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Gaps

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AAW39821-23 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 2A10, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                       Gaps
viral antigen. It is used in the construction of a chimeric MAD comprising heavy and light chains having murine V regions and human C regions. The chimeric MADs are more effective than murine MAD 2812 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MADs can be used as immunoconjugates, in association with e.g. toxins for HIV treatment. See also AAQ12057-63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
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                                                                                                                                                                                                                  Score 45; DB 12; Length 132; Pred. No. 0.24;
                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                              AAW39823 standard; peptide; 9 AA.
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88.9%;
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Best Local Similarity 86.5°
Local 8; Conservative
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                                                                                                                                                                                       Sequence
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9 AA;

Sequence

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                                                                                                                                                                                                                                                                                  Variable domain, lambda light chain, catalytic antibody; degradation; cocaine, cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
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Pred. No. 0.33;
), Mismatches 1; Indels
Score 44; DB 19; Lengtn >;
Pred. No. 7.88+05;
Pred. 1; Indels
                                                                                                                                                                                                                                                           Light chain of the catalytic antibody 2A10.
                                          0; Mismatches
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88.9%;
               91.7%;
88.9%;
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                                            8; Conservative
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Best Local Similarity
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             Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                       1 QQLVEYPFT 9
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AAW39804
ID AAW39
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade cocaine. A series of cocaine transitions state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl occaine, The 2AhO antibody (AAW39809 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2AlO has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can
                                                                                                       Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
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                                                                           Variable domain of the Kappa light chain of catalytic antibody 2A10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
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Pred. No. 0.33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16; Pages 73-74; 147pp; English.
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88.9%;
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                                                                                                                                                           overdose; addiction.
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-077166/07.
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Best Local Similarity
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QQFVEYPFT 102
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             AAW39804;
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Matches
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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The manied antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating CCR2. They are useful for inhibiting or treating cell subject of lateovyte trafficiary for treating CCR2-andised disorders such as their inhibiting restences; attended and atherosclerosis, arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restences; attended sorders such as affor inhibiting restences; attended sorders such as and for inhibiting restences; attended allergy, anaphylaxis, and in the manufacture of a medicament for treating CCR2-2 mediated disease. They are useful in therapy or diagnosis, and in the manufacture of a medicament of interacting creation, shock, stenosis, allograft rejection, filteractic disease, asthma, inflammatory glomerulopathies, acquired increvention, including angioplasty and/or stent placement in a mammal. The present in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, and inhibiting modifical inflammal, and subject of the present sequence is mouse germline kappa light chain variable
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inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasis; VK; kappa light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O'Brien S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.1.
100.0%; Fi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-FEB-2000; 2000US-0497625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-FEB-2001; 2001WO-US03537.
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nes 7; Conserv
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WO9749800-A1

31-DEC-1997.

25-JUN-1997; 25-JUN-1996;

Landry DW;

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AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806 represents the heavy chain) was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can
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                                                                                                                                                                                                                                                                         New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.0%; Score 36; DB 66.7%; Pred. No. 13; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Pages 71-72; 147pp; English.
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                                                                                                                           COLUMBIA NEW YORK
                                          97WO-US10965.
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94 QHFVDYPFT 102
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31-DEC-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW39815-17 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 389, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 31+Denzoic acid from 31+Phenyl cocaine. The 389 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 389 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                      Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Variable domain of the Kappa light chain of catalytic antibody 3B9
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66.7%; Pred. No. 7.8e+05;
iive 1; Mismatches 2;
  Light chain CDR3 of catalytic antibody 3B9
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                                                                                                                                                                                                                                                                                                                                                                        (UYCO ) UNIV COLUMBIA NEW YORK
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(UYCO) UNIV COLUMBIA NEW YORK

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16-JUN-1998

AAW39801;

AAW39801

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Sequence

Query Match

Best Loca Matches

96US-0672345.

25-JUN-1996;

DB 19; Length 113;

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AAW39801-05 represent the amino acid sequences of the variable domain of the Kappa light chain of catalytic antibodies which are able to degrade occaine. A series of cocaine pransition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release silf-benzoic acid from 3H-phenyl occaine. The 12H1 antibody (AAW39808 represents the heavy chain) was identified using TSA2, and has a per minute Kcat of 0.016. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                          New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WSX*receptor and related antibodies and ligands - used to develop products for diagnosis and therapy, e.g. for improving haematopoigsis or for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ligand; activator; antibody; agonist; proliferation; obserty; differentiation; anaemia; treatment; neoplasia; arteriosclerosis; Type II diabetes; polycystic ovarian disease; cardiovascular disease; postcoarthritis; dermatological disorder; hypertension; insulin resistance; hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, WSX receptor; clone #17; identification; purification;
                                                                                                                                                                                                                                                                                                                                                                                                                           75.0%; Score 36; DB 19; Length 113; 66.7%; Pred. No. 13; ive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW24063 standard; Protein; 241 AA.
                                                                                                                                                    Claim 18; Page 73; 147pp; English.
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96US-0585005
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Matches 6; Conservative
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94 QHFVDYPFT 102
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                                  P-PSDB; AAV09802
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08-JAN-1996;
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The present sequence is an agonist antibody clone to the human WSX receptor, which can be used to identify and purify ligands and activators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor, leading to enhanced proliferation or differentiation of a cell expressing the WSX receptor. It can also differentiation of a cell expressing the WSX receptor. It can also intake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or contake in an obese mammal. WSX receptor ligands can be used to expecially a human is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to repopulate marrow transplantation therapy. It can also be used to repopulate collocation therapy. It can also be used to repopulate to look cells in a mammal. The products can also be used to repopulate collocation disorders, arteriosclerosis, Type II diabetes, polycystic ovarian disease, cardiovascular diseases, cardiovascular diseases, cardiovascular diseases, can cholelithiasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels 0;
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Pred. No. 30;
1; Mismatches 2; Indels ·
                      Example 14; Pages 122-123; 219pp; English.
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Matches 6, Conservative
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GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                     US-09-674-716B-7
48
1 QQLVEYPFT 9
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 32, Appl Sequence 50, Appl Sequence 1310, Ap Sequence 936, App Sequence 47635, A Sequence 10, Appl Sequence 11, Appli	. 6, 245, 245, 23,
SUMMARIES	US-09-840-459-32 US-08-779-457-50 US-09-880-748-936 US-09-880-748-936 US-09-848-761-47635 US-09-848-788-40 US-09-973-451.10 US-10-164-359-4 US-09-107-058-8 US-09-114-8 US-09-144-886-97 US-10-045-545-4 US-10-045-545-1 US-10-045-545-3	US-09-976-787-6 US-09-865-198-6 US-09-809-391-745 US-09-976-787-24 US-09-865-198-23
DB		22 6 2 2 2
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% Que <i>ry</i> Match	77777777777777777777777777777777777777	64.6 64.6 64.6 64.6
Score	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	31 31 31 31
Result No.	111111 1211111 13111111	15 16 18 19

RESULT 2

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Sequence 1 Sequence 1 Sequence		; o o ;
8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	AND	Length 100 Indels
75 -8 -8 -608 -6756 -12613 -12852 -12863 -128 -128 -128 -128 -128 -128 -128 -128	ANTIBODIES PREFOR	10; 5; 0;
09-144-886-09-976-788-09-976-788-09-976-988-18-823-09-9815-242-99-976-78-98-976-78-98-976-78-98-976-78-98-976-78-98-978-98-978-98-978-98-978-98-978-98-978-98-978-98-978-98-98-98-98-98-98-98-98-98-98-98-98-98	CR2 ANTII THEREFOR 0,459 3537 n 3.0	37; DB No. 3. matches
US-09-144-886-75 0 US-09-976-787-8 0 US-09-976-787-8 0 US-09-881-823-6 0 US-09-881-823-6 0 US-09-815-242-12613 0 US-09-815-242-12613 0 US-09-915-787-29 0 US-09-965-198-28 0 US-09-965-198-28 0 US-09-965-198-28 0 US-09-965-198-28 0 US-09-965-198-28 0 US-09-965-118-28 0 US-09-965-118-28 0 US-09-952-217-1118 0 US-09-922-217-1118 0 US-09-309-196-116	her H. ANTI-CCI OF USE TI S/09/840 -02 /US01/031 497,625 359,193 121,781	Sco Pr 0;
	S/098 y J. stoph stoph han H	0.0%; e.0%;
00001111110000 1111100000 11111100000 1111100000 11100000 111000000	Gregory J. Gregory J. Gregory J. J. Christopher Walter S. Tarran J. Slobhan H. J. Slobhan H. J. Slobhan H. J. Theresa HUMANIZED AN MURER HOSO Z. 2001-02-02 UMBER: 09/497 Z0001-02-03 UMBER: 09/497 Z0001-02-03 UMBER: 09/359 1999-07-22 1999-07-22 1998-07-23 SS: 107 Cor Windows Ve	77 10 vativ
	1-09-840-459-32 Sequence 32 Application US/09840459 Sequence 32 Application US/09840459 Sequence 32 Application US/09840459 GEMERAL INFORMATION: APPLICANT: LaRosa, Gregory J. APPLICANT: Horveth, Christopher APPLICANT: O'Briten, Slobhan H. APPLICANT: O'Refe, Theresa TITLE OF INVENTION: HUMANIZED ANTI-TITLE OF INVENTION: METHODS OF USE TITLE OF INVENTION: METHODS OF USE TITLE OF INVENTION: METHODS OF USE TITLE OF INVENTION WIMBER: US/09/8 PRIOR PLILING DATE: 2001-02-02 PRIOR PLILING DATE: 2001-02-02 PRIOR PLING DATE: 1999-07-23 PRIOR PLING DATE: 1999-07-23 PRIOR PLING DATE: 1999-07-23 PRIOR PLING DATE: 1998-07-23 PRIOR PRIOR PLING DATE: 1998-07-23 PRIOR	Similarity 7; Conser VEYP 7
	D-459-3, No. 10	Sal Sal
	WESCULI I USG-0840-459-32 Sequence 32 Application US/09840459 FRETEIN NO. US2020150578A1 GENERAL INFORMATION: APPLICANT: LaRosa, Gregory J. APPLICANT: Horverth, Christopher APPLICANT: O'Brien, Slobhan H. FRIGR REFERENCE: 1855.1052-0.2 FRIOR APPLICATION NUMBER: 09/497, 625 FRIOR PLING DATE: 2001-02-02 FRIOR PLING DATE: 1999-07-22 FRIOR APPLICATION NUMBER: 09/121, 781 FRIOR PLING DATE: 1999-07-22 FRIOR APPLICATION NUMBER: 09/121, 781 FRIOR PLING DATE: 1999-07-23 NUMBER OF SEQ ID NOS: 107 SEQ ID NO 32 LENGTH: 100 TYPE: PRT ORGANISM: Mus musculus US-09-840-459-32	Query Ma Best Loc Matches Qy 1

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RESULT 5
US-09-864-761-47635
US-09-864-761-47635
Sequence 47635, Application US/09864761
Sequence 47635, Application US/09864761
GENERAL INFORMATION:
SAPPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENEEXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION UNMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
SPRIOR APPLICATION NUMBER: US 60/180,312
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US-09-880-748-936

i Sequence 936, Application US/09880748

i Publication No. U52003005937A1

i GENERAL INFORMATION:

APPLICANT: Ruben et al.

I TILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF533

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PRICH FILING DATE: 2000-17

PRIOR APPLICATION NUMBER: 60/270,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR PLICATION NUMBER: 60/277,379

PRIOR PLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PLICATION NUMBER: 60/293,499

PRIOR PLICATION NUMBER: 60/293,499
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                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 9; Length 251;
Pred. No. 14;
1; Mismatches 2; Indels
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1310
LENGTH: 251
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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US-09-880-748-936
                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1310
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234 QQLISYPLT 242
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US-09-880-748-1310

US-09-880-748-1310

Sequence 1310, Application US/09880748

Publication No. U52003005937A1

GENERAL INFORMATION:

APPLICANT: Ruben

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR PLILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/210,816

PRIOR APPLICATION NUMBER: 60/210,816

PRIOR APPLICATION NUMBER: 60/210,816

PRIOR APPLICATION NUMBER: 60/210,816

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16
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                   Sequence 50, Application US/08779457
Sequence 50, Application US/08779457
Publication No. US20020193571A1
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Kyung, Jin Kim
APPLICANT: Kyung, Jin Kim
APPLICANT: Rodrigues, Maria L.
TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generatech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
ZIP: 94080
ZIP: 94080
ZIP: 94080
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IDEN PC compatible
COMPUTER: PREADBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IDEN PC compatible
COMPUTER: MARCHINE PC COMPATIBLE
COMPUTER: PLAINER WINPATIN:
PLIIGATION NUMBER: US/08/779,457
PLIIGATION NUMBER: US/08/779,457
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/58505
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: 1ee, Wendy M.
REGISTRATION NUMBER: P0996F2
TELEPHONE: 415/225-1994
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEFAX: 01/371-7168
INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 241 amino acids
TYPE: Amino Acid
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TOPOLOGY:
US-08-779-457-50
      US-08-779-457-50
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US-09-973-451-10

US-09-973-451-10

Sequence 10, Application US/09973451

Patent No. US2002013228A1

GENERAL INFORMATION:
APPLICANT: JACOBSON, Myron K.
APPLICANT: JACOBSON, Minston
TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE
TITLE OF INVENTION: THE REQUEST THEREOF, AND ANTIBODIES IMMUNOREACTIV
TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV
TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV
TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV
TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV
TITLE OF INVENTION INVERSE: US/09/302,812

CURRENT FILING DATE: 1999-04-30

PRIOR APPLICATION NUMBER: 60/083,768

PRIOR APPLICATION NUMBER: 60/083,768

PRIOR APPLICATION DATE: 1999-05-01

NUMBER OF SEQ ID NOS: 38

LENGTH: 766

TURENT: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10164359
Sequence 4, Application US/10164359
Publication No. US2030012776A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid and Protein Expressed Thereby and Their Involvement
TITLE OF INVENTION: Nucleic Acid and Protein Expressed Thereby and Their Involvement
TITLE OF INVENTION: UNCHESTED STREET APPLICATION NUMBER: 8010/164,359
CURRENT APPLICATION NUMBER: PCT/US00/33438
PRIOR APPLICATION NUMBER: PCT/US00/33438
PRIOR APPLICATION NUMBER: 60169,418
PRIOR FILING DATE: 2006-12-07
PRIOR FILING DATE: 1999-12-07
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match 68.8%; Score 33; DB 9; Length 107; Best Local Similarity 66.7%; Pred. No. 23; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                    OTHER INFORMATION: anti-Rh(D) chain 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
ORGANISM: Homo sapiens
; FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 QQLNSYPYT 96
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172 QELIEYP 178
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US-10-164-359-4
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Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION:
FILE REPERENCE: 05956-42U.
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: ERALIER APPLICATION NUMBER: 09/240,274
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR PLING DATE: EARLIER FILING DATE: 1996-10-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.1
OTHER INFORMATION: EST HUMAN HIT: AW612517.1, EVALUE 7.00e-43
OTHER INFORMATION: SWISSPROT HIT: P54253, EVALUE 1.00e-43
US-09-864-761-47635
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    PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PRILING DATE: 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||||
6 LVEYPF 11
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Gaps

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RESULT 11
US-09-144-886-97
US-09-144-886-97
Sequence 97. Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
    APPLICANT: Marks, James D
    APPLICANT: Marks James D
    TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
    TITLE OF INVENTION: Botulinum Neurotoxins
    TITLE OF INVENTION: Botulinum Neurotoxins
    TILE REFERENCE: 250.171780
    CURRENT APPLICATION NUMBER: US/09/144,886
    CURRENT APPLICATION NUMBER: 1998-08-31
    NUMBER OF ERQ ID NOS: 98
    SOFTWARE: Patentin Ver. 2.0
    SEQ ID NO 97
    LENGTH: 109
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US-09-144-886-97
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TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
bcl-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%; Score 32; DB 10; Length 105;
llarity 55.6%; Pred. No. 35;
Conservative 3; Mismatches 1; Indels
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                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: RC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELERX: (212) 391-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 66.7%; Score 32; DB 9;
Best Local Similarity 55.6%; Pred. No. 36;
Matches 5; Conservative 2; Mismatches ;
                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                               STATE: New York
COUNTRY: United States of America
ZIP: 10036
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/761,117
APPLING DATE: 16-Jan-2001
CLASSIPICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Innear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-761-117-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
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                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 5; Conserv
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72 QQILEYAYT 80
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Pred. No. 35;
3; Mismatches 1; Indel8
                                                                                                         Length 105;
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                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09107058
Patent No. US20010010922A1
GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
APPLICANT: Niu, Hui-Feng
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
TELEX: 42253 COOP UI
INFORMATION POR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: ISN PC compatible
COMPUTER: ISN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,058
FILING DATE:
CLASSIFICATION:
                                                                                                       Score 32; DB 9;
Pred. No. 35;
3; Mismatches
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dalla-Favera, Riccardo
Chaganti, Raju S.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: United States of America
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/09761117; Patent No. US20010012887A1; GENERAL INFORMATION;
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US-09-107-058-8
                                                                                                       66.7%;
55.6%;
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                     Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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  ; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-359-4
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STREET: 1185 Av
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||::|| :|
72 QQILEYAYT 80
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66 QQILEYAYT 74
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US-09-761-117-8
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RESULT 15
US-09-976-787-6
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Publication No. US20030027124A1
GENERAL INPROMATION:
GENERAL INPROMATION:
TITLE OF INVENTION: TISSUE
TITLE OF INVENTION: TISSUE
FILE REFERENCE: 176 60991;
CURRENT APPLICATION NUMBER: US/10/045,545;
FRICE FILING DATE: 2002-01-14;
FRICE FILING DATE: 2001-01-12;
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 1:
IENGTH: 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Maines, Mahin D.
TITLE OF INVENTION: METHODS OF MODIFYING CELL STRUCTURE AND REMODELING
TITLE OF INVENTION: TISSUE
                                                                                                                                                                APPLICANT: Maines, Mahin D.
TITLE OF INVENTION: METHODS OF MODIFYING CELL STRUCTURE AND REMODELING
TITLE OF INVENTION: TISSUE
FILE REFERENCE: 176/60991
CURRENT APPLICATION NUMBER: US/10/045,545
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 60/261,500
PRIOR APPLICATION NUMBER: 60/261,500
RIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 17
SSQ ID NO 4
LENGTH: 295
TYPE: PRT
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Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 9; Length 295;
Pred. No. 98;
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US-10-045-545-3
Sequence 3, Application US/10045545
Publication No. US20030027124A1
GENERAL INFORMATION:
                                                                                                                Sequence 4, Application US/10045545 Publication No. US20030027124A1 GENERAL INFORMATION:
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Similarity 85.7%;
6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%;
                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Rattus norvegicus
US-10-045-545-4
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Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 6; Conserv
                 90 QQYIGYPYT 98
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1 QQLVEYPFT 9
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                                                                                 RESULT 12
US-10-045-545-4
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US-10-045-545-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09976787
; Batent No. US20020064528A1
; GENERAL INFORMATION:
    APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; *TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; TILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT APPLICATION NUMBER: US 09/493,539
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 2000-01-28
; PRIOR FILING DATE: 1999-01-29
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 6
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Pred. No. 98;
0; Mismatches 1; Indels
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Pred. No. 2.7e+05;
0; Mismatches 3; Indels
FILE REFERENCE: 176/60981
CURRENT APPLICATION NUMBER: US/10/045,545
CURRENT FILING DATE: 2002-01-14
FRIOR APPLICATION NUMBER: 60/261,500
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SENGTH: 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: April 22, 2003, 13:11:13 Job time : 10.4821 secs
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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US-09-976-787-6
                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QQLVEYPFT 9
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Query Match
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Matches 5; Conserv
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probable membrane
scrA protein - Sta
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                                                                                       April 22, 2003, 12:48:24; Search time 4.91071 Seconds (without alignments) 97.882 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                        283224
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                       283224 segs, 96134422 residues
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Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
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G2MSU1
S09681
F97302
T42185
AE1752
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E83163
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B95249
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D84505
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C72544
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JQ1462
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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1 GYWMS 5

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hypothetical prote cation efflux syst cadmium, zinc, cob SWI/SNF family hel helicase, Snf2/Rad multidrug resistan hypothetical prote Ig heavy chain V r Ig hypothetical prote Ig heavy chain V r Ig hypothetical prote Ig heavy chain V r Ig hypothetical prote Ig heavy chain V r hypothetical prote Ig heavy chain V r	hypothetical prote
T47495 A33830 AC4700 AC4700 AC4700 AC4700 AC4700 AC4700 B72029 B72042 B72742 B73694 S13694 A83766 S03326	D84436 ALIGNMENTS
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851 1063 1063 1215 1215 1215 101 1112 1112 1115 1116 137	157
00000000000000000000000000000000000000	97.9
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001
C;Date: 02-Feb-2001
C;Date: 02-Feb-2001
C;Date: 02-Feb-2001
C;Accession. A84376
R;NG; W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabloo, Jung, K.H.; Alam, M.; Freitas, T.
Jung, K.H.; Alam, M.; Freitas, T.
Froc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L.A., A;Accession, A84376
A;Accession, A84376
A;Accession, A84376
A;Accession, A84376
A;Residues: 1-67 -STO>
A;Cross-references: GB:AE004437; NID:g10581666; PIDN:AAG20373.1; GSPDB:GN00138
C;Gene: VNG2253H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GARSUI

19 heavy chain V region (UPC10) - mouse

(5)Species: Mus musculus (house mouse)

(5)Bate: 03-Mug-1984 #sequence_revision 03-Aug-1984 #text_change 23-Mar-2001

(5)Accession: A02081

M. Muffray, C.; Sikorav, J.L.; Ollo, R.; Rougeon, F.

An: Immunol. (Paris) 132D, 77-88, 1981

A; Title: Correlation between D region structure and antigen-binding specifity: evidence:

A; Reference number: A02081; MUID:83021113; PMID:6181731

A; Residues: 1-117 (AUD-8)

C; Comment: This chain was isolated from an Ig gamma-2a myeloma protein binding 2,6-levan-

C; Superfamily: immunoglobulin v region; immunoglobulin homology

C; Superfamily: immunoglobulin homology cincles

F; 5-96/Disulfide bonds: #status predicted
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A84376
hypothetical protein Vng2253h [imported] - Halobacterium sp. NRC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 67;
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llarity 100.0%; Pred. No. 15;
Conservative 0; Mismatches
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Best Local Similarity
Matches 5; Conserv
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Gaps

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h Similarity 100.0%; Score 33; DB 1; Length 117; Similarity 100.0%; Pred. No. 26; 5; Conservative 0; Mismatches 0; Indels

Gaps

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hypothetical protein homolog lin2562 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Species: P:; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
I; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshhi, H
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 201
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Accession: AE1752

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Abî phage protein homolog lin2373 [imported] - Listeria innocua (strain Clip11262)
C,Species Listeria innocua
C,Accession: AH1728
R,Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
J, Doninguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Faihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A,Authors: Kreft, J.; Kunnst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A,Authors: Kreft, J.; Kunnst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A,Reference number: AB1077; MulD:21537279; PMID:11679669
A;Accession: AH1728
A;Accession: AH1728
A;Accuse type: DNA
A;Residues: 1-298 cGLA>
A;Residues: 1-298 cGLA>
A;Cross-references: GB:AL592022; FIDN:CAC97600.1; FID:gl6414896; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.9%; Score 30; DB 2; Length 298; ilarity 80.0%; Pred. No. 2.3e+02; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
A;Reference number: 222068; MUID:98391744; PMID:9722640
A;Accession: T42185
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-86 <BUR>
A;Residues: 1-86 <BUR>
A;Resperimental source: SHBL:AF074613; PIDN:AAC70153.1
A;Resperimental source: strain BDL933; serotype 0157:H7
A;Genome: DJasmid pO157
A;Note: L7085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Status: Preliminary A; Accession: F9700
A; Status: preliminary A; Cacession: F9700
A; Residues: 1-1043 - KUR>
A; Residues: 1-1043 - KUR>
A; Cross-references: GB:AE001437; PIDN:AAK81209.1; PID:G15026351; GSPDB:GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics: A; Genetics: A; Genetics: A; Genetics: Cacession: Comparation: A; Genetics: Cacession: Cace
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T42185
Conserved hypothetical protein L7085 - Escherichia coli plasmid p0157
C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accesgion: T42185
R;Burland, V.; Aslao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
Nucleic Acids Res. 26, 4196-4204, 1998
A;Title: The complete DNA sequence and analysis of the large virulence plasmid of Escher
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                                                                                                                                                                                                                                                                                                                                                                                    ditrate transport protein - Klebsiella pneumoniae plasmid pES1
N;Alternate names: cirrate carrier
C;Species: Klebsiella pneumoniae: cirrate
C;Species: Klebsiella pneumoniae
C;Species: Klebsiella pneumoniae
C;Date: 12-Feb-1993 #text_change 26-Aug-1999
C;Accession: SO9681
R;van der Rest, M.E.; Schwarz, E.; Oesterhelt, D.; Konings, W.N.
Eur. J. Biochem. 189, 401-407, 1990
A;Title: DNA sequence of a citrate carrier of Klebsiella pneumoniae.
A;Reference number: SO9681; MUD:90249385; PMID:2186908
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A; Residues: 1-444 <RES>
A; Residues: 1-444 <RES>
A; Residues: 1-444 <RES>
A; Crosters: references: EMBL; X51479; NID:g43800; PIDN:CAA35844.1; PID:g43801
C; Genetics: plasmid pES1
C; Superfamily: citrate utilization determinant
C; Reywords: membrane protein
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                                                                                                                                         31 GYWMS 35
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C;Species: Peeudomonas aeruginosa ceruginosa (strain PAOI)
C;Species: Beeudomonas aeruginosa ceruginosa cipate: 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E39163
Resquence __revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E39163
Resquence __revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E39163
A;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
A;Aritle: Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic pathox A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                              C;&pecies: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Jory, S.; Olson, M.V.
Alture 406, 959-964, 2000
A;Reference numbers sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE004803; GB:AE004091; NID:g9950035; PIDN:AAG07250.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA3863
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-350 <STO>
A;Cross-references: GB:AE004508; GB:AE004091; NID:g9946611; PIDN:AAG04125.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein PA3863 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                       Nypothetical protein PA0736 [imported] - Pseudomonas aeruginosa (strain PAO1)
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C;Species: Homo sapiens (man)
C;Dete: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T00729.
R;Kochrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, May 1999
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80.0%; Pred. No. 2.7e+02;
iive 1; Mismatches 0; Indels
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Pred. No. 2.8e+02;
1; Mismatches 0; Indels
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A;Accession: T08724
A;Molecule type: mRNA
A;Residues: 1-417 <KOB>
A;Cross-references: EMBL:AL050275
A;Experimental source: fetal kidney; clone DKFZp566D213
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity
Matches 4, Conserva
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A;Molecule type: DNA
A;Residues: 1-375 <STO>
                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
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19 GYWLS 2
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                                                                                                                                                                                                                                                                                                                                                                    H86836
Carbamate kinase (EC 2.7.2.2) [imported] - Lactococcus lactis subsp. lactis (strain IL14
C;Species: Lactococcus lactis subsp. lactis
C;Accession: H86836
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Reference number: BR836
A;Status: preliminary
A;Molecule type: DNA
A;References: GB:AE005176; PID:g12724712; PIDN:AAK05794.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Genetics:
A;Genetics:
C;Keywords: phosphotransferase
C;Keywords: phosphotransferase
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R; Smith, D. R.; Doucette-Stamm, L. A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicainre, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Accession: G69142
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Mesidues: 1-348 cMTH>
A; Residues: 1-348 cMTH>
A; Cross-references: GB: AE000818; GB: AE000666; NID: G2621384; PIDN: AABB4839.1; PID: G262138
A; Experimental source: strain Delta H
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G69142
GDP-D-mannose dehydratase - Methanobacterium thermoautotrophicum (strain Delta H)
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 315;
                                                                     Length 298;
                                                              90.9%; Score 30; DB 2; Length 298
80.0%; Pred. No. 2.3e+02;
ive 1; Misma#ches 0; Indels
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Pred. No. 2.4e+02;
1; Mismatches 0;
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C;Superfamily: GDP-D-mannose dehydratase
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Similarity 80.0%;
4; Conservative 1
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Best Local Similarity
Matches 4; Conserv
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156 GYWMT 160
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45 GYWLS 49
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A; Gene: lin2373
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undecaprenyl-phosphate galactosephosphotransferase homolog - Actinobacillus actinomycete. CiSpecies: Actinobacillus actinomycetemcomitans
CiSpecies: Actinobacillus actinomycetemcomitans
CiSpecies: 2-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
CiAccession: T00113
Biochim: Alabaphys. Acta H42, 409-414, 1998
Biochim: Biophys. Acta H42, 409-414, 1998
A;Title: A gene cluster for 6-deoxy-L-talan synthesis in Actinobacillus actinomycetemcom A;Reference number: Z14111; MUID:99023768; PMID:9805002
A;Accession: T00113
A;Accession: T00113
A;Accession: T00113
A;Accession: T00113
A;Accession: T00113
A;Accession: T00113
A;Crosse-references: EMBL:AB010415; NID:g3132248; PIDN:BAA28142.1; PID:g3132265
A;Experimental source: strain NCTC 9710
C;Superfamily: xps2A protein
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R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 cKUR>
A;Cross-references: GB:AE005672; PIDN:AAK76187.1; PID:g14973641; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
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                                                            Length 417;
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                                         Score 30; DB 2; Length 41.7
Pred; No. 3.16+02;
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Pred. No. 3.3e+02;
1; Mismatches 0; Indels
                                             90.9%; Scc...
80.0%; Pred. No. 5...
1; Mismatches
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Matches 4; Conserv
                                                          Query Match
Best Local Similarity
Matches 4; Conserv
C;Genetics:
A;Note: DKFZp566D213.1
                                                                                                                                                              402 GYWLS 406
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A,Gene: SP2129
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salmonella

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJNE=8902113; PubMed=6181731;
MEDIJNE=8902113; PubMed=6181731;
Auffray C., Sikorav U.L., Ollo R., Rougeon F.;
Auffray C., Sikorav U.L., Ollo R., Rougeon F.;
MCOrrelation between D region structure and antigen-binding
specificity: evidences from the comparison of closely related
immunoglobulin VH sequences.
Ann. Immunol. (Paris) 132D:77-88 (1981).
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG GAMMA-2A MYELOMA
PROTEIN BINDING 2, 6-LEVAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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PIR; A02081; G2MSU1.
INCEPPO; IPR003006; Ig_MHC.
INCEPPO; IPR003596; Ig_V.
EnterPro; IRN00406; IGV.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
NON TER 117 AA; 13001 MW; B20A1074F8E99E7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 heavy chain V region UPC10.
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                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA
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                        SCRTA_BACSU
SPRA_HABIN
SPRA_HABIN
X119_MYCTU
GAOA_DACDE
VQVS_CABEL
VP4_ROTF6
VP4_ROTF6
VP4_ROTF7
WP4_ROTF7
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CIT1 KLEPN
ID CIT1 KLEPN STANDARD;
AC P164B2;
DT 01-AUG-1990 (Rel. 15, Created)
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31 GYWWS 35
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P01811;
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                                                                                                                                                  April 22, 2003, 12:46:53 ; Search time 2.5 Seconds (without alignments) 82.953 Million cell updates/sec
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P57057
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Copyright (c) 1993 - 2003 Compugen_Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                          112892 seqs, 41476328 residues
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CZCA ALCEU
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CIT1 KLEPN
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AMPR PROST
ARCC ENTFC
ARCD LACSK
ARCD CLOPE
PTSB STAXY
SYG ÄRRPE
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              - protein search, using sw model
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33
1 GYWMS 5
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RESULT 3
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                                                                                                                                                            Klebsiella pneumoniae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cltrate-proton symporter (Citrate transporter) (Citrate carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transport; Transmembrane; Inner membrane; Citrate utilization;
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EXTRACELLULAR (POTENTIAL)
4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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TIGRPAMS; TIGRO0883; 260106; 1.
PROSITE; PS00116; SUGAR_TRANSPORT_1; 2.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
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InterPro, IPR004736; Cit H. symport.
InterPro, IPR003662; sub_transporter.
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"DNA sequence of the SFT1 gene from Kluyveromyces lactis.";

"DNA sequence of the EMBL/GenBank/DDBJ databases

"Le FUNCTION: F-ACTIN CAPPING PROTEINS BIND IN A CA(2+)-INDEPENDENT

MANNER TO THE FAST GROWING ENDS OF ACTIN FILAMENTS (BARBED END)

THEREBY BLOCKING THE EXCHANGE OF SUBUNITS AT THESE ENDS. UNLIKE
OTHER CAPPING PROTEINS (SUCH AS GELSOLIN AND SEVERIN), THESE
OTHER CAPPING PROTEINS (SUCH AS GELSOLIN AND SEVERIN),

PROTEINS DO NOT SEVER ACTIN FILAMENTS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                    Kluyveromyces lactis (Yeast).
Bukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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                                                                                                                                                                                                                     16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
F-actin capping protein alpha subunit (Fragment).
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InterPro; IPR002189; F-actin_cap_A.
Pfam; PF01267; F-actin_cap_A; 1.
PRINTS; PR00191; FACTINCAPA.
Probom; PD006960; F-actin_cap_A; 1.
PROSITE; PS00748; F_ACTIN_CAPPING_A_1; 1.
PROSITE; PS00749; F_ACTIN_CAPPING_A_2; 1.
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053092;
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                                                                                                     Rock J.L., Bammaciogullari S., Parzy D., Barnaud G., TeysBou R.,
BuisBon Y., Philippon A., Arlet G.J.;
"Cloning and sequencing of ampC and ampR genes from Providencia
stuartii.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN IS A POSITIVE REGULATOR OF GENE EXPRESSION
OF BETA-LACTAMASE (AMPC).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecium (Streptococcus faecium), and
Enterococcus faecalis (Streptococcus faecalis).
Bacteria, Firmicutes, Lactobacillales, Enterococcaceae, Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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MEDLINE=94141928; PubMed=8308897;
Marina A., Bravo J., Fita I., Rubio V.;
"Crystallization, characterization and preliminary crystallographic
studies of carbamate kinase of Streptococcus faecium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Carbamate kinase from Enterococcus faecalis and Enterococcus faeciu
Coning of the genes studies on the enzyme expressed in Escherichia
coli, sequences similarity with N-acetyl-L-glutamte kinase.";
Submitted (REB-1998) to the EMBL/GenBank/DDBJ databases.
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Marina A., Uriarte M., Barcelona B., Fresquet V., Cervera J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.9%; Score 30; DB 1; Length 292; 80.0%; Pred. No. 82; 0; Indels rative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO00847; HTH LysR.
InterPro; IPRO0119; LysR_subst.
Pfam; PF001026; HTH 1; 1.
Pfam; PF00406; LysR_substrate; 1.
PROSITE; PS00049; HTH LYSR_FMILY; 1.
PROSITE; PS00044; HTH LYSR_FMILY; 1.
PROSITE; PS00046; HTH LYSR_FMILY; 1.
PROSITE: PS00046; HTH LYSR_FMILY; 1.
PROSITE; PS000464; HTH LYSR_FMILY; 1.
PS0004665; HTH LYSR_FMILY; 1.
PS0004665; HTH LYSR_FMILY; 1.
PS00046665; HTH LYSR_FMILY; 1.
PS0004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y17315; CAA76738.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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Best Local Similarity
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                                                                 SEQUENCE FROM N.A.
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                        NCBI_TaxID=588;
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                                                                                       STRAIN=VDG 96;
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  Providencia
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                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-98361904; PubMed-9696763;

Zuniga M., Champonier-Verges M., Zagorec M., Perez-Martinez G.;

Zuniga M., Champonier-Verges M., Zagorec M., Perez-Martinez G.;

Structural and functional analysis of the gene cluster encoding the enzymes of the arginine deiminase pathway of Lactobacillus sake.";

4. Bacteriol. 180:4154-4159(1998).

-i- FUNCTION: CATALYZES AN ELECTRONEUTRAL EXCRANGE BETWEEN ARGININE AND ORNIHINE TO ALLOW HIGH-FFFICIENCY ENERGY CONVERSION IN THE ARGININE DEIMINASE PATHWAY (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-i- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
                                                                         phosphate.
--- PATHMAY: Arginine degradation via arginine deiminase; third step.
--- SUBUNIT: HOMODIMER (PREDOMINANTLY) AND HOMOTETRAMER.
--- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
--- SIMILARITY: BELONGS TO THE CARBAMATE KINASE FAMILY.
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0
J. Mol. Biol. 235:1345-1347(1994).
-!- CATALYTIC ACTIVITY: ATP + NH(3) + CO(2) = ADP + carbamoyl
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 157 MISSING (IN REF. 2).
168 168 I -> D (IN REF. 2).
309 AA, 32795 MW, 5014514A7FEEB290 CRC64;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P99474; IEB9.
InterPro; IPR001048; Aa_kinase.
InterPro; IPR001046; Bac_carb_kinase.
InterPro; IPR003964; Bac_carb_kinase.
InterPro; IPR003964; Bac_carb_kinase.
TIGRFAMS; TIGR00746; arcc; 1.
Transferase; Kinase; Arginine metabolism.
ONFILCT 33 157 MISSING (IN REFCONFILCT 168 168 I -> D (IN REFSEQUENCE 309 AA; 32795 MW; 5014514A7FEEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ223331; CAA11270.1; -. EMBL; AJ223332; CAA11271.1; -. PIR; S44002;
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tes 4; Conserv
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or send an email to license@1sb-sib.ch).
                                                                     EMBL; AP003165; BAB79876.1; -.
InterPro; IPR00223; AA/Fal_prmeasel.
InterPro; IPR004841; Permease.
InterPro; IPR004754; R/O_antiport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                       EMBL; X97768; CAA66366.1; -.
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GYWLS 100
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P51184;
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MEDLINE=97199138; PubMed=9053381;
Ohtani K., Bando M., Swe T., Banu S., Oe M., Hayashi H., Shimizu T.;
"Collagenase gene (colA) is located in the 3'-flanking region of the perfringolysin O (pfcA) locus in Clostridium perfringens.";
FEMS Microbiol. Lett. 146:155-159(1997).
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-!- FUNCTION: CATALYZES AN ELECTRONEURAL EXCHANGE BETWEEN ARGININE
AND ORNITHINE TO ALLOW HIGH-EFFICEMOY ENERGY CONVERSION IN THE
ARGININE DEIMINASE PROMISSION IN SIMILARITY.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=13 / Type A;
PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Pred. No. 1.3e+02;
1; Mismafches 0; Indels
                                                                                                                               Amino-acid transport; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                  BE91A01F6A2203CC CRC64;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                 EMBL; AJ001330; CAA04686.1; -.
InterPro; IPR002293; AA/rel_prmease1.
InterPro; IPR004841; Permease.
InterPro; IPR004754; R/O_antiport.
Pfan; PF00324; aa_permeases; 1.
TIGRFAMs; TIGR00905; 2A0302; 1.
                                                                                                                                                                                                                                                                                                                                                                  51881 MW;
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80.0%;
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94 GYWLS 98
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Q46170;
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Mol. Gen. Genet. 241:33-41(1993).

-I- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
SUGAR PHOSPHOTRANSFERSE SYSTEM (FTS), A MAJOR CARBOHYDRATE ACTIVE
TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
AND THE TRANSMERANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
PHOSPHORYLATION SITE (THE DOWNE IS PHOSPHO-HPR); IIA TRANSFERS IT TO
PHOSPHORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
115-UNN-2002 (Rel. 41, Last annotation update)
PTS system, sucrose-specific IIBC component (EIIBC-SCR) (Sucrose-permease IIBC component) (Phosphotransferase enzyme II, BC component) (EC 2.7.1.69) (EII-SCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Сарв
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STRAIN-DSM 20367 / Isolate C2A;
MEDLINE-940495686; PubMed=8232209;
MEDLINE-940405686; FubMed=8232209;
MEDLINE-940409686; FubMed=8232209;
MEDLINE-94040566; FubMed=8232209;
MEDLINE-94040566; FubMed=8232209;
SEQUENCE FROM IT Of the phosphotransferase system from
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Pfan; PF00324; aa_pormeases; I.
TIGRROMS; TIGRO0905; 2A0302; I.
Transport; Antiport; Amino-acid transport; Transmembrane;
Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING (IN REF. 1).
MISSING (IN REF. 1).
A -> V (IN REF. 1).
G -> E (IN REF. 1).
W, A7BA24F7B53A344B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus xylosus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                                                                                                                                                                                                                                                              Complete proteome
SEQUENCE 583 AA
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P04480;
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CEA CITRR
CID - CEAA CITRR
AC P0448
DT 13-AU
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                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate
-!- + glycyl-tRNA(Gly).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
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MEDLINE=99310339; PubMed=10382966;
MEDLINE=99310339; PubMed=10382966;
MEDLINE=99310339; PubMed=10382966;
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukuii S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobtc hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i6-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2002 (Rel. 41, Last annotation update)
Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS).
GLYS OR APE1639.
                                                                                                                                                                                                                                                                                              InterPro; IFR001955; PTS_EIIB.

InterPro; IFR001955; PTS_EIIB.

Refam; PF00376; PTS_EIIB.

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Refam; PF00376; PTS_EIIB.

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Refam; PF00376; PTS_EIIB.

Refam; PTS_
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80.0%; Pred. No. 1.3e+02;
.ive 1; Mismatches 0; Indels
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          -!- SIMILARITY: CONTAINS 1 PTS EIIB DOMAIN.
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325
480 AA;
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Best Local Similarity
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MOD_RES
MOD_RES
SEQUENCE
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-!- FUNCTION: THIS COLICIN IS A CHANNEL-FORMING COLICIN. THIS CLASS OF TRANSMEMBRANE TOXINS DEPOLARIZE THE CYTOPLASMIC MEMBRANE, LEADING TO DISSIPATION OF CELLULAR ENERGY.

-!- FUNCTION: COLICINS ARE POLYEPETIDE TOXINS PRODUCED BY AND ACTIVE AGAINST, ESCHERICHIA AOLI AND CLOSELY RELATED BACTERIA.

-!- SIMILARITY: BELONGS TO THE CHANNEL FORMING COLICIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morlon J., Lloubes R., Varenne S., Chartier M., Lazdunski C.; "Complete nucleotide sequence of the structural gene for colicin A, a gene translated at non-uniform rate."; J. Mol. Biol. 170:271-285 (1983).
                                                                                                                                                                                                                                                                   PRINTS, PRO1043; TRNASYNTHGLY.
TIGRRAMs; TIGR00389; G1yS dimeric; 1.
PROSITE; PS50862; AA TRNA_LIGASE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE=88174422; PubMed=2832701;
Morlon J., Chartier M., Bidaud M., Lazdunski C.;
Mhe complete nucleotide sequence of the colicinogenic plasmid ColA.
High extent of homology with ColE1.";
Mol. Gen. Genet. 211:231-243 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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MEDLINE=22235820; PubMed=1373773;
Parker M.W., Postma J.P.M., Pattus F., Tucker A.D., Tsernoglou D.;
"Refined structure of the pore-forming domain of colicin A at 2.4-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 1; Length sos
Pred. No. 1.66+02;
Or Indels
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13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                    HSSP, P56206; 1ATI.
INCEPTO, IPRO02106; AACRNA_ligaseII.
INCEPTO; IPRO04154; HGTP_anticodon.
INCEPTO; IPRO02314; tRNA-synt_2b.
INCEPTO; IPRO02315; tRNA-synt_gly.
Pfam; PF00159; tRNA-synt_gly.
Pfam; PF03129; HGTP_anticodon; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=84036205; PubMed=6313941;
EMBL; AP000062; BAA80640.1; -.
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Reymond P., Geourjon C., Roux B., Durand R., Fevre M.;
Reymond P., Geourjon C., Roux B., Durand R., Fevre M.;
Sequence of the phosphoenolypyruvate carboxykinase-encoding CDNA from the rumen anaerobic fungus Neocallimastix frontalis: comparison of the rumen anaerobic fungus Neocallimastix frontalis: comparison of the rumen and sequence with animals and yeast.";
Gene 110:57-63(1992).
--- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                             EMBL, M3/40/2; ANSIANI IKEBCA.
PIR; A03504; IKEBCA.
PBB; 1COL; 15-UUL-93.
PBB; 1COL; 15-UUL-93.
PINCAFPRO; IPR00229; Channel_colicin.
PFANTYS; PR0024; Colicin; 1.
PROSITE; PS00276; CHANNEL_COLICIN.
PROSITE; PS00276; CHANNEL_COLICIN; 1.
PROSITE; PS00276; CHANNEL_COLICIN; 1.
Antiblotic; Bacteriocin; Plasmid; Transmembrane; 3D-structure.
TRANSMEM 528 548
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                    90.9%; Score 30; DB 1; Length 592; llarity 80.0%; Pred. No. 1.6e+02; Conservative 1; Mismatches 0; Indels
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Eukaryota, Fungi, Chytridiomycota, Neocallimasticales;
Neocallimasticaceae; Neocallimastix.
                                                                                                                                                                                                                                                                                                                                                                                62992 MW; B80FA1F52A8CFC5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P22130;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         608 AA.
                               EMBL; X01008; CAA25503.1; -. EMBL; M37402; AAA72879.1; -.
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                                                                                                                                                   Local Similarity
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|36 GYWLS 140
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P22130;
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01-MAY-1991 (Rel. 18, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ENV polyprotein precursor [Contains: Knob protein GP70; Spike protein PISE].
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InterPro; IPR002050; Env_polyprotein.
Pfam; PF00429; ENV_polyprotein; 1.
Coat protein; Glycoprotein; Polyprotein; Transmembrane; Signal.
1 42 KNOB PROTEIN GP70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gibbon ape leukemia virus.
Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
VCBI_TaxID=11840;
                                                                                                                                                                                                                    EMBL; M59372; AAA33533.1; -.

PIR; JQ1462; JQ1462;
InterPro; IPR000034; PEP_carboxykin.

Promom; PD004739; PEP_carboxykin; 1.

PROSITE; PS00505; PEPCR GTP; 1.

Qluconeogenesis; Lyase; Decarboxylase; GTP-binding.

NP BIND 217 224 GTP (POTENTIAL).

ACT SITE 269 Z69 POTENTIAL.

SEQUENCE 608 AA, 66904 MW; C4D2B249A92B7D26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
C4D2B249A92B7D26 CRC64;
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Delassus S., Sonigo P., Waln-Hobson S.;
"Genetic organization of gibbon ape leukemia virus.";
Virology 173:205-213(1989).
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SPIKE PROTEIN PISE.
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P21415;
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                                                                                                                                                                                                                                                 MEDLINE=97420683; PubMed=9276668;
Takai K., Sako Y., Uchida A., Ishida Y.;
Takai K., Sako Y., Uchida A., Ishida Y.;
"Extremely thermostable phosphoenolpyruvate carboxylase from an extreme thermostable, Rhodothermus obamensis.";
J. Blochem. 122:32-40(1997).
-!-FUNCTION: TO FORM OXALOACETATE, A FOUR-CARBON DICARBOXYLIC ACID SOURCE FOR THE TRICABBOXYLIC ACID CYCLE. THE OPTIMUM TEMPERATURE FOR ACTIVITY IS 75 DEGREES CELSIUS. THE BNZYME EXHIBITS A PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p135I1, P94142;
01-JNN-1990 (Rel. 13, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cobalt-zinc-cadmium resistance protein czcA (Cation efflux system
                                                             Phosphoenolpyruvate carboxylase (BC 4.1.1.31) (PEPCASE) (PEPC) PPC OR PEPC.
                                                                                                                            Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
Crenotrichaceae; Rhodothermus.
NCBI_TaxID=29549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
Ralstonia.
NCBI_TaxID=510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.9%; Score 30; DB 1; Length 936;
80.0%; Pred. No. 2.5e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          OPTIMUM OF 8.0. CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle. AcT SITE 155 155 BY SIMILARITY. ACT SITE 55 55 55 SS BY SIMILARITY. SEQÜENCE 936 AA; 107886 MW; C9AA94C3F26C345A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphoenolpyruvate + CO(2).
--- CORACTOR: ABSOLUTE REQUIREMENT FOR DIVALENT CATIONS.
--- PATHWAY: Tricarboxylic acid cycle.
--- SUBUNIT: HOMOTETRAMER.
--- SUBILARITY: BELONGS TO THE PEPCASE FAMILY.
              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                              Rhodothermus marinus (Rhodothermus obamensis)
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Plasmid pMOL30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0150; PEPCARBILASE.
PROSITE; PS00393; PEPCASE 2; 1.
PROSITE; PS00781; PEPCASE 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001449; PEPcase.
Pfam; PF00311; PEPcase; 1.
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GYWMA 602
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Alpha-glucuronidase precursor (EC 3.2.1.139) (Alpha-glucosiduronase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR005154; Glyco hydro 67.
Pfam; PF03648; Glyco hydro 67; 1.
Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
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"The alpha-glucuronidase-encoding gene of Trichoderma reesei.";
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(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                Trichoderma reesei (Hypocrea jecorina).
Eukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Hypocreaceae; Hypocreales; Hypocreales; Cordariomycetes; NCBI_TaxID=51453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO FAMILY 67 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 847;
                                  90.9%; Score 30; DB 1; Length 667;
80.0%; Pred. No. 1.8e+02;
iive 1; Mismatches 0; Indels
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  73729 MW; SFFB32F00D8631BE CRC64;
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STRAIN=QM9414 / Rut C-30;
MEDLINE=96257277; PubMed=8654984;
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847 AA;
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180 GYWLS 184
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                                                                                                                                                                          Pagens W., Schel P.O., Nies D.H.;
Backens W., Scheel P.O., Nies D.H.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-I. FUNCTION: HAS A LOW CATION TRANSPORT ACTIVITY FOR CO(2+), IT IS
-ESSENTALE FOR THE EXPRESSION OF COBALT, ZNC, AND CADMIUM
RESISTANCE. CZCA AND CZCB TOGETHER WOULD ACT IN ZN(3+) EFFLUX
NEARLY AS EFFECTIVELY AS THE COMPLETE CZC EFFLUX SYSTEM (CZCABC).
-I. SUBCELLIAGAR LOCATION: Integral membrane protein (Probable).
-I. INDUCTION: BY CADMIUM, COPPER AND ZINC.
-I. SIMILARITY: BELONGS TO THE ACRB/ACRD/ACRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                              STRAIN=CH34;
MEDLINE=90017477; PubMed=2678100;
Nies D.H., Nies A., Chu L., Sllver S.;
MEXpression and nucleotide sequence of a plasmid-determined divalent cation efflux system from Alcaligenes eutrophus.";
Proc. Natl. Acad. Sci. U.S.A. 86:7351-7355(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X98451; CAA67084.1; -.
BHR; A31840; A31830.
InterPro; IPR001035; CzcA.
InterPro; IPR004763; CzcA.
Emm; PF006973; ACK tran; 1.
TIGRFAM9; TIGR00914; ZA6601; 1.
Plasmid; Transport; Zinc; Cobalt; Cadmium resistance; Transmembrane.
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80.0%; Pred. No. 2.8e+02;
tive 1; Mismatches 0; Indels
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115668 MW; 1E9587923996AEBC CRC64;
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STRAIN=CH34;
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1063 AA;
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Search completed: April 22, 2003, 12:51:50 Job time : 4.5 secs

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Query Match
100.0%; Score 33; DB 17; Length 67;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels
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09iag7 hippopotamy
09iag3 hippopotamy
09iag2 hippopotamy
09iag1 hyperopisus
09iag1 hyperopisus
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                                                       April 22, 2003, 12:47:43; Search time 10 Seconds (without alignments) 103.024 Million cell updates/sec
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        GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                671580 seqs, 206047115 residues
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sp_plant:*
sp_rodent:*
sp_virus:*
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sp_vertebrate:*
sp_monlassified:*
sp_monlassified:*
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sp_bacteria:*
sp_fungi:*
sp_fungan:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_bacteriap:*
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Maximum DB seq length: 200000000
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PEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMed=11016950;

MEDLINE=2050483; PubMed=11016950;

MEDLINE=
                         Ogiaf6 marcusenius Ogiaf5 marcusenius Ogiaf5 marcusenius Ogiae1 marcusenius Ogiae2 mormyrus ru Ogiae6 paramormyro Ogiae0 pollimyrus Ogiae0 pollimyrus Ogiae0 pollimyrus Ogiae0 stomatorhin Ogiae6 stomatorhin Ogiae3 stomatorhin Ogiae3 escherichia Ogiae3 escherichia Ogiae3 escherichia
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032816 lactococcus
0997x3 philotrypes
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Q925x5 listeria in
Q9bt16 homo sapien
                marcusenius
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Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Q9JMR3
Q9ZGR9
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Q91AF4
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Q925X5
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Q9IAF7
Q9IAF6
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Gaps ; 0

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PRELIMINARY;
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GYWMS 372
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Sullivan J.P., Lavoue S., Hopkins C.D.;

Sullivan J.P., Lavoue S., Hopkins C.D.;

Sullivan d.P., Lavoue S., Hopkins C.D.;

Sullivan J.P., Lavoue S., Hopkins C.D.;

Teleostei) and a model for the evolution of their electric organs.";

J. Exp. Biol. 203:665-683 (2000).

EMBL, AP201625; AAF43336.1; -..

EMBL, AP201624; AAF43336.1; -..

InterPro; IRR004331; RAG2.

Ffam, PP03089; RAG2; 1.

NON TER 177 377

SEQÜENCE 377 AA, 41387 MW; D52A9E361A56AB43 CRC64;
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SEQUENCE FROM N.A.

Sullivan J.P., Lavoue S., Hopkins C.D.;

Sullivan J.P., Lavoue S., Hopkins C.D.;

Sullivan J.P., Lavoue S., Hopkins C.D.;

"Molecular systematics of the African electric fishes (Mormyroidea:

"Molecular systematics of the African electric organs.";

Teleostei) and a model for the evolution of their electric organs.";

D. Exp. Balol. 203:665-683(2000).

EMBL, AF201616; AAF44321; RAG2.

InterPro; IPR004321; RAG2.

InterPro; IPR004321; RAG2.

NON TER.

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Q1-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
Boulengeromyrus knoepffleri.
Bukaryota; Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Boulengeromyrus.
                                                                                                                      Bukāryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Osteoglossomorpha,
Osteoglossiformes, Mormyridae, Campylomormyrus.
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                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
Campylomormyrus tamandua.
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Best Local S:
Matches 5,
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Q91867
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SEQUENCE FROM N.A.

MEDLINE=20115608; PubMed=10648209;
Sullivan J.P., Lavoue S., Hopkins C.D.;
Sullivan J.P., Lavoue S., Hopkins C.D.;
"Molecular systematics of the African electric fishes (Mormyzoidea:
"Molecular systematics of the African electric organs.";
J. Exp. Biol. 203:665-683(2000).
Interpro; IPR004321; RAG2.
Interpro; IPR004321; RAG2.
Pfam; PR03089; RAG2; 1.

NON TER 1

NON TER 377 377
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"Molecular systematics of the African electric fishes (Mormyroidea:
"Molecular systematics of the African electric fishes (Mormyroidea:
Teleostei) and a model for the evolution of their electric organs.";
J. Exp. Biol. 203:665-683(2000).
ENBL; AP201618; AAF43329.1; -.
Fran, PP03089; RAG2:
NON TER 1
NON TER 377 377
SEQÜENCE 377 AA; 41403 MW; 0A4599C6604C8123 CRC64;
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neoptengii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Brienomyrus.
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostai; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Brienomyrus.
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llarity 100.0%; Pred. No. 2.2e+02;
Conservative 0; Mismatches 0; Indels 0
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                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment)
Brienomyrus hopkinsi.
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01-OCT-2000 (TrEMBLrel. 15, Last asquence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
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PRT;
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                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=112141;
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RESULT

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MEDLINE=20115608; PubMed=10648209;
Sullivan J.P., Lavoucue S., Hopkins C.D.;
Teleostei) and a model for the evolution of their electric organs.";
J. Exp. Biol. 203:665-683(2000).
BEMBL; AR201623; AAF4334.1; -.
InterPro; IPR004321; RAG2.
Pfam; PF03089; RAG2; 1.
NON_TER 1 1
NON_TER 377 377
SEQÜENCE 377 AA; 41357 MW; DDA7ED06162C799A CRC64;
                                                                                                                                                                                                                                                                   MEDIJIRE=20115608; bubMed=10648209; Sullivan J.P., Lavoue S., Hopkins C.D.; Sullivan J.P., Lavoue S., Hopkins C.D.; Medicaliza eystematics of the African electric fishes (Mormyroidea: molecular systematics of the African electric fishes (Mormyroidea: Most.) and a model for the evolution of their electric organs."; J. Exp. Biol. 203:665-683(2000).

EMBL, ARZOIGE2; ARR43333.1; -.

InterPro; IPR004321; RAG2.

Pfam; PF03089; RAG2; 1.

NON_TER 1 1

NON_TER 377 377

SEQÜENCE 377 AA; 41360 MW; COE574061A4C986A CRC64;
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01-0CT-2000 (TrEWBLrel. 15, Last sequence update)
01-0CT-2000 (TrEWBLrel. 15, Last annotation update)
1-0CT-2000 (TrEWBLrel. 15, Last annotation update)
Recombination-activating protein 2 (Fragment).
Campylomormyrus sp. JPS1-2000.
Campylomormyrus sp. JPS1-2000.
Actinopterygii; Neopterygii; Teleostel; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Campylomormyrus.
                                                                                                                             Campylomormyrus numenius.
Bukaryota; Merezoa; Chordat; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Campylomormyrus.
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100.0%; Pred. No. 2.2e+02;
Live 0; Mismatches 0; Indels 0
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                                     01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
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368 GYWMS 372
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Q9IAG9
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MEDILINE-20115608; PubMed=10648209;
Sullivan J.P., Lavoue S., Hopkins C.D.;
Sullivan J.P., Lavoue S., Hopkins C.D.;
"Molecular systematics of the African electric fishes (Mormyroidea: Teleostei) and a model for the evolution of their electric organs.";
Teleostei) and a model for the evolution of their electric organs.";
Teleostei) and a model for the Perula State of their electric organs.";
EMBL, AP201621; AAF43332.1;
InterPro; IRR044321; RAG2.
Pfam; PF03089; RAG2;
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Metaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Brienomyrus.
                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Brienomyrus.
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377 AA; 41522 MW; 2E93DC79A8B6EC4A CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
                                          091AH2;
01-0CT-2000 (TrEWBLrel. 15, Created)
01-0CT-2000 (TrEWBLrel. 15, Last sequence update)
01-DEC-2001 (TrEWBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
Brienomyrus niger.
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                          377 AA
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Best Local Similarity 100..
Lag 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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368 GYWMS 372
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Q9IAG2
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AC Q9IAG3
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1-000 (TrEMBLrel. 15, Created)
01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Geompomyrus donnyi.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ostinopterygii; Neopterygii; Teleostei; Osteoglossicomorpha;
Osteoglossiformes; Mormyridae; Genyomyrus.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
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Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0;
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Q91AG4;
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Q9IAG4
ID Q9IAG4
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"Molecular systematics of the African electric fishes (Mormyroidea:
Teleostei) and a model for the evolution of their electric organs.";
J. Exp. Biol. 203:665-683(2000).
EMBL; AF201630; AAF43341.1;
-.
InterPro; IPR004321; RAG2.
Pfam; PF03089; RAG2; 1.
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MEDLINE=20115608; PubMed=10648209;

Sullivan J.P., Lavouce S., Hopkins C.D.;

Sullivan J.D., Lavouce S., Hopkins C.D.;

Sullivan J.D., Lavouce S., Hopkins C.D.;

Teleostei) and a model for the evolution of their electric organs.";

J. Exp. Biol. 203:665-683 (2000).

Exp. AF201631; AAF43342.1; -.

InterPro; IPR004321; RAG2.

Pfam; PF03089; RAG2; 1.

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NON_TER 377 377

SEQÜENCE 377 AA; 41491 MW; 1BE26037590CA937 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Recombination-activating protein 2 (Fragment).
Hippopotamyrus pictus.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei, Osteoglossiformes, Mormyridae, Hippopotamyrus.
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2010 (TrEMBLrel. 19, Last annocation update)
01-DEC-2010 (TrEMBLrel. 19, Last annocation update)
Recombination-activating protein 2 (Fragment).
Hippopotamyrus discorbynchus (Zambezi parrotfish).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygli; Neopterygli; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Mormyridae; Hippopotamyrus.
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NON TER 377 377
SEQUENCE 377 AA, 41293 MW, 9F7C51AF89B736C4 CRC64;
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Q91AG2;
01-OCT-2000 (TrEMBLrel. 15, Created)
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MEDLINE=20115608; PubMed=10648209;
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Sullivan J. P., Layoue S., Ropkins C.D.;
Sullivan J. P., Layoue S., Ropkins C.D.;
Molecular systematics of the African electric fishes (Mormyroidea: Molecular systematics of the African electric organs.";
J. Exp. Biol. 203:665-683(2000).
EMBL; AF201633; AAR43344.1; -.
Pfam; PF03089; RAG2; 1.
NON_TER 1
NON_TER 377 377
SEQÜENCE 377 AA; 41324 MW; C3C5A2BBE34EF6FC CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 15, Last annotation update)
Recombination-activating protein 2 (Fragment).
Hyperoplaus bebe.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha; Osteoglossiformes; Mormyridae; Hyperopisus.
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hippopotamicon-activating protein 2 (Fragment).
Hippopotamyrus wilverthi.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
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100.0%; Score 33; DB 13; Length 377;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels
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Best Local Similarity
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                                                                                                                     NCBI_TaxID=112149;
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
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1: /SIDS2/gcgdata/
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Maximum DB seq length: 2000000000
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33
1 GYWMS 5
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                                                                                                                                                                        OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
•		ا حث				
Result No.	Score	Query	Query Match Length DB	DB	ID	Description
1	33	100.0		21	AAY32257	Light chain CDR H1
1 6	(M)	100.0				Mouse anti-CD23 MA
ı	9.6	100.0		21	AAY32263	Humanised anti-CD2
4	33	100.0	1254	22	ABB62006	Drosophila melanog
'n	30	6.06				Novel human diagno
•	30	90.9				V39, monoclonal an
7	30	6.06				Human secreted pro
. 00	30	6.06		20		Chlamydia pneumoni
6	30	6.06				Novel signal trans
10	30	6.06	242		AAY76114	Rat HT glycoprotei

(GLAX ) GLAXO GROUP LTD.

Skin cell protein, Rat protein isolat Rat protein isolat Rat protein isolat Staphylococcus epi Enterococcus faeca	GALV retrovirus su Lactococcus lactis Arabidopsis thalia Activating polypep Arabidopsis thalia Human secreted pro	acid seq ke homol PRO214 p PRO214 a polypept	Human FROZI4, Homo sapi Human PROZI4 prote Human TANGO 206 po Mouse TANGO 206 po Human TANGO 206 va Human TANGO 206 va Human TANGO 206 va Human TANGO 206 va	TANGO 206 TO
22 AAB56053 23 ABB72253 23 ABB72290 23 ABB72301 23 ABP39269 22 AAU35317	AAB1986 ABB5504 AAG3198 AAB1987 AAG3198			22 AAB48135 22 AAB48136 22 AAB48137 22 AAB48138 23 AAB5431 23 ABB5431 23 AAU33652 23 AAU37919 21 AAY81542 23 ABP25669
		,	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.9.		000000000000000000000000000000000000000		, , , , , , , , , , , , , , , , , , ,
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11 12 13 14 15	110 118 118 110 110 110	7 6 5 5 4 3 V	2 2 2 2 2 2 2 2 2 2 3 4 3 4 4 4 4 4 4 4	6 U U U U U U 4 4 4 4 4 4 N O C O O O O I I I W 4 N

## ALIGNMENTS

CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementerarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria, nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; slogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graft-versus-host disease; CoPD; bronchitis; diabetes; B-cell malignancy; therapy. Light chain CDR H1 of mouse anti-CD23 MAb C11. AAY32257 standard; Peptide; 5 AA. 99WO-GB01434. 98GB-0009839. 15-FEB-2000 (first entry) 07-MAY-1999; 09-MAY-1998; WO9958679-A1 Mus musculus 18-NOV-1999. AAY32257; RESULT 1  N

us-09-674-716b-9.open.rag

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59 GYWMS 63
                        07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GYWMS 5
                                                09-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY32263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            유
                                                                                                                                                                                                                                                                                                                                                                                                                o,
                                                                                                                    This sequence represents complementarity determinating region 1 (CDR HI) of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11 (see also AAY32263). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise utilities to the amino acid sequences of C11 light and heavy chain CDRs (see AAY3254-59) to render them. Teapable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus exthematous, Hashimoto's thyroiditis, multiple sclerosis, clabetes, uveit1s, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogran's syndrome, allergies, allergic asthma, intrinsic asthma, acte asthma, acted asthma, colitis, bronchitis or czema, graft-versus-host disease, CODP, insulitis, bronchitis disbetes), and B-cell malignancies (claimed). They are also useful for etermining the binding agents.
                                                          Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythepatosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psorlasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; slogren's syndrome; allergy; aethma; rhinitis; eczema; insulitis; graff.-vergus-host disease; COPD; bronchitis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                ö
Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 33; DB 21; Length 5; 100.0%; Pred. No. 7.8e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse anti-CD23 MAb C11 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY32260 standard; Protein; 137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "CDR H1"
78..96
/note= "CDR H2"
129..131
/note= "CDR H3"
                                                                                               Claim 1; Page 40; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B-cell malignancy; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 5; Conservative
                      WPI; 2000-053101/04.
                                   N-PSDB; AAZ34742
                                                                                                                                                                                                                                                                                                                                                                5 AA;
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                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY32260;
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This sequence represents the heavy chain variable region (VH) of murine anti-CD23 (FCERII) monoclonal antibody Cl1. The invention provides altered antibodies, such as chimeric or humanised antibodies (see AAY32262 and AAY32263), which comprises sufficient of antibodies (see AAY32262 and AAY32263), which comprises sufficient of the amino acid sequences of the Cl1 light and heavy chain complementarity determining regions (see AAY32254-59) for render them capable of binding to the CD23 type II molecule expressed on hammatopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, lubus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, clubus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, lubus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, claberes, uveltis, dermatitis, psoriasis, uritoraria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulerative colitis, trohn's disease, is spring, asthma, acute asthmatic excension; xinnitis, eccema, graft-versus-host disease, COPD, insulitis, bronchitis (particularly tronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful cetermining the binding agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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Pred. No. 69;
                                                                                                                                                                                                                                                                     Crowe SJ, Ellis JH, Rapson NT, Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Fig 1; 81pp; English.
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99WO-GB01434.
                                                                                          98GB-0009839.
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                                                                                                                                                                               (GLAX ) GLAXO GROUP LTD
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N-PSDB; AAZ34745.
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(first entry)

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGITG-ABL30511), expressed DNA sequences (ABLIGITG-ABL30511),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                  Drosophila, developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 12810; 21pp + Sequence Listing; English.
                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 12810.
ABB62006 standard; Protein; 1254 AA.
                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75.
N-PSDB; ABL06109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY
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                                                                                    26-MAR-2002
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ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This amino acid sequence represents the heavy chain of humanised anti-CD23 (FCERI) monoclonal antibody C11, composed of a human framework (HSIGKVI) and the heavy chain complementarity determining regions (see AAY32257-59) of murine antibody C11. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, such as chimaris or humanised antibodies, which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions to render them comprise sufficient of the maino acid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on hamancopoietic cells. The antibodies are used to block soluble charactoric in human therapy, for the treatment of arthritis, lugus erythematorous, Hashimoto's hypoiditis, multiple solerosis, clabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, crohn's disease, Sjogram's syndrome, allergies, allergies cathma, intrinsic asthma, acte asthmatic exacerbation, rhinitis, estema, graft-versus-host disease, COPD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly chronic bronchitis) or diabetes (particularly chronic bronchitis) or diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 33; DB 21; Length 444; 100.0%; Pred. No. 2.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rapson NT,
                                                                                                                                                                                                                                                                                                  /note= "framework region 4"
112..444
/note= "constant region"
                                      note= "framework region 1"
                                                                                                                                                                                                                    region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crowe SJ, Ellis JH,
                                                                                                                                                                           /nocc
69..100
'--a= "framework r
ocation/Qualifiers
                                                                                                         36..49
/note= "framework r
50..68
/note= "CDR 2"
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101..103
--- "CDR 3"
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                                                                                "CDR 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonnefoy JMP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                      W09958679-A1
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Key
Region
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Matches
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Myers EW;

Li PWD,

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(ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                    ö
                                                                                                                   Length 1254;
                                                                                                                                                    0; Indels
                                                                                                                   h 100.0%; Score 33; DB 22; Similarity 100.0%; Pred. No. 6.6e+02; 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #7524.
                                                                                                                                                                                                                                                                                                       ABG07533 standard; Protein; 40 AA.
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                   1254 AA;
                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                      1139 GYWWS 1143
                                                                                                                                                                                      1 GYWMS 5
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                                                                                      Sequence
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Gaps ó

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RESULT 4
ABB62006

4

us-09-674-716b-9.open.rag

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Human, secreted protein; prevention; treatment; protein therapy; gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; lymphoma; developmental abnormality; foetal deficiency; blood disorder; lymphoma; leukemia; immune system disorder; autoimmune disease; hepatic disease; renal disease; inflammation; allergy; asthma, sepais; diabetes; AIDS; Altheimer's disease; cognitive disorder; schizophrenia; osteoporosis; arthritis; psoriasis; digestive; endocrine; infection.
                                                                                                                                                                                                                                                                                                                                                                                                            AAR95459-R95509 are antigen binding peptides ("abtides") derived from the monoclonal antibody SM-3 which recogniese a specific polymorphic epithelial mucin tummour antigen found on human breast cancer cells. The abtides are identified from random peptide libraries using specific ligand binding. Abtides mimic the binding specificity of large molecules such as antibodies and receptors but have a much smaller size allowing their production at a lower cost and reducing the extent of their immunogenicity aiding in vivo delivery. The abtides are useful for the diagnosis, detection, imaging and treatment of disease, e.g. tumours, prostate cancer and breast
                                                                                                                                                                                                                                                                                    New isolated peptide(s) with specific binding activities - obtd. by screening random peptide libraries, for use in diagnostic and therapeutic compsns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.9%; Score 30; DB 17; Length 43; 80.0%; Pred. No. 77; 0; Indels .ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein fragment encoded from gene 70.
                                                                                                                                                                                                                                                                                                                                                                          Claim 38; Page 75; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY07813 standard; Protein; 64 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0092956.
98US-0092956.
97US-0056368.
97US-0056369.
                                                        95WO-US11934.
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                                                                                                 95US-0488161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                (CYTO-) CYTOGEN CORP
                                                                                                                                                                                                                                                WPI; 1996-188471/19.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 GYWLS 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JUN-1998;
15-JUL-1998;
19-AUG-1997;
19-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9909155-A1.
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                                                        20-SEP-1995;
                                                                                                 07-JUN-1995;
21-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1999.
                    28-MAR-1996
                                                                                                                                                                                                         Alvarez VL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polymuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polyperide are also used in diagnostics as expressed sequence tags for identifying expressed sequence. (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving contrating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in dispositios, foremsics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Aggioungland or appear in the printed agancetic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the vive or the produces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V39, monoclonal antibody SM-3 derived antigen binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 22; Length 40;
Pred. No. 71;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID No 37892; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR95472 standard; peptide; 43 AA.
                                                                                                                                                                                                                           Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.94;
                                                                               30-MAR-2001; 2001WO-US08631.
                                                                                                                     31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-NOV-1996 (first entry)
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                                                                                                                                                                                                                                                                  WPI; 2001-639362/73.
N-PSDB; AAS71720.
                                                                                                                                                                                                                           Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 AA;
WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||:|
GYWLS 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GYWMS 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9609413-A1.
                                      11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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181 AA;
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                                                                 (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                          1 GYWMS 5
            20-NOV-1998;
                                  04-NOV-1998;
                                            21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                      |||:|
48 GYWLS
                                                                                       Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU17327;
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU17327
                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                          This invention describes novel isolated human secreted proteins and their encoding nucleic acid sequences. The products of the invention are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the presence or amount of expression of the new polypeptides in a sample or by determining the presence or absence of mutations in the new polynucleotides. Specific uses are described for each of the 70 polynucleotides. Specific uses are the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune of sections in the section of all diseases, lamphomas, inflammation, allergies, asthma, seppis, diabetes, halphimer's and cognitive disorders, schizophrenia, osteoporosis, arthritis, psoriasis, digestive/endocrine clinomare represented in AAX37169-X37441.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                              New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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                                                                                                                      DW;
Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.9%; Score 30; DB 20; Length 64;
80.0%; Pred. No. 1.2e+02;
/ative 1; Mismatches 0; Indels
                                                                                                            Feng P;
Lafleur I
Shi Y, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia pneumoniae transmembrane protein sequence.
                                                                                                           A, Duan R, Ebner R, Endress GA, C, Florence KA, Komatsoulis GA, Olsen HS, Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ļ
                                                                                                                                                                                                                                        Claim 1b; Page 264; 280pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY35482 standard; Protein; 181 AA.
97US-0056535.
97US-0056555.
97US-0056528.
97US-0056528.
97US-0056728.
                                                                                       (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                WPI; 1999-190160/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 AA;
                                                                                                                                                                           N-PSDB; AAX37438.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GYWMS 5
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                                                      19-AUG-1997;
            19-AUG-1997
  19-AUG-1997
                                19-AUG-1997
                                            19-AUG-1997
                                                                                                                     Florence C,
Moore PA,
Young PE;
                                                                                                             Brewer LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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AAY35482
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Neuroprotective, cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV, antibacerial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alabeimer's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; ardicatory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlbS; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX31990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent critis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 1244; Disclosure; 1912pp; English.
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04-PEB-2000; 2000US-0180628.
24-PEB-2000; 2000US-0184664.
02-MAR-2000; 2000US-0186350.
16-MAR-2000; 2000US-0189874.
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                                                                         98US-0107078.
97FR-0014673.
98WO-IB01890
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Best Local Similarity
Matches 4; Conserv
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                                 2000US-0205515.
2000US-0205515.
2000US-02014867.
2000US-0215135.
2000US-0215135.
2000US-0215135.
2000US-0215135.
2000US-0215135.
2000US-02250513.
2000US-0225266.
2000US-0225267.
2000US-0225267.
2000US-0225267.
2000US-0225267.
2000US-0225267.
2000US-0225268.
2000US-0225268.
2000US-0225269.
2000US-023249.
2000US-0232399.
2000US-0232399.
2000US-0232399.
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2000US-0232399.
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2000US-0232399.
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2000US-0236369.
2000US-0236370.
2000US-0236802.
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2000US-0235484.
2000US-0235834.
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2000US-0236327.
2000US-0236367.
117-MAR-2000;
18-AZR-2000;
07-JUN-2000;
28-JUN-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
14-AUG-2000;
11-AUG-2000;
11-AUG-2000;
11-AUG-2000;
11-AUG-2000;
11-AUG-2000;
11-AUG-2000;
12-AUG-2000;
12-AUG-2000;
13-AUG-2000;
13-AUG-2000;
13-AUG-2000;
13-AUG-2000;
10-AUG-2000;
10-AUG-2000;
11-AUG-2000;
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02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
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13-OCT-2000; 2000US-0249937.
20-OCT-2000; 2000US-0241086.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241787.
20-OCT-2000; 2000US-0241826.
20-OCT-2000; 2000US-0241826.
20-OCT-2000; 2000US-0241826.
20-OCT-2000; 2000US-0244617.
20-OCT-2000; 2000US-0246475.
20-OCT-2000; 2000US-0246476.
20-OCT-2000; 2000US-0246476.
20-OCT-2000; 2000US-0246476.
20-OCT-2000; 2000US-0246521.
20-OCT-2000; 2000US-024921.
20-OCT-2000; 2000US-025198.
20-OCT-2000; 2000US-025198. 

(HUMA-) HUMAN GENOME SCI INC

Ruben SM, Barash SC, Rosen CA,

WPI; 2001-465460/50. N-PSDB; AAS27244.

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders

Claim 1; SEQ ID No 892; 880pp; English

The invention relates to novel isolated polypeptides (I),

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polynucleotides (II). (I) (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiancies, autoimmune tisorders (e.g. congenital and acquired immunodeficiancies, autoimmune transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis O.) bleeding disorders, hemoglobin abnormalities and cher blood-related disorders (e.g. hepatitis disorders (e.g. disorders (e.g. disorders), primary haematopoietic disorders, hyperproliferative disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. disorders (e.g. disorders), neurodegenerative disorders (e.g. disorders (e.g. disorders), respiratory disorders (e.g. stroke), renal alsorders (e.g. g. domerulonephritis), cardiovascular disorders (e.g. disorders) in respiratory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocrine disorders (e.g. dadisorder) reproductive system disorders (e.g. disorders), inversional disorders (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU1705-AAU17083 represent novel signal transduction con pathoway protein, amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell; secreted; transmembrane; inflammation; cancer; neurological disease; angiogenesis; tumour vasculfastion; growth disorder; developmental disorder, skin wound; hair follicle disorder; anti-inflammatory; cytostatic; neuroprotective; vulnery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotides useful for the treatment of various conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30; DB 22; Length 210;
Pred. No. 3.9e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Onrust R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat HT glycoprotein homologue, SEQ ID NO:393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watson JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY76114 standard; Protein; 242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 222; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   including wounds and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0069726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-NZ00051
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 90.9%;
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strachan L, Sleeman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-072177/06.
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68 GYWLS 72
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09-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GYWMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY76114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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The invention relates to novel nucleic acid sequences derived from rat

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dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to transit inflamation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of concer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences ANYTS942-Y76121 represent polypeptides encoded by the properties of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murison JG;
                                                                                                                                                                                                                                                                                       by CDNA sequences derived from several mouse, rat or human skin cell types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY760094-Y76109 and AAY7619 are proteins with an N-terminal signal sequence, indicating that they are secreted. Sequences AAY75986-Y75989, AAY76001-Y76071, AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more putative transmembrane domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat; skin cell; cytostatic; antiinflammatory; anti-HIV; nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide used in the identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 21; Length 24
Pred. No. 4.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Onrust R, Sleeman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 297-298; 352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB56053 standard; Protein; 242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skin cell protein, SEQ ID NO: 393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-2000; 2000WO-NZ00075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0312283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-007495/01.
N-PSDB; AAC99755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200069884-A2
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224 GYWLS 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-NOV-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB56053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                     85999999999999999<del>8</del>8
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ABB72290 standard; Protein; 242 AA.

04-APR-2002

ABB72290;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of CDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammarcory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kumble KD;
                                                                                                                                                                                                                                                                                                                                                                                                      Human; rat; mouse; skin cell; skin wownd; cancer; growth defect;
developmental defect; inflammatory disease; dermatological; vulnerary;
immunomodulator; anti-inflammatory; cytostatic; neuroprotective.
neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns.
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.9%; Score 30; DB 23; Length 242;
80.0%; Pred. No. 4.4e+02;
.ive 1; Mismatches 0; Indels
                                                                                               22; Length 242;
                                                                                                 ; Ub c...
. 4.4e+02;
...a 0; Indels
                                                                                                                                                                                                                                                                                                                                                                         Rat protein isolated from skin cells SEQ ID NO: 393.
                                                                                               Score 30; DB
Pred. No. 4.4e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sleeman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                         ABB72253 standard; Protein; 242 AA.
                                                                                             Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-2000; 2000US-206650P.
25-JUL-2000; 2000US-221232P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modulating immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-2001; 2001WO-NZ00099
                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strachan L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-122020/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 4; Conserv
                                                                242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 AA;
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                                                                                                                                                                                 224 GYWLS 228
                                                                                                                                                            1 GYWMS 5
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                                                                                                                                                                                                                                                                                                                                          04-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus sp.
                                                                                                                                                                                                                                                                                                         ABB72253;
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                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                          RESULT 12
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The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                 Kumble KD;
                                                                                             Human, rat, mouse, skin cell, skin wound; cancer, growth defect, developmental defect, inflammatory disease, dermatological, vulnerary; immunomodulator, anti-inflammatory, cytostatic, neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, rat, mouse; skin cell; skin wound; cancer; growth defect; developmental defect; inflammatory disease; dermatological; vulnerary; immunomodulator; anti-inflammatory; cytostatic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                               Murison JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.9%; Score 30; DB 23; Length 24
80.0%; Pred. No. 4.46+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat protein isolated from skin cells SEQ ID NO: 625.
                                                               Rat protein isolated from skin cells SEQ ID NO: 502.
                                                                                                                                                                                                                                                                                                                                                                               Onrust R,
                                                                                                                                                                                                                                                                                                                                                                               Sleeman M,
                                                                                                                                                                                                                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB72301 standard; Protein; 242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 308; 466pp; English.
                                                                                                                                                                                                                                                                24-MAY-2001; 2001WO-NZ00099.
                                                                                                                                                                                                                                                                                                24-MAY-2000; 2000US-206650P.
25-JUL-2000; 2000US-221232P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modulating immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                               Strachan L,
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-122020/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 AA
                                                                                                                                                                                              WO200190357-A1.
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224 GYWLS 228
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                                                                                                                                                                                                                                29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                               Watson JD,
                                                                                                                                                                Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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224 GYWLS 228

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Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
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                                                                                                                                                                                                                                                  New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4114.
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                                                                                                                                                           (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                     Claim 4; Page 390; 466pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0134001
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                                                                                                                                                                                                                                                                                            modulating immune responses
                                                                                                                  24-MAY-2000; 2000US-206650P.
25-JUL-2000; 2000US-221232P.
                                                                                         24-MAY-2001; 2001WO-NZ00099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                    Strachan L,
                                                                                                                                                                                                               WPI; 2002-122020/16.
N-PSDB; ABL34986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 AA;
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224 GYWLS 228
                                       WO200190357-A1.
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                                                                 29-NOV-2001
                                                                                                                                                                                       Watson JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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ABP39269
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Gaps

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Score 30; DB 23; Length 242; Pred. No. 4.4e+02; 1; Mismatches 0; Indels

90.9%;

(GENO-) GENOME THERAPEUTICS CORP.

97US-055779P 97US-064964P

14-AUG-1997; 08-NOV-1997;

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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to sorcem for compounds able to interfere with the S. epidermidis liferion. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                   Novel isolated nucleic acid encoding a Staphylococcus epidermidis
polypeptide, useful for diagnosing and treating bacterial infections
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                                                                                                                                          Disclosure; SEQ ID 4114; 267pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: April 22, 2003, 12:51:15 Job time : 14.6786 secs
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Bush D;
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                                WPI; 2002-381255/41.
N-PSDB; ABN91814.
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Matches 4; Conserv
Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                   243 AA;
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52 GYWLS 56
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Murison JG,

Onrust R,

Sleeman M,

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; Patent No. US20020168711A1
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 64;
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US-09-906-838-109
US-09-907-613-109
US-09-907-613-109
US-10-176-918-290
US-10-176-918-290
US-10-176-918-290
US-10-137-865-290
US-10-137-865-290
US-10-137-865-290
US-10-137-865-290
US-10-137-865-290
US-10-137-865-290
US-10-137-865-290
US-10-140-474-290
US-09-909-204-109
US-09-909-204-109
US-09-906-666-109
US-09-906-666-109
US-09-906-666-109
US-09-906-109
US-09-903-138-1122
US-09-903-1498-109
US-09-903-1498-109
US-09-903-1498-109
US-09-903-1498-109
US-09-903-1498-109
US-09-903-1498-109
US-09-903-1498-109
US-10-142-419-290
US-10-118-61-122
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; OTHER INFORMATION: Xaa equals stop translation
US-10-144-929-162
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Best Local Similarity 80.0.
    ORGANISM: Homo sapiens
       |||:|
45 GYWLS 49
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LOCATION: (64)
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US-09-764-868-892
        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                      April 22, 2003, 12:53:59 ; Search time 5.26786 Seconds (without alignments) 76.055 Million cell updates/sec
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1: \( \cgn2 \frac{6}{\prodata} \) | | | \( \cgn2 \frac{6}{\prodata} \) | | | | \( \cgn2 \frac{6}{\prodata} \) | \( \cgn2 \frac{6}{\prodata} \
                       GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-764-868-892
US-09-866-050A-502
US-09-866-050A-625
US-09-866-050A-625
US-09-866-050A-625
US-09-866-050A-625
US-10-050-704-180
US-10-144-929-156
US-09-907-824-109
US-09-907-824-109
US-09-907-824-109
US-09-907-824-109
US-09-907-824-109
US-09-907-824-109
US-09-907-824-109
US-09-907-824-109
US-09-907-824-109
US-09-907-826-109
US-09-906-742-109
US-10-121-049-290
US-10-121-049-290
US-10-121-049-290
US-10-121-049-290
                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                             301932 seqs, 80129803 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REPERSENCE: 11000.1011c4U
CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT APPLICATION NUMBER: US/09/866,050A
SOFTHARE FASESEQ for Windows Version 4.0
SEQ ID NO 625
LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 109100 Application US/09815242

Fatent NO. US2000661569A1
GENERAL INFORMATION:
APPLICANT: Hagelbeck, Robert
APPLICANT: Carri Carnit C
                                                                                                                                                                                                                Length 242;
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80.0%; Pred. No. 2.3e+02;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                        Score 30; DB 9; Length 242
Pred. No. 2.3e+02;
1; Mismatches 0; Indels
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7 Publication No. US20030040471A1
7 GENERAL INFORMATION:
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Matches 4; Conserv
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US-09-815-242-10910
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US-09-866-050A-625
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US-09-866-050A-625
                                                                                         ; ORGANISM: Rat
US-09-866-050A-502
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                 LENGTH: 242
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FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
FILOR TOTALING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 1510
SOUTHWARE: PatentIN Ver. 2.0
SEQ ID NO 892
LENGTH: 210
TYPE: PRT
TYPE: PRT
CRANISM: HOMO SADIENS
US-09-764-868-892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 393, Application US/09866050A; Sequence 393, Application US/09866050A; Publication No. US20030040471A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions isolated From Skin Cells
TITLE OF INVENTION: Compositions for Their Use
TITLE OF INVENTION: and Methods for Their Use
TITLE OF INVENTION: 1010.101.04U
CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
SOFTWARE: FSELSEQ for Windows Version 4.0
SEQ ID NO 393
LENGIN: NAMER: TUBER SECOND SECOND
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GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Rumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c4U
CURRENT APPLICANT: 11000.1011c4U
CURRENT FILING DATE: 2001-05-24
NUMMER OF SEQ ID NOS: 725
SEQ ID NO 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 90.9%; Score 30; DB 9; Length 210; Best Local Similarity 80.0%; Pred. No. 2e+02; Matches 4; Conservative 1; Mismatches 0; Indels
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Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0,
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68 GYWLS 72
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; ORGANISM: Rat
US-09-866-050A-393
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US-09-866-050A-393
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US-09-866-050A-502
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TYPE: PRT
ORGANISM: Homo sapiens
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US-09-905-291A-109
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-050-704-180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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US-10-144-929-156
; Sequence 156, Application US/10144929
; Publication No. US20030069405A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.,
; TITLE OF INVENTION: 70 Human Secreted Proteins
; CURRENT APPLICATION NUMBER: US/10/144,929
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/251,329
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US-10-050-704-180

$ sequence 180, Application US/10050704

$ bublication No. US2000050442A1

$ publication No. US2000050442A1

$ GENERAL INFORMATION:

$ TITLE OF INVENTION:

$ FILE REFRENCE: PZ039P1

$ CURRENT APPLICATION NUMBER: US/10/050,704

$ CURRENT FILING DATE: 2002-01-18

$ PRIOR APPLICATION NUMBER: C9/684,524

$ PRIOR APPLICATION NUMBER: E7/US00/08979

$ PRIOR FILING DATE: 2000-10-10

$ PRIOR FILING DATE: 2000-04-06

$ PRIOR FILING DATE: 2000-04-06

$ PRIOR FILING DATE: 1999-04-09

$ PRIOR FILING DATE: 1999-04-09

$ PRIOR FILING DATE: 1999-04-06

$ PRIOR PILING DATE: 1999-04-06

$ PRIOR PILING DATE: 1999-04-06

$ NUMBER OF SEQ ID NOS: 344

$ SOFTWARE: PATENTIN VOT: 2.0
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10910
                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10910
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LOCATION: (251
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87 GYWLS 91
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PRIOR FILING NOTE: 1999-06-18

PRIOR FILING NOTE: 1999-06-18

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SEQUENCY STREET ST
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Score 30; DB 9; Length 420;
Pred. No. 3.9e+02;
1; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-20
PRIOR PRILING DATE: 1999-11-20
PRIOR PRILING DATE: 1999-11-20
PRIOR PRILING DATE: 1999-11-20
PRIOR PRILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PRILING DATE: 1999-12-02
PRIOR PRILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-04
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-07
PRIOR PRILING DATE: 1999-12-07
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, avi
APPLICANT: Botstein, David
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Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Mather, Jennie P.
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Eaton, Dan L.
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US-09-902-853-109
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/902,853
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                                                               PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PELICATION NUMBER: PCT/US99/28565
PRIOR PELICATION NUMBER: PCT/US99/30095
PRIOR PELICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-06
PRIOR PELICATION NUMBER: PCT/US99/30910
PRIOR PELICATION NUMBER: PCT/US99/30910
PRIOR PELICATION NUMBER: PCT/US99/30999
PRIOR PELICATION NUMBER: PCT/US09/30999
                 APPLICATION NUMBER: PCT/US99/21547
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PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
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Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botetein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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; ORGANISM: Homo sapiens
US-09-905-291A-109
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US-09-902-853-109
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Soy, Margaret Ann
APPLICANT: Everart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, F. Mickey
APPLICANT: Wood, William, F. Mickey
APPLICANT: Wood, William, E. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acide Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US 60/143,048
FRIOR APPLICATION NUMBER: US 60/145,698
FRIOR PELING DATE: 1999-00-02-2
FRIOR APPLICATION NUMBER: US 60/146,222
FRIOR APPLICATION NUMBER: US 60/146,222
FRIOR APPLICATION NUMBER: PCT/US99/20594
FRIOR PELING DATE: 1999-00-18
FRIOR PELING DATE: 1999-09-18
FRIOR PELING DATE: 1999-09-15
FRIOR PELING DATE: 1999-09-15
FRIOR PELING DATE: 1999-09-15
FRIOR PELING DATE: 1999-10-05
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APPLICANT: Genentech, Inc.; APPLICANT: Betstein, David; APPLICANT: Besnoyers, Luc; APPLICANT: Baton, Dan L. APPLICANT: Baton, Dan L. APPLICANT: Ferrara, Napoleone; APPLICANT: Ferrara, Napoleone; APPLICANT: Filvaroff, Ellen
                                                                                                                                                                             Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                           Gurney, Austin L.
Hillan, Kenneth, J
                                                                                                       Gerritsen, Mary E
                                                                                 Gerber, Hanspeter
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Mather, Jennie P.
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           ong, Sherman
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                       Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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402 GYWLS 406
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APPLICANT: Stewart, Timothy A. APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Williams, P. Mickey APPLICANT: Williams, P. Mickey TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same PILE REFERENCE: 10466-14 CURRENT APPLICATION NUMBER: US/09/907,824 CURRENT FILING DATE: 2001-07-17
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                                                                                                                                                                                                                                                                                                              PRIOR PELICATION NUMBER: 09/665,350
PRIOR PELIANG DATE: 2000-09-18
PRIOR PELIANG DATE: 2000-09-18
PRIOR PELIANG DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 05/145,048
PRIOR PELIANG DATE: 1999-07-07
PRIOR PELIANG DATE: 1999-07-26
PRIOR PELIANG DATE: 1999-07-26
PRIOR PELIANG DATE: 1999-07-26
PRIOR PELIANG DATE: 1999-09-08
PRIOR PELIANG DATE: 1999-09-08
PRIOR PELIANG DATE: 1999-09-18
PRIOR PELIANG DATE: 1999-09-18
PRIOR PELIANG DATE: 1999-09-15
PRIOR PELIANG DATE: 1999-10-05
PRIOR PELIANG DATE: 1999-11-30
PRIOR PELIANG NUMBER: PCT/US99/28564
PRIOR PELIANG DATE: 1999-12-02
PRIOR PELIANG DATE: 1999-12-03
PRIOR PELIANG DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 420
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Publication No. US20020198366A1
GAPERAL INFORMATION:
APPLICANT: Genencech, Inc.,
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Betsein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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CRGANISM: Homo Sapien
US-09-907-824-109
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Best Local Similarity
Matches 4; Conserv
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PRICE REFERENCE:
CURRENT PILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 06/049911
PRIOR APPLICATION NUMBER: 60/049911
PRIOR PLILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-08-16
PRIOR PILING DATE: 1997-08-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-19
PRIOR PILING DATE: 1997-00-19
PRIOR PILING DATE: 1997-00-19
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-27
PRIOR PILING DATE: 1997-10-27
                                                          ; Sequence 290, Application US/10028072; Publication No. US20030004311A1; GENERAL INFORMATION:
                                                                                                                                                       APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sherwood, Steven
Smith, Victoria
Stewart, Timothy
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                      Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumas, Danie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
RESULT 14
US-10-028-072-290
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Williams, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF THE SOBOLOGY-18
FRIOR APPLICATION NUMBER: 09/66,350
FRIOR PELING DATE: 2000-09-18
FRIOR PELING DATE: 1999-07-18
FRIOR PELING DATE: 1999-09-18
FRIOR PELING DATE: 1999-09-18
FRIOR PELING DATE: 1999-09-18
FRIOR PELING DATE: 1999-09-18
FRIOR PELING DATE: 1999-10-18
FRIOR PELING DATE: 1999-10-20-18
FRIOR PELING DATE: 1999-11-20
FRIOR PELING DATE: 1999-12-20
FRIOR APPLICATION NUMBER: PCT/US99/3099
FRIOR PELING DATE: 1999-12-20
FRIOR PELING DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                         Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                                   Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                     Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                        Paoni, Nicholas F
                                                                                                                                                                                                                               Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
                                                                 Goddard, A.
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ORGANISM: Homo Sapien
US-09-904-011-109
                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE: 1997-10-29

PRIOR PELICATION NUMBER: 60/063735

PRIOR PELICATION NUMBER: 60/063735

PRIOR PELICATION NUMBER: 60/063735

PRIOR PELICATION NUMBER: 60/063735

PRIOR PELICATION NUMBER: 60/063755

PRIOR PELICATION NUMBER: 60/063755

PRIOR PELICATION NUMBER: 60/063755

PRIOR PELICATION NUMBER: 60/064809

PRIOR APPLICATION NUMBER: 60/064809

PRIOR APPLICATION NUMBER: 60/064809

PRIOR APPLICATION NUMBER: 60/064809

PRIOR PELING DATE: 1997-11-12

PRIOR PELING DATE: 1997-11-12-14

PRIOR PELING DATE: 1997-11-12-14

PRIOR PELING DATE: 1997-11-12-14

PRIOR PELING DATE: 1997-11-12-14

PRIOR PELING DATE: 1997-11-2-14

PRIOR PELING DATE: 1997-11-2-16

PRIOR PELING DATE: 1998-01-2-16

PRIOR PELING DATE: 1998-01-16

PRIOR PELING DATE: 1998-01-16

PRIOR PELING DATE: 1998-01-16

PRIOR PELING DATE:
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FRIOR APPLICATION NUMBER: 60/004627
FRIOR APPLICATION NUMBER: 60/004627
FRIOR APPLICATION NUMBER: 60/004627
FRIOR APPLICATION NUMBER: 60/004627
FRIOR APPLICATION NUMBER: 60/004624
FRIOR APPLICATION NUMBER: 60/004624
FRIOR APPLICATION NUMBER: 60/004624
FRIOR APPLICATION NUMBER: 60/004627
FRIOR APPLICATION NUMBER: 60/004627
FRIOR APPLICATION NUMBER: 60/004627
FRIOR APPLICATION NUMBER: 60/004627
FRIOR APPLICATION NUMBER: 60/004640
FRIOR APPLICATION NUMBER: 60/004640
FRIOR PLILING DATE: 1998-06-15
FRIOR PLILING DATE: 1998-06-16
FRIOR PLILING DATE: 1999-06-16
FRIOR FRIILING DATE: 1999-07-07
FRIOR FRIILING DATE: 1999-0
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Gaps

RESULT 15
US-09-906-742-109
US-09-906-742-109
; Sequence 109, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:

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APPLICANT: Generate, Naid
APPLICANT: Generate, Naid
APPLICANT: Bankenati, Naid
APPLICANT: Bankenati, Naid
APPLICANT: Benerati, Naid
APPLICANT: Benerati, Naid
APPLICANT: Benerati, Naid
APPLICANT: Beneration and APPLICANT: Beneration and APPLICANT: Gao, Well-Clang
APPLICANT: Gao, Well-Clang
APPLICANT: Gao, Well-Clang
APPLICANT: Gao, Well-Clang
APPLICANT: Garden and APPLICANT: Market, Austin J. J.
APPLICANT: Market, Austin J. J.
APPLICANT: Market, Market, J.
APPLICANT: Mood, Malliann, P.
APPLICANT: Mood, Malliann, P.
APPLICANT: Mood, Malliann, J.
APPLICANT: Mood, J.
APPLICANTON NUMBER: PCT/USS9/2034
APPLICANTON NUMBER: PCT/USS9/2039
APPLICANTON NUMB
```

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Query Match
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYMMS 5
Db 402 GYMLS 406
Search completed: April 22, 2003, 13:11:14
Job time: 6.26786 Becs
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Appl Appl Appl Appl Appl Appl Appli Appli

Sequence Sequence Sequence

Sequence Sequence Sequence

233, 332, 110, 117,

Sequence Seq

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* GENERAL INFORMATION:

* APPLICANT: Alvarez, Vernon L.

* TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries

* NUMBER OF SEQUENCES: 103

* CORRESPONDENCE ADDRESS:

* ADDRESSES: Pennie & Edmonds

* STREET: 1155 Avenue of the Americas

CITY: New York

COUNTRY: USA

ZIP: 1036

COMPUTER: READABLE FORM:

* MEDIUM TYPE: Floppy disk

COMPUTER: EDMP PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIR Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

* APPLICATION NUMBER: US/08/488,161

FLING DATE: 0'-1UN-1995

CLASSIFICATION: 436

ATTORNET/AGENT INFORMATION:

* REPERENCE/DOCKET WINDER: 109.979

* TELECOMMUNICATION INVERS: 1101-176

* TELECOMMUNICATION INVERS: 1101-176

* TELECOMMUNICATION INVERS: 1101-176

* TELERAX: (212) 790-9090

* TELECOMMUNICATION INVERSES: 1101-176

* TELERAX: (212) 780-9741/8864

* TELERAX: (212) 780-9741/8864
US-08-318-157B-23
US-08-053-4551B-32
US-08-25-534A-19
US-07-942-245-37
US-08-244-626-10
US-07-942-245-17
US-09-376-330-20
US-09-376-330-20
US-08-355-80A-95
PCT-US93-09166-3
US-08-318-157B-9
US-08-318-157B-9
US-08-318-157B-9
US-08-318-157B-9
US-08-318-157B-9
US-08-318-157B-9
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US-08-318-157B-10
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Pred. No. 45;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 39, Application US/08488161; Patent No. 5885577; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
    10
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US-08-488-161-39
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GYWLS
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Sequence 39, Appl
Sequence 4114, Ap
Sequence 5, Appli
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 39, Appl
Seguence 39, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, App. Sequence 22, App. Sequence 22, App. Sequence 21, App. Sequence 11, App. Sequence 11, App. Sequence 12, App. Sequence 12, App. Sequence 19, App. Sequence 20, 
                                                                                                                                                April 22, 2003, 12:48:49; Search time 4.375 Seconds (without alignments) 33.626 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, A
Sequence 2, A
Sequence 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
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Sequence 1
Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued Patents AA:*

.. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/RB_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                           GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-488-161-39
US-09-273-685-39
US-09-134-001C-4114
US-09-134-001C-4114
US-09-134-001C-4114
US-08-480-434-31
US-08-68-480-434-31
US-08-65-451B-31
US-08-65-451B-31
US-08-65-451B-31
US-08-65-451B-31
US-08-65-451B-31
US-08-65-451B-31
US-08-65-451B-31
US-08-46-431-114
US-08-46-431-119
US-08-69-434-19
US-08-69-434-19
US-08-69-434-19
US-08-69-434-19
US-08-05-451B-19
US-08-05-451B-19
US-08-05-434-18
US-08-05-434-18
US-08-05-434-18
US-08-05-44-65-12
                                                                                                                                                                                                                                                                                                                                                                                                                     hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
                                                                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                  US-09-674-716B-9
33
1 GYWMS 5
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Match Length DB
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                                                                                                                                                                                                                                    Title:
Perfect score:
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                                                                                                            OM protein
                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                     Run on:
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No.
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Gaps

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2; Length 43; ;

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Sequence 4114, Application US/09134001C

Sequence 4144, Application US/09134001C

Patent No. 6380370

GENERAL INFORNATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: UVCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BD1DERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: B0100 NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

SRIOR PPLICATION NUMBER: US 60/055,779

WUMBER OF SEQ ID NOS: 5674

LENGTH: 243

WUMBER OF SEG ID NOS: 5674
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US-09-115-127-5
US-09-115-127-5
; sequence 5, Application US/09315127
; Patent No. 6446390
; GENERAL INFORMATION:
; APPLICANT: THE University of Tennessee, c/o Richard Cox
; TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
; TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy
; FILE REFERENCE: 44137-5023, U. of Tennessee
; CURRENT APPLICATION NUMBER: US/09/315,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBR: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 1101-196-228
FEREFERENCE/DOCKET NUMBER: 1101-196-228
FELESHORF/DOCKET NUMBER: 1101-196-228
FELESHORF/CATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
FELEX: 66141 PENNIE
SEQUENCE CHARRATERISTICS:
SEQUENCE CHARRATERISTICS:
LENGTH: 43 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.9%; Score 30; DB 4; I
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide PCT-US95-11934-39
                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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US-09-134-001C-4114
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                                                        Sequence 39, Application US/09273685
; Betent No. 6015561
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Vernon L.
; TITLE OF INVENTION: Peptide Libraries
; TITLE OF INVENTION: Peptide Libraries
; TOWERSPONDENCES: 103
; CORRESPONDENCES: Râmonds
; STREET: 1155 Avenue of the Americas
; STATE: New York
; STATE: New York
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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; Sequence 39, Application PC/TUS9511934
; GeneRAL INFORMATION:
; APPLICANT: Cyclen Corporation
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; TITLE OF INVENTION: Peptide Libraries
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 3; Length 43;
Pred. No. 45;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/273,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFLING DATE:
CLASSIFICATION:
PRIGNA PELICATION:
PRICE APPLICATION:
APPLICATION NUMBER: 08/488,161
FILING DATE:
APTORNEY FAGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 110.176
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEX: 66/41 PENNIE
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: A amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTY: USA
VIP: 10036
CMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC COMPATER:
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ilarity 80.0%;
Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-09-273-685-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
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GYWLS 10
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                                                   US-09-273-685-39
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07-JUN-1995
                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                  5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DI
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-480-434-31
    FILING DATE:
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1 GFWMS 5
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                                                                                                                                                                                                                                                                  LENGTH:
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Sequence 6, Application US/09315127

Sequence 6, Application US/09315127

Sequence 6, Application US/09315127

Sequence 6, Application US/09315127

GENERAL INFORMATION:

TITLE DF INVENTION: Stable Envelope Proteins for Retroviral, Viral and TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy FILE REFERENCE: 44137-5023, U. of Tennessee

CURRENT APPLICATION NUMBER: US/09/315,127

CURRENT PILING DATE: 1999-05-20

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: SEQ ID NO. 4, OTHER INFORMATION: envelope protein produced by retroviral vector of content information: seq. id no. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

Fatent No. 5911248

GENERAL INFORMATION:

TITLE OF INVENTOR:

TITLE OF INVENTOR:

TITLE OF INVENTOR:

ANTIBODIES THERETO, AND USES THEREOF

CORRESPONDENCE: 88

NUMBER OF SEQUENCE: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

STATE: New York

STATE: New York

COUNTRY: U.S.A.
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                                                                                                                                                                                                  Score 30, DB 4; Length 667;
Pred. No. 5.8e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ISM PC compatible
SOFTWARE: PETENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
  CURRENT FILING DATE: 1999-05-20 NUMBER OF SEQ ID NOS: 23 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 5 LENGTH: 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                     ; ORGANISM: Artificial Sequence US-09-315-127-5
                                                                                                                                                                                                    Query Match 90.9%;
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 GYWLS 184
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LENGTH: 667
TYPE: PRT
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                                                                                                                   TYPE: PRT
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TELERAN (1415) 634-3604

ATTOMASTICATION (1455) 701

ATTOMASTICATION (1455) 701

BEGGGSTRATTON WINDERS (152) 227

REFERENCE (1415) 634-3604

TELERAN (1415) 634-364

TELERAN (1415)
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Sequence 11, Application US/08204656B
Sequence 11, Application US/08204656B
Patent No. 553882
GENERAL INFORMATION:
APPLICANT: Matsui, Ikuo
APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Honda, Koichi
APPLICANT: Honda, Koichi
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: 011gosaccharide Using The Enzyme
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.9%; Score 29; DB 2; Length 5; 80.0%; Pred. No. 2e+05;
                                                                                                                      COMPUTER READER FORM:

COMPUTER READER FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/053,451B

FILING DATE: 26-APR-1993

CLASSIPICATION: 424

ATTONEY/AGENT INFORMATION:

NAME: Halluin, Albert P.

REGISTRATION NUMBER: 25,227

REFERENCE/DOCKET NUMBER: 25,227

REFERENCE/DOCKET NUMBER: 25,227

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPAX: 415-854-3694

TELEEX: 66141 PENIE

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: 8110 Gatehouse Road, Sulte 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                             NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
STREET: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
CITY: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 8110 Gatehou
CITY: Falls Church
STATE: virginia
COUNTRY: U.S.A.
ZIP: 22042
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: un)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: unknow
; MOLECULE TYPE: DNN
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-053-451B-31
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1 GFWMS 5
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US-08-204-656B-11
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                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29; DB 2; Length 5;
Pred. No. 2e+05;
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             Score 29; DB 2; Length 5; Pred. No. 2e+05; 0; Indels 1; Mismatches 0; Indels
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Patent No. 595584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Ditlow, Charles C.
APPLICANT: Calenoff, Emanuel
             87.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                           Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-22
                                                                              1 GYWMS 5
                                                                                                            1 GFWMS 5
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               Query Match
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19.508-467-831-11

19.508-quence 11, Application US/08467831

19.508-quence 12, Application US/0846781

19.508-quence 12, Application US/0846781

19.508-quence 12, Application US/08467, BIRCH

19.508-quence 12, Application US/08468467, BIRCH

19.508-quence 12, Application US/08467, BIRCH

10.508-quence 12, Application US/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 87.9%; Score 29; DB 1; Best Local Similarity 100.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches (
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TELEX: 248345
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-terminal
                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHEFICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal
US-08-470-702-11
                                                                    LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FRAGMENT TYPE:
US-08-467-831-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 GYWM 13
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APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAHIRI, SACHIO
APPLICANT: MIYAHIRI, SACHIO
APPLICANT: MIYAHIRI, SACHIO
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: 12042
ZIP: 22042
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
FILING DATE: 02-WAR-1994
ATTORNEY/AGENTIND NUMBER: US/08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENTIND NUMBER: US/08/ATO.703
WARDEL OF THE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 87.9%; Score 29; DB Best Local Similarity 100.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches
APPLICATION NUMBER: US/08/204,656B
FILING DATE: 02-MAR.1994
CLASSIFICATION: 435
ATTORNEY FAGNY INFORMATION:
NAME: Weiner, Marc S.
REGISTRATION NUMBER: 32,181
REFREENCE/DOCKET NUMBER: 234-252P
TELEPHONE: (703) 205-8050
TELEPHONE: (703) 205-8050
TELER: 248345
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08470702
Patent No. 5631149
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 248345
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO FRAGMENT TYPE: N-terminal US-08-204-656B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDENRES: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 GYWM 13
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TELEX: 24
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US-08-470-702-11
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Length 119;
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                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: C5-APR-1993
CLASSIFICATION: 424
ATTONEY/AGENT INPOMMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 25,227
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELESTAX: 415-854-369
TELEX: 66141 PENNIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 87.9%; Score 29; DB 2; Le. Best Local Similarity 80.0%; Pred. No. 1.7e+02; Matches 4; Conservative 1; Mismatches 0;
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: April 22, 2003, 12:55:42 Job time : 5.375 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-053-451B-125
                                                                                                                                      COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
              STREET: 1122.
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
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                                            RESULT 14
US-08-053-451B-114
US-08-053-451B-114
US-08-053-451B-114
Sequence 114, Application US/08053451B
APPLICANT: Chan's Francis W.
APPLICANT: Charles C.
APPLICANT: Calenoff, Emanus C.
TITLE OF INVENTION: ATHEROSCIEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Patent No. 595584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Ditlow, Charles C.
APPLICANT: Ditlow, Charles C.
TIV-LE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
UMBER OF SEQUENCES 176
CORRESPOSEDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEFAM: 415-854-3694
TELEFAM: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TYPE: amino acid
   Best Local Similarity 100.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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US-08-053-451B-125
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Gaps

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April 22, 2003, 12:48:24 ; Search time 18.6607 Seconds (without alignments) 97.882 Million cell updates/sec
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                         283224 seqs, 96134422 residues
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                              1 BIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
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98
                                                                                                                                                                                                                                                                    BLOSUM62
                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                             Searched:
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283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Ig heavy chain V r	Ig heavy chain V r	heavy	y heavy	heavy	y heavy chain	y heavy chain	y heavy chain	y heavy chain	g heavy chain	g heavy	g heavy chain	g heavy chain	g heavy	g heavy chain	g heavy chain V-	g heavy	g heavy	g heavy chain	g heavy	heavy chain	g heavy chain	g heavy	g heavy	heavy chain	chain	onoclonal anti		Ig heavy chain V r
QI	S26460	538714	824521	AVMS06	AVMSAB	AVMS61	AVMS09	AVMSB7	AVMS82	A25803	AVMS57	HVMSAM	MHMS76	PC1213	177394	809958	826462	PH1091	PH1092	A27630	A41940	132513	S67945 🕶	G29380	PH1093	868211	PC4436	H12	842467
DB	- 8	~	~	н	-	н	-1	m	-	N	7	٦	-	~	N	~	N	7	N	N	N	N	N	N	N	0	~	~	7
Length 1	101	115	106	115	113	113	113	113	115	115	113	113	111	139	64	121	100	110	110	119	121	141	125	139	110	220	444		137
% Query Match	100.0	100.0	94.9	4.	O	•	92.9	92.9	92.9	90.8	-	86.7	7	74.5	69.4	69.4	68.4	68.4	68.4	68.4	68.4	68.4	67.3		65.3	64.3	64.3	62.2	62.2
Score	86	86	93	93	91	91	91	91	91	89	86	85	75.5	73	68	68	67	67	67	67	67	67	99	65	64	63	63	61	61
Result No.		1 73	m	4	Ŋ	9	7	00	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

heavy chain heavy chain heavy chain		neavy chain			
2 S46466 2 PL0122 2 S44107				2 PH1288 2 S26926 2 S00981	2 PH1290
55 100 126	132 116 118	137	137 142 127	133 100 119	119
59.2	2 2 2 2 1 2 2 2 2 1 3 2 2 2 1	58.5 58.2 58.2	58.2 58.2 57.1	57.1 56.1 56.1	56.1
50 50 50	55 57 57	57	527	55 55 55	55
30	1 W W W	33.0	39 40 40	4 4 4 2 6 4 4 4	45

## ALIGNMENTS

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Ig heavy chain V region - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999 C; Accession: 826460
R; Kavaler, J.
Submitted to the EMBL Data Library, April 1991
A; Reference number: 826459
A; Reference number: 826460
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-101 - KRNA
A; Residues: 1-101 - KRNA
A; Residues: 1-101 - KRNA
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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Gaps 100.0%; Score 98; DB 2; Length 101; 100.0%; Pred. No. 1.1e-08; tive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0 Matches 19; Conservative

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## 32 EIRLKSDNYATHYAESVKG 50 1 EIRLKSDNYATHYAESVKG 19 g ઠ

RESULT 2

Systy.

Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S38714
R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A;Reference number: S38713
A;Accession: S38714
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <CIMA;Gross-references: EMBL:X76014; NID:g416092; PIDN:CAA53601.1; PID:g1334076
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-99/Domain: immunoglobulin homology <IMM>

Gaps ö Length 115; Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels

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Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Musulus 1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
Cispeciesion: B9818; A02072
Rivana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A;Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A;Reference number: A93818; MUID:78158406; PMID:417344
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A; Residues: 1-113 <VRA>
C; Comment: This chain was isolated from a myeloma protein that binds inulin.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
F;22-98/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V-III region (ABE-47N) - mouse
Cypecies Mus musculus (house mouse)
Cybate: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
CyAccession: A90400; A02072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                         92.9%; Score 91; DB 1; Length 113; llarity 94.7%; Pred. No. 1.7e-07; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 113;
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F;22-98/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                             1 EIRLKSDNYATHYAESVKG 19
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                                                                                                                                         Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: B93818
                                                                                               Query Match
                                                                                                                                                         Best Loca
Matches
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C;Accession: C92811, A02072
R;Johnson, N.; Slankard, J.; Paul, L.; Hood, L.
A;Title: The complete V domain amino acid sequences of two myeloma inulin-binding protein A;Reference number: A92811; MUID:82099361; PMID:6798111
A;Accession: C92811
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C; Accession: A93818; A02072
R; Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S. A. 75, 1957-1961, 1978
A; Reference number: A93818; MUD: 78158406; PMID: 417344
C; Comment: This chain was isolated from a myeloma protein that binds inulin.
C; Superfamily; aimmunoglobulin V region; immunoglobulin homology
C; Keywords: heteroteramer; immunoglobulin
F; 15-100/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-115 <JOH>
C; Comment: This chain was isolated from a myeloma protein that binds inulin.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
P;15-100/Domain: immunoglobulin homology <IMM>
                                                                               S24521

Ig heavy chain V region - mouse
Ig heavy chain V region - mouse
(Species: Mus musculus (house mouse)
(Spacies: Mus musculus (house mouse)
(Spacies: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
(Spaciession: S24521
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(Spaciession: S24521
(Spaciession: S24490
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(Spaciession: S24430
(Spaciession: S2
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Pred. No. 8.2e-08;
1; Mismatches 0; Indels
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Local Similarity 94.7%; Pred. No. 7.5e-08;
Les 18; Conservative 1; Mismatches 0; Indels
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Ig heavy chain V region (AMPCI) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: IB-Aug-1992 #sequence_revision 18-Aug-1982 #text_change 31-Mar-1997
C;Accession: A02073
R;Rudikoff, S.; Potter, M.
A;Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a nayReference number: A92810; MUID:81216632; PMID:6787122
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Proc. Natl. Acad. Sci. U.S.A. 77, 3630-3634, 1980
Proc. Natl. Acad. Sci. U.S.A. 77, 3630-3634, 1980
Ajfitle: Nucleotide sequence of immunoglobulin heavy chain joining segments between trans A; Reference number: A02074; MUID:81013937; PMID:6251474
A;Accession: A02074
                                                                                                                                        Ig heavy chain V-III region (T957) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C;Accession: A92810; A02072
F;Rudikoff, S;. Potter, M.
J Immunol: 127, 191-194, 1981
A;Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a n
A;Reference number: A92810; MUID:81216632; PMID:6787122
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A; Residues: 1-113 < RUD>
C; Comment: This chain was isolated from a myeloma protein that binds inulin.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 15-100/Domain: immunoglobulin homology < IMM>
F; 22-98/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                            A Accession: A92810
A Molecule type: protein
A Molecule type: protein
A;Residues: 1-13 <RUD>
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
F;15-100/Domain: immunoglobulin homology <IMM>
F;22-98/Disulfide bonds: #status predicted
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C.species: Mus musculus (house mouse)
C.bate: 30-Sep-1980 #sequence_revision 30-Sep-1980 #text_change 31-Mar-1997
C.scession: A02074
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A;Residues: 1-111 <BER>
A;Note: the sequence was also determined from the differentiated gene
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89.5%; Pred. No. 1.6e-06;
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89.5%; Pred. No. 1.1e-06;
iive 0; Mismatches 2;
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Matches 17; Conservative
   50 QIRLASDNYATHYAESVKG
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hes 17; Conserv
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R;Herbst, H.; Grutter, T.; Aebersold, R.; Braun, D.G.
Biol. Chem. Hoppe-Seyler 367, 843-851, 1986
A;Fitle: The complete amino-acid sequence of the variable domain of a monoclonal anti-st A;Reference number: A25803; MUID:87076047; PMID:3539142
A;Accession: A25803
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C;Accession: D92811; A02072 —
C;Accession: D92811; A02072 —
J: Immunol. 128, 302-307, 1982
J: Immunol. 128, 302-307, 1982
A;Title: The complete V domain amino acid sequences of two myeloma inulin-binding protein A;Reference number: A92811; MUID:82099361; PMID:6798111
A;Reference number: A92811; MUID:82099361; PMID:6798111
A;Residues: 1-115 <-JOH>
A;Residues: 1-115 <-JOH>
C;Comment: This châin was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology < IMM>
F;15-100/Domain: immunoglobulin homology < IMM>
F;22-98/Disulfide bonds: #status predicted
R;Vrana, M.; Rudikoff, S.; Potter, M.
Biochemistry 16, 1170-1175, 1977
A;Title: Heavy-chain variable-region sequence from an inulin-binding myeloma protein. A;Feference number: A90400; MUID:77134726; PMID:402936
A;Accession: A90400
A;Molecule type: protein
A;Residues: 1-113 <VRA>
C;Comment: This chain was isolated from a myeloma protein that binds inulin. C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>F;15-100/Domain: immunoglobulin homology <IMM>F;15-100/Domain: immunoglobulin predicted
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C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g heavy chain V-III region (W3082) - mouse
;Species: Mus musculus (house mouse)
jatte: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
;Accession: D92811; A02072
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A;Reaiduea: 1-115 <HBR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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92.9%; Score 91; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                   92.9%; Score 91; DB 1; Length 113
94.7%; Pred. No. 1.7e-07;
tive 0; Mismatches 1; Indels
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Matches 18; Conservative
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RESULT 9

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RESULT 10

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Ig heavy chain precursor V region (mAb H8) ~- mouse (fragment)
C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house mouse)
C,Accession: PG1213
R,Hong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; Kim, A.H.; M.H.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; Kim, A.F.; Rieference number: PC1213
A,Reference number: PC1213
A,Reference number: PC1213; MUD:93077049; PMID:1446832
A,Reference number: PC1213
A,Residues: 1-139 < H0N.>
A,Residues: 1-139 < H0N.>
A,Residues: 1-139 < H0N.>
A,Residues: 1-199 PD0 minnoglobulin A region, immunoglobulin homology
C,Reywords: heteroterramer; immunoglobulin
C,Reywords: heteroterramer; immunoglobulin Newsology
C,Reywords: heteroterramer heterote estatus predicted < MAT>
F;20-139/Product: Ig heavy chain V region #stetuus predicted < MAT>
F;20-139/Product: Ig mmunoglobulin homology < IMM>
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A,Residues: 1-64 <RES>
A;Cross-references: GB:M64568; NID:g198472; PIDN:AAA39341.1; PID:g198473
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                          77.0%; Score 75.5; DB 1; Length 111; 89.5%; Pred. No. 5.3e-05; ive 0; Mismatches 1; Indels
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Pred. No. 0.00017;
4; Mismatches 1
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Best Local Similarity 73.7%;
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P49417 vibrio angu
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O25360 helicobacte
P12605 human parai
O67301 aquifex aeo
P26192 porcine rot
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P40355 saccharomyc
P01767 homo sapien
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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115 AA; 12810 MW; B67AD6638A121A5F CRC64;
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Local Similarity 94.7%; Pred. No. 1.4e-08;
Les 18; Conservative 1; Mismatches 0;
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MEDIINE-82099361; PubMed-6798111;
Johnson N., Slankard J., Paul L., Hood L.;
The complete V domain amino acid sequences of binding proteins.";
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
11g heavy chain V-III region A4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HV32 MOUSE STANDARD; FRT; 115 AA. P01801; P01801; Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
115 heavy chain V-III region J606.
Mus musculus (Mouse)
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VJ31 YEBAST
HV3F HUVAN
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SEQUENCE.
MEDLINE=78158406; PubMed=417344;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum DB seq length: 200000000
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98
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75.5
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Result Š. ö

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NY MEDILINES-1815406; PubMed=417344;

XI MEDILINES-1815406; PubMed=417344;

Yeana M., Rudikoff S., Potter M.;

Yeana M., Rudikoff S., Potter M.;

"Sequence variation among heavy chains from inulin-binding myeloma profesing.";

"Proc. Natl. Acad. Sci. U.S. A. 75:1957-1961(1978).

"I Proc. Natl. Acad. Sci. U.S. A. 75:1957-1961(1978).

"I Proc. Natl. Acad. Sci. U.S. A. 75:1957-1961(1978).

"I Proc. Natl. Acad. Sci. U.S. A. 75:1957-1961(1978).

"E PROC. Natl. Acad. Sci. U.S. A. 75:1957-1961(1978).

"T PROC. Natl. Acad. Sci. U.S. A. 75:1957-1961(1978).

"T PROC. Natl. Acad. Sci. Ig. MHC.

"T Proc. Natl. Acad. Sci. Ig. Ac.

"T Proc. Natl. Acad. Sci. Ig.

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Biochemistry 16:1170-1175(1977).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN.
PIR, A90400; AVMSB7.
HSSP, PORBIO, 2FBJ.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_V.
SMART; SMO047; ig; 1.
SMART; SMO0406; IGV.
Immunoglobulin V region.
DISULPIO
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Vrana M., Rudikoff S., Potter M.;
"Heavy-chain variable-region sequence from an inulin-binding myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annocation update)
16-JUL-1999 (Rel. 38, Last annocation update)
16 heavy chain V-III region ABE-47N.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Sciurognathi; Muridae; Musinae; Musi.
         15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V-III region B109.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TAXID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 92.9%; Score 91; DB 1; Length 113; Local Similarity 94.7%; Pred. No. 2.9e-08; es 18; Conservative 0; Mismatches 1; Indels
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P01799;
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HV30 MOUSE
ID HV30 MOUSE
DT 21-JUL
DT 21-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 16-JUL
DT 16-JUL
DT 18-JUL
DT
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RX VERIANCE.

RX WEDLINE=78158406; PubMed=417344;

RY VERIAN M.; Rudikoff S., Potter M.;

RY VERIAN M.; Rudikoff S., Potter M.;

RT Proceine.";

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Proceine.";

PROSEILANBOUS: THIS CHAIN WAS ISOLATED FROW A MYELOWA PROTEIN THAT CC.

EINDS INULIN.

RR HSSP: PO1810; ZFBJ.

DR HSSP: PO1810; ZFBJ.

DR InterPro; IPR00356; Ig_WHC.

DR InterPro; IPR00356; Ig_W.

BR Efan; PF00047; ig; 1.

DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region.

FT DISULFID ...
Vrana M., Rudikoff S., Potter M.;

"Sequence variation among heavy chains from inulin-binding myeloma proteins.";

"Droceins."; Acad. Sci. U.S.A. 75:1957-1961 (1978).

-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN.

PIR; A93818; AVMSAB.

R HSSP; POIGH10, 2PB.

InterPro; IPRO03096; Ig.V.

R InterPro; IPRO03096; Ig.V.

R SMART; SMO0406; IGv; 1.

Immunoglobulin V region.

P SMART; SMO0406; IGv; 1.

INON TER. 113 113

SEQUENCE 113 AA; 12675 MW; 76658C12ICS99285 CRC64;
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101737;
21-071-1986 (Rel. 01, Last sequence update)
21-071-1986 (Rel. 01, Last sequence update)
15-071-1999 (Rel. 38, Last annotation update)
15-071-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 2.9e-08;
Matches 18; Conservative 0; Mismatches 1; Indels
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113 113
113 AA; 12675 MW; 76658C121C598285 CRC64;
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HV29 MOUSE STANDARD; FRT; 113 AA.
AC P01798;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
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Best Local Similarity 94.74
Matches 18, Conservative
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113 113 AA; 12732 MW; 26618F626B59859E CRC64;
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P01804;
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P01803;
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                                                                                                                                             HV34 MOUSE
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Rudikoff S., Potter M.;
Rudikoff S., Potter M.;
"Immunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment.";
J. Immunol. 127:191-194(1981).
-1- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOWA PROTEIN THAT
                                                                                                                                                                                                                         Aimenoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                       MEDLINE=82099361; PubMed=6798111;
Johnson N., Slankard J., Paul L., Hood L.;
"The complete V domain amino acid sequences of two myeloma inulin-
                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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92.9%; Score 91; DB 1; Length 115;

Best Local Similarity 94.7%; Pred. No. 2.9e-08;

Matches 18; Conservative 0; Mismatches 1; Indels
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SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;
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01-OCT-1993 (Rel. 27, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G heavy chain V-III region T957.
                                                                             21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1986 (Rel. 38, Last annotation update)
119 heavy chain V-III region W3082.

Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
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PIR, A92810; AVMS57.

HSSP, P01810; 2FBJ.

InterPro; IPR003006; Ig_MC.

InterPro; IPR003596; Ig_V.

Pfam; PF00047; ig; 1.

SMART; SMO0406; IGv.

Immunoglobulin V region.

DISULFID 22 98 B
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    68
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    50 EIRLKSHNYATHYAESVKG
                                                          STANDARD;
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P01800;
                                                        HV33 MOUSE
P01802;
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                                               HV33_MOUSE
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Rudikoff S., Potter M.;

Rudikoff S., Potter M.;

Rudikoff S., Potter M.;

Immunoglobulin heavy chains from anti-inulin myeloma proteins:

revidence for a new heavy chain joining segment.";

U. Immunol. 127:191-194 (1981).

EL J. Immunol. 127:191-194 (1981).

EL MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN.

PRINDS INULIN.

PRINDS INULIN.

RISP; PO1789; IMPP.

RISP; PO17
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MEDLINE=81013937; PubMed=6251474;
MEDLINE=81013937; PubMed=6251474;
Bernard O., Gough N.M.;
"Nucleotide sequence of immunoglobulin heavy chain joining segments between translocated VH and mu constant regions genes.";
Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).
-i. MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1986 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 heavy chain V-III region HPC76 (Fragment).
18 heavy chain V-III region from the fragment of the frag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.-UU.-1986 (Rel. 01, Created)
21.-UU.-1986 (Rel. 01, Last sequence update)
21.-UU.-1996 (Rel. 38, Last annotation update)
15.-UU.-1999 (Rel. 38, Last annotation update)
1g heavy chain V region AMPC1.
Mus musculus (Mouse).
Mammalia (Mouse).
Mammalia Butharia Rodentia; Sciurognathi; Muridae; Murinae; Mus.
COTT. TaxID=10090;
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       Length 113;
                                                                                                                                                        2; Indels
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113 AA; 12691 MW; 7A6D906AAA966E9E CRC64;
Query Match

Best Local Similarity 89.5%; Pred. No. 1.9e-07;
Matches 17; Conservative 0; Mismatches 2;
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Matches 17; Conservative
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SEQUENCE FROM N.A. (H107).
MEDLINE-80199926; PubMed=6769593;
Early P., Huang H., Davis M., Calame K., Hood L.;
"An immunoglobulin heavy chain variable region gene is generated from three segments of DNA: VH, D and JH.";
Cell 19:981-992(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1996 (Rel. 01, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 heavy chain V regions TEPC 15/8107/HPCM1/HPCM2/HPCM3.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia; Sciurognathi, Muridae, Murinae, Mus. 11 TaxID=10090;
                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Rodentia; Sciurognathi, Muridae, Murinae; Mus. NCBI_TaxID=10090;
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MEDLINE-81197602; PubMed=7231520;

Gearhart P.J., Johnson N.D., Douglas R., Hood L.;

Gearhart P.J., Johnson N.D., Douglas R., Hood L.;

IgG antibodies to phosphorylcholine exhibit more diversity than their IgM counterparts.";

Nature 291:29-34 (1981).

-! - MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Match 49.0%; Score 48; DB 1; Length 122; Local Similarity 52.9%; Pred. No. 0.43; e.g. 9; Conservative 4; Mismatches 4; Indels
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MEDIJNE=76222762; PubMed=819932;

Rudikoff S., Potter M.;

Size differences among immunoglobulin heavy chains from phosphorylcholine-binding proceins.';

Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQÜENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;
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Rudikoff S., Barstad P., Potter M., Hood L.,
Unpublished results, cited by:
Hood L., Campbell J.H., Blgin S.C.R.;
Annu. Rev. Genet. 9:305-353(1975).
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                                                                                                                                          SEQUENCE.
MEDLINE=81054880; PubMed=6776528;
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InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SMO406; IGv; 1.
Immunoglobulin V region.
NON_TER 122
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52 RNKANDYTTEYSASVKG 68
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REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.
HSSP; P01789: 1MCP
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21-JUL.1986 (Rel. 01, Last sequence update)
15-JUL.1999 (Rel. 38, Last annotation update)
15-JUL.1999 (Rel. 38, Last annotation update)
19 heavy chain V region IR2 precursor.
Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TAXID=10116;
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BEDLINESBA064537, PubMed=6292865;
Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
"Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 10:6041-6049(1982).
-!- MISCELLANBOUS: THE MENA WAS ISOLATED FROM AN IGE-SECRETING
IMMUNOCYTONA THISES SPONTANBOUSLY IN LOU/C/WSL RATS.
PIR! A02075; EVRTR2.
                                                                                                                                                                                                                                                                                                                                      77.0%; Score 75.5; DB 1; Length 111; 89.5%; Pred. Nof. 1.1e-05; tive 0; Mismatches 1; Indels 1
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InterPro; IPR003006; Ig MHC.
InterPro; IPR003066; Ig_V.
Pfam; PP00047; ig; 1.
SWART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
                                                                                                           1 EIRLKSDNYATHYAESVKG 19
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nes 17; Conservative
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Matches 10; Conserv
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AC P01805;
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SEQUENCE
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1D HV21_MC
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DT 15-UUL.
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HV25 MOUSE
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HV25_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                       Barstad P.;
Thesis (1975), California Institute of Technology / Pasadena, U.S.A.
-!- MISCELLANGOUS: THIS CHAIN WAS ISOLATED FROM A WYELOMA PROTEIN THAT
BINDS PHOSPHORYLCHOLINE.
PIR; A02070; AVMSTS.
HSSP; P01789; LMCP.
InterPro; IPR003006; Ig_MRC.
InterPro; IPR003066; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv.
Immunoglobulin V region.
NON_TER 123 123
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region HPCM6.
Mus musculus (Wouse).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 03, Last annotation update)
15-JUL-1999 (Rel. 03, Last annotation update)
15 heavy chain V region H8.

Mus musculus (Mouse).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; MuschI_TaxID=10090;
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49.0%; Score 48; DB 1; Length 123;
Best Local Similarity 52.9%; Pred. No. 0.44;
Matches 9; Conservative 4; Mismatches 4; Indels
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Best Local Similarity 52.9%; Pred. No. 0.44;
Matches 9; Conservative 4; Mismatches 4; Indels
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                                                                                                          SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;
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MEDLINE-81197602; PubMed=7231520;
Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE
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          PIR, A02070; AVMST5.
HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003396; Ig_v.
Pfam; PF00047; Ig; 1.
SWART; SM00406; IGv; 1.
Immunoglobulin V region; Hybridoma.
NON_TER 123 123
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P01788;
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P01791;
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ID HV22 M

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DT 21-707.

DT 13-707.

DE 19 -807.

Mus mus

OC Eukaryo

OC Mammal.

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MEDLINE-81197602; PubMed=7231520;

Gearhart P.J., Johnson N.D., Douglas R., Hood L.;

Gearhart P.J., Johnson N.D., Douglas R., Hood L.;

"Igd antibodies to phosphorylcholine exhibit more diversity than
"Igd antibodies to phosphorylcholine exhibit more diversity than
"Independent of the phosphorylcholine of the phosphorylcholine.";

"In their IgM counterparts.";

"In their IgM counterparts.";

"In their IgM counterparts.";

"In NATURE 291:29-34(1981).

"In NOW TER.
"In their IgM counterparts.";

"In their Igm counterparts.
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RT "IgG antibodies to phosphorylcholine exhibit more diversity than their IgM counterparts.";

RL Nature 291:29-34(1981).

Nature 291:29-34(1981).

- HISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHOKYLCHOLINE.

DR HASP; PO1789; MPC.

RICHAPPO; IPRO03006; Ig_WHC.

REAPP: PRO047; ig; 1.

REAPP: PRO047; ig; 1.

RAMRT; SMORAT; Good of Ig_V.

RAMRT; SMON46; IGV; 1.

RAMRT; SMON46; IGV; 1.

RAMRT; SMON46; IGV; 1.

RAMRT; SMON46; IGV; 1.

REAPP: PRO047; ig; 1.

RAMRT; SMON46; IGV; 1.

RAMRT; SMON46; IGV; 1.

RAMRT; SMON46; IGV; 1.

REAPP: PRO046; IGV; 1.

RAMRT; SMON46; IGV; 1.

RAMRT; SMON46; IGV; 1.

RAMRT; SMON46; IGV; 1.

RAMRT; SMON46; IGV; 1.

RAMRT; RAMRT
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Best Local Similarity 52.9%; Pred. No. 0.44;
Matches 9; Conservative 4; Mismatches 4; Indels
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52.9%; Pred. No. 0.44;
cive 4; Mismatches 4
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 AA.
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Job time : 10.5 secs
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Best Local Similarity 52.2.
Best Local 9; Conservative
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			41	
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Q93nc6 myxococcus P82987 homo sapien

Q99119 xestia c-ni Q98615 hizobium 1 Q98616 hyphantria u O34751 bacillus au O55078 pyrococcus Q94783 oryza sativ O97289 plasmodium O69247 bacillus 1i O66071 bacillus 1i Q96079 drosophila Q94780 drosophila Q94780 drosophila Q94780 drosophila Q9480 drosophila Q9430 drosophila Q9430 drosophila Q940753 rattus norv Q940753 rattus norv Q9407 aratus norv Q9407 aratus norv Q9212 aratus norv Q9212 manabaena sp Q9212 mattus norv Q9212 mattus norv Q9212 mus musculu Q9212 mattus norv Q9212 sattus norv Q93180 spodoptera

OM protein

Run on:

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SEQUENCE FROM N.A.
STRAIN=BALB/C;
MEDLINE=2010447; PubMed=1922069;
MEDLINE=22010447; PubMed=1922069;
MEDLINE=2201047; PubMed=1922069;
Monthomologous recombination at sites within the mouse JH-Cdelta locus accompanies cmu deletion and switch to immunoglobulin D secretion.";
Mol. Cell. Biol. 11:5660-570(1991).
EMBL; M64568; AAA39341.1; -
HSSP; PO1799; 1MCP.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 68; DB 11; Length 64;
Pred. No. 0.00061;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 AA; 7594 MW; FE83625079AC2F28 CRC64;
                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
JH-Cdelta locus (Fragment).
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469 AA.
                                                                                                                                                                                                                                                                    ALIGNMENTS
                       Q9PZ19
Q98BT5
Q96360
                                                                                                   Q960N9
Q9VJ80
P70535
Q9UL88
                                                                                                                                                               Q8YXI3
O94206
                                                                                                                                                                                               Q920L2
Q921P5
Q9P196
Q8U0R3
Q9J8C9
Q9J8C9
                                                         059078
Q94F83
                                                                                                                                      Q9VA95
Q99UF7
                                                                                                                                                       O9EOL9
                                                                                                                                                                                         053670
                                                                                                                                                                                                                                                                                                              PRT;
                                                                           097289
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                                                                                                                               2 IRLKSDNYATHYAESVKG 19
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Best Local Similarity 72.2
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                   749
1074
11261
11288
11394
1485
751
131
1485
751
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751
1485
381
403
532
NCBI_TaxID=10090;
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SEQUENCE
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Q8R3V9
ID O8R3V
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Q61750
q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q88651 agrobacteri
Q45562 clostridium
O35037 archaeoglob
Q8tzk5 pyrococcus
Q92f6 streptococc
P7337 sprechocyst
P7337 sprechocyst
Q8yck5 brucella me
Q8yck5 anabaena sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q61750 mus musculu
Q87379 mus musculu
Q91xel mus musculu
Q91bz2 pseudomonas
Q91bz3 pseudomonas
Q91ds arabidopsis
Q91171 homo sapien
Q84x61 lymantria d
                                                        April 22, 2003, 12:47:43 ; Search time 38 Seconds (without alignments) 103.024 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
         GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                      671580 segs, 206047115 residues
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                                                                                                                                                                                                                Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
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                                          - protein search, using sw model
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Q9RBZ2
Q9RBZ3
Q9FND5
Q9FND5
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Q8U651
Q45962
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Q99ZF6
P73837
Q8YCK5
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Q8R3V9
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                                                                                                            1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                      Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mbc:*
sp_organelle:*
sp_phage:*
sp_plant:*
sp_codent:*
sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                           unclassified: *
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Match Length
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Minimum DB Maximum DB

Database

Searched:

Sequence:

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Gaps

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8 111 112 113 114 115

Result Š ô

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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Similarity to hear shock protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eutorophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=COLUMBIA;
MEDLINE=98069011; PubMed=9405937;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=20015131; PubMed=10545263;

Alarcon-Chaidez F.J., Penaloza-Varquez A., Ullrich M., Bender C.L.;

"Characterization of plasmide encoding the phytotoxin coronatine in Plasmid 42:210-22011999.

EMBL, AF169828, AAD50908.1; -.

Plasmid 42:210-22011999.

Plasmid 42:210-22011999.

Plasmid 42:210-22011999.

Plasmid 43:210-22011999.
SEQUENCE FROM N.A.

STRAIN=204180;
MEDIJNE=20015131; PubMed=10545263;
Alarcon-Chaidez F.J., Penaloza-Vazquez A., Ullrich M., Bender C.L.;
Forazacterization of plasmids encoding the phytotoxin coronatine in Pseudomonas syringee.";
Plasmid 42:210-220(1999).
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                               50.0%; Score 49; DB 2; Length 361; 52.6%; Pred. No. 6.7; tive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.0%; Score 47; DB 2; Length 357; 58.8%; Pred. No. 14; 6; Indels tive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 AA; 40339 MW; F21B4028AA5A9BD2 CRC64;
                                                                                                                                                                                            361 AA; 41448 MW; 0416AA0203BE5A27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Transposase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             syringae (pv. glycinea)
                                                                                                                                                  EMBL; AF170066; AAD50977.1; -. Plasmid.
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Best Local Similarity 58.8
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                 10; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas
                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9RBZ3
Q9RBZ3;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 20, Last annotation update)
Unknown (Protein for IMAGE:4224494) (Fragment).
Mus musculus (Mouse).
Eukaryocta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1S870-like transposase.
Pseudomonas ayringae (pv. glycinea).
Plasmid p4180A.
Bacteria; Proteobacteria; gamma subdivision; Fseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                   Score 51, DB 11; Length 469;
Pred. No. 4.2;
3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL, BCO24405. AAH24405.1; -. Hypothetical protein. SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;
                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypotherical 52.0 kDa protein.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 55.6%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas.
NCBI_TaxID=318;
[1],
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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09RB2
1D 09RB
AC 09RB
AC 01-M
DT 01-M
DT 01-D
D 10-D
D 1
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Gaps

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RESULT 7 Q9UL71

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SEQUENCE FROM N.A. Denlings D.L., Lee K.-Y., Horodyski F.M., Valaitis A.P., Horodyski F.M., Valaitis A.P., Horodyski F.M., Valaitis A.P., Horotain of the insect immune protein hemolin and the high induction during embryonic diapause in the gypsy moth,
                                                                                                                                                                                                                                               45.9%; Score 45; DB 5; Length 422; 53.3%; Pred. No. 37;
                                                             Lymantia dispar.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR453868; AR149765.1;
InterPro; IPR003599; Ig.
InterPro; IPR03599; Ig.
InterPro; IPR033599; Ig.
Efam; PP0047; ig; 3.
SMART; SM00409; IG; 3.
SMART; SM00409; IGC; 3.
                                                                                                                                                                                                                 422 AA; 47234 MW; ODC52EC4BF142617 CRC64;
                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                     1 EIRLKSDNYATHYAE 15
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42 EVRFKADNYSTALLE
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pTiC58.
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                                                                                                                                                                                                                                                    Query Match
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Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia,
Noctuoidea, Lymantriidae, Lymantria.

[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
             "Structural analysis of Arabidopsis thaliana chromosome 5. II. Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned Pl clones.";
DNA Res. 4:291-300(1997).
EMBL, AB016702; BAB11602.1; -...
EMBL, AB017062; BAB11602.1; JOINED.
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                    46.9%; Score 46; DB 10; Length 2910; 60.0%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

BEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                      Q9UL/1;
0-1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 121; Score 45; DB 4; Length 121; Local Similarity 50.0%; Pred. No. 8.7; Pred. No. 8.7; Pred. 8; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                     4; Indels
                                                                                                                                    2910 AA; 325351 MW; A847EC3FE1427DF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035043; AAD56279.1; -.
HSSP: PO1772; 2F84.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_V.
Ffam: PF0017; ig; 1.
RONN TER
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                                                                                                                                                                                                                                                                                                                                                        121 AA
                                                                                                                                                                                                     2; Mismatches
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                                                                                                                                                                                     Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LKSDNYATHYAESVKG 19
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51 ISGDGGSTYYADSVKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                             297 LKEDNHQEEYAESVE 311
                                                                                                                                                                                                                                      4 LKSDNYATHYAESVK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                      Heat shock.
     Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                      SEQUENCE
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Q8WR61;
                                                                                                                                                                       Query Match
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MEDINES-1608551; PubMed=11743194; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Hahling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchowk O., Epp A., Liu F., Houmiel X., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.; "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens CSB."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=2160850; PubMed=11741193; Monks D.E., Kitajima J.P., Mood D.M., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Moo L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Zhou Y., Chen Y., Easen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 450;
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EMBL; AE007935; AAK31044.1; -.
Monooxygenase; Plasmid; Complete proteome.
SEQUENCE 450 AA; 50163 MW; D3ADB8261D68C026 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Nitrilotriacetate monooxygenase, component A.
                                                                                                                                                                    ATU6084 OR AGR PTI 161.
Agrobacterium tumefaciens (strain C58 / ATCC 33970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
40;
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Matches

RESULT 8

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Nature 390;364-370(1997).
EMBL; AE001010; AAB89893.1;
EMBL, AE000956; AAB89112.1;
TIGR; AF21352; -.
TIGR; AF2139; -.
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                                                                                                                                                                                                                                                                                                      7 DNYATHYAESVK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus furiosus
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SEQUENCE FROM N.A.
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NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1314;
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Matches
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Q99ZF6
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MEDLINE=9804943; PubMed=9389475;

MEDLINE=9804943; PubMed=9389475;

MEDLINE=9804943; PubMed=9389475;

MEDLINE=9804943; PubMed=9389475;

MEDLINE=9804943; PubMed=9389475;

MECHAN R.A., Dodgen R.J., Gwinn M., Hickey B.K., Peterson J.D.,

MICHAGES D., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Pleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness B.R., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Kirkness B.R., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Kirkness B.R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Pujii C., Garland S.A.,

Wentex J.C.,

Wentex J.C.,
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      Gaps
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SEQUENCE PROM N.A.
STRAINS-ING 7423.
Brehm J.K., Pennock A., Young M., Cultram J.D., Minton N.P.;
Brehm J.K., Pennock A., Young M., Cultram J.D., Minton N.P.;
Physical characterisation of the replication origin of the cryptic
plasmid open of the cryptic plasmid or of 100 (10).
EMBL, X62684; CAA44562.1; -.
Brania O.O-0(0).
From Characterisation of the replication of the cryptic
plasmid or of 100 (10).
Plasmid.
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                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Frinicutes, Bacillus/Clostridium group, Clostridia, Clostridiales, Clostridiaceae, Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 2; Length 362;
Pred. No. 45;
2; Mismatches 4; Indels
         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 AA; 43052 MW; FC8A02436E259A49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Archaeota; Archaeoglobi; Archaeoglobales; Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                 362 AA
      Mismatches
                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                               PRT;
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         3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 53.8 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
         Conservative
                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaeoglobus fulgidus.
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                                                                                                                                                                                                                                                                                                                                               Clostridium butyricum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EIRLKSDNYATHY 13
                                             7 DNYATHYAESVK 18
                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   Plasmid pCB101.
      7;
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035037
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Q45962
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      Matches
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STRAIN=SEPTO / ATCC 700294 / SEROTYPE M1;
MEDINE=2192684; Dubmed=11296296;
MEDINE=2192684; Dubmed=11296296;
MEDINE=2192684; Dubmed=112966296;
Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Zworov A.N., Kenton S., Lai H.S., Lin S.P., Ojan Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenee.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                               Gaps
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Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Straptococcaceae; Straptococcus.
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STRAIN=VCI / DSM 3638 / ATCC 43597 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
BHJ, ABC10292; AAABS110.1;
Hypothetical protein; Complete proteome.
SEQUENCE 290 AA; 34518 MW; 7697BAS8D6794B7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.9%; Score 43; DB 17; Length 290;
61.5%; Pred. No. 51;
ive 1; Mismatches 4; Indels
                                                                                                                                                    Length 182;
                                                                                                                                                                                                                   2; Indels
InterPro, IPR001584; Rve.
Pfam, PR0665; rve; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 182 AA; 20733 MW; 860E5DBDE445CDE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein PF1986.
                                                                                                                                                 43.9%; Score 43; DB 17;
58.3%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 AA.
                                                                                                                                                                                                                   3; Mismatches
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8; Conservative
                                                                                                                      Query Match
Best Local Similarity 56.3.
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us-09-674-716b-11.open.rspt

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Query Match
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**MEDLINE=97061201; PubMed=8905231;

**MEDLINE=97061201; PubMed=8905231;

**Raneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Miyajima N., Hirosawa M., Sugiura M., Fasamoto S., Kimura T.,

Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,

Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
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                                                                                                                                                                                                                                                            DB 16; Length 310; 56;
                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001258; NHL.
Pfam; PF01436; NHL, 3.
Hypothetical protein; Complete proteome.
SEQUENCE 474 AA; 53482 MW; 52B2F006F34BE7ED CRC64;
                                                                                                                                                                                                  310 AA; 36047 MW; 4A9A7C575CF2B47D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
BMBIJ0523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 02, Created)
(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
EMBL, AB006564; AAKA4105.1; -.
InterPro; IPR002606; FAD_Synth.
Pfan; PF01687; FAD_Synth; 1.
ProDom; PP003662; FAD_Synth; 1.
TIGRFAMS; TIGR00083; FibF; 1.
Complete proteome.
SEQUENCE 310 AA; 36047 WW; 4A9A7C575CF2B47D C3
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                                                                                                                                                                                                                                                         h 43.9%; Score 43; DB Similarity 37.5%; Pred. No. 56; 6; Conservative 7; Mismatches
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STRAIN=16M / ATCC 23456 / BIOTYPE 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (strain PCC 6803)
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87 EVSVKSDAYAEHFLAKPTG 105
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Matches 8; Conservative
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Best Local Similarity
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01-FEB-1997
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08YCK5
1D 09YCK
AC 08YCK
DT 01-MA
DT 01-MA
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OC BRILLI
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P73837
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RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N. Anderson I. Bhatacharya A., Iykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Salkov B., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N. O'veallaghan D., Letesson J.-J.,
RT G. Brucella melitensis.";
RT Brucella melitensis.";
RT Brucella melitensis.";
RT Brucella melitensis.";
RM EMBL; AE009688; AALS3765.1; --
DR InterPro; IPR001637; GlnA adenyltn.
DR ProDom; PD001057; GlnA adenyltn.
COMPLET OF PRODOM; PD001057; GlnA adenyltn.
DR ProDom; PD001057; GlnA adenyltn.
COMPLET OF STORE A.S. SCORE 43; DB 16; Length 476;
Best Local Similarity 47.4%; Pred. No. 92;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps

QY 1 EIRLKSDNYATHYARSVKG 19
DD 261 EAALKHDMYATFWAKPIQG 279
Search completed: April 22, 2003, 12:53:52
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Light chain CDR H2	Mouse anti-CD23 MA	Antibody 33F12 cat	Humanised anti-CD2	Mouse germline hea	Mouse antibody 38C	BW 835 VH. Synthe	SM3 heavy chain va	Amino acid sequenc	Lead binding MAb 4
SUMMARIES			ΙD	AAY32258	AAY32260	AAB50426	AAY32263	AAE06973	AAB50425	AAR34018	AAY03869	AAW46958	AAW01589
			DB	21	21	22	21	22	22	14	20	19	18
			Match Length DB ID	19	137	286	444	100	299	115	116	119	120
	æ	Query	Match	100.0	100.0	100.0	100.0	96.9	96.9	94.9	94.9	94.9	94.9
			Score	96	86	86	86	95	95	93	93	93	93
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2G3 hybridoma VH d MAD Br-3 heavy cha Mouse Br-3 heavy c Br-3 Heavy Chain PS-23 single chain PS-23 single chain 3B10xPS-23 bispeci Antibody ABX-CBL h Murine PSCA antibo Mouse heavy chain MAD 4197X heavy ch Anti-cataract immu Heavy chain variab Heavy chain variab 113F1 hybridoma VH Lead binding MAD 7 Scaffold protein S A3 derivative #15, Murine anti-TNYBa1p Humanised CA2 heav Heavy chain variab Hawy chain variab Assertion anti-TNYBa1p Humanised CA2 heav Heavy chain variab Hawy chain variab Antine anti-TNYBa1p Humanised CA2 heav	Mouse heavy chain Anti-TNF antibody Chimeric antibody Heavy chain variab Mouse Mab IC11 H c VH region of Ab to 14G1 heavy chain v Anti-dangyl single 8019 VH antibody. H. pylori 26 kDa p H. pylori 26 kDa p
21 AAV90812 28 AAW6212 29 AAW86259 21 AAU72866 21 AAU72866 22 AAU52866 22 AAU52866 22 AAS55297 22 AAS55297 22 AAS55297 23 AAU76696 16 AAR70829 11 AAR70829 11 AAR20816 21 AAR30816 21 AAR30816 22 AAS5410 22 AAS5410 23 AAR30816 24 AAR30816 25 AAX5440 26 AAX4089 27 AAX684 28 AAX2244 28 AAX2244 28 AAX2244	22 AAE10850 22 AAG67763 22 AAG67763 12 AAR12358 14 AAR13484 17 AAR30484 17 AAR30488 18 AAR3689 19 AAM6485 21 AAB10002
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# ALIGNMENTS

CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; conplementerarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; glomerulonephritis; crohn's disease; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sydgren's syndrome; allergy; aschma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy. Light chain CDR H2 of mouse anti-CD23 MAb C11. AAY32258 standard; Peptide; 19 AA. 98GB-0009839. 99WO-GB01434 15-FEB-2000 (first entry) (GLAX ) GLAXO GROUP LTD. Mus musculus. WO9958679-A1. 07-MAY-1999; 09-MAY-1998; 18-NOV-1999. AAY32258;  Shearin J;

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This sequence represents the heavy chain variable region (VH) of murine anti-CD23 (FCERII) monoclonal antibody Cl1. The invention provides altered antibodies, such as chimeric or humanised antibodies, such as chimeric or humanised antibodies (see AAY32263 which comprises sufficient of the antibodies (see AAY32263), which comprises sufficient of the antibodies (see AAY32264 59) to render them capable of binding to the CD21 type II molecule expressed on capable of binding to the CD21 type II molecule expressed on the CD23 formation in human therapy, for the treatment of arthritis, lupus erythematous, Habilmoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermaitis, psoriasis, uritoaria, nephrotic syndrome, glomerulomephritis, inflammatory bowel disease, ulcerative colitis, crohn's disease, Sjogren's syndrome, allergic asthma, intrinsic asthma, acte asthmatic exacerbation, rhinitis, ecema, graft-versus-host disease, COPD, insulitis, bronchitis containing the proncit chambetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                             Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 98; DB 21; Length 137; 100.0%; Pred. No. 1.4e-08; ive 0; Mismatches 0; Indels C
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targeted drug delivery.
                                                                                                                                                                                                                          Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB50426 standard; Protein; 286 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Fig 1; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-2000; 2000WO-US14366.
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                                                            99WO-GB01434.
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                                                                                                                                                                       (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                    WPI; 2000-053101/04.
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                                                         07-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                     This sequence represents complementarity determinating region 2 antibody C11 (see also AAY32263). The linention provides altered antibodies, such as chimeric or humanised antibodies, which comprise authodies, such as chimeric or humanised antibodies, which comprise the subdies is such as chimeric or humanised antibodies, which comprise the sufficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to render them capable of binding to the CD23 type II molecule expressed on haemacopoietic cells. The antibodies of type II molecule expressed on haemacopoietic cells. The antibodies of type II molecule expressed on haemacopoietic cells. The antibodies of abetes, uveitis, dermatitis, portasis, multiple sclerosis, diabetes, uveitis, dermatitis, profiles, untiliple sclerosis, colitis, Crohn's disease, sinflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjognen's syndrome, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, cathma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, (particularly chronic bronchitis) or diabetes (particularly type II diabetes), and B-cell malignancies (claimed). They are also useful certaining the binding acute of the expension of the binding acute of the collines between CD23 and various ligands and
                                                                                                                                        Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy, asthma; rhinitis; eczema; insulitis; graft.vergus-host disease; COPD; bronchitis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 98; DB 21; Length 19; 100.0%; Pred. No. 1.4e-09; ive 0; Mismatches 0; Indels
      Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse anti-CD23 MAb C11 heavy chain variable region.
   Rapson NI,
   Bonnefoy JMP, Crowe SJ, Ellis JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY32260 standard; Protein; 137 AA.
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78..96
/note= "CDR H2"
129..131
/note= "CDR H3"
                                                                                                                                                                                                                             Claim 1; Page 40; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        determining the binding agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B-cell malignancy; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-FEB-2000 (first entry)
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Les 19; Conservative
                                                            WPI; 2000-053101/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 AA;
                                                                                        N-PSDB; AAZ34743
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Query Match

Best Loca Matches

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AAY32260 RESULT

Region Region Region

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Gaps

"CDR 3"

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                                                                                                                           The present sequence may be used in the activation of new ketone prodrug compounds containing active agents. The ketone derivatives are useful as carriers for antitumour agents such as cytocoxic agents, where the antitumour agent is a microtubule stabilising agent such as paclitaxel, epothilone or its therapeutically active analogue or an anthracycline antibiotic such as doxorubicin or its therapeutically active analogue. The ketone derivatives are useful for targeted drug delivery. The inactive molecules in the ketone compounds are converted to active molecules by retro-Michael reaction. The antibody has bifunctional activity and specifically immunoraects with cell surface antigen of a target cell. The active ingredients can be mixed effectively with excipients as per deelired amount along with the buffering agent to enhance the effectiveness and activity of the
                                                                                                                                                                                                                                                                                                                                                          0; Indels 0; Gaps
                                                                     New ketone compounds containing active agents useful as carriers for e.g. antitumor agents, antibiotics or fluorescent molecules -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        urticaria; nephrotic syndrome; glomerulonephritis;
inflammatory bowel disease; ulcerative collitis; Crohn's disease;
Sjogren's syndrome; allergy, asthma; rhinitis; eczema; insulitis;
graft-versus-host disease; COPD; bronchitis; diabetes;
                                                                                                                                                                                                                                                                                                                                  100.0%; Score 98; DB 22; Length 286; 100.0%; Pred. No. 3.4e-08; ive 0; Mismatches 0; Indels C
             Lerner RA;
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/note= "framework region 3"
101..103
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/note= "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36..49
/note= "framework region
             List B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised anti-CD23 MAb C11 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY32263 standard; Protein; 444 AA.
                                                                                                         Disclosure; Fig 10; 45pp; English.
             Rader C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "CDR 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50..68
/note= "CDR 2"
                                                                                                                                                                                                                                                                                                                                                                                                 203 EIRLKSDNYATHYAESVKG 221
                                                                                                                                                                                                                                                                                                                                                                                   1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B-cell malignancy; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31..35
/note=
             Barbas CF, Shabat D,
                                     WPI; 2001-061339/07.
                                                                                                                                                                                                                                                                                                              286 AA;
                                                 N-PSDB; AAC90472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                       compound
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                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
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This amino acid sequence represents the heavy chain of humanised anti-CD23 (FCERII) monoclonal antibody Cl1, composed of a human cramework (HSIGKIVI) and the heavy chain complementarity determining regions (see AAY32257-59) of murine antibody Cl1. The DNA was constructed by splice overlap FCR. The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of the Cl1 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on capable of binding to the CD23 type II molecule expressed on capable of binding to the CD23 type II molecule expressed on capable of antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, upon erythematosus, Hashimco's thyroiditis, multiple sclerosis, upuse erythematosus, Hashimco's thyroiditis, multiple sclerosis, upuse erythematosus, Hashimco's thyroiditis, multiple sclerosis, upuse erythematosus, Hashimco's thyroiditis, multiple sclerosis, capabees, uveitis, dermatitis, inflammatory bowel disease, ulcerative colitis, crohn's disease, Sjogren's syndrome, allergies, allergie asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, cecema, graft-versus-host disease, COPD, insulitis, bronchitis asthma, and B-cell malignancies (claimed). They are also useful for studdying interactions between CD23 and various ligands and consistent and becall malignancies (claimed). They are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor specific antibodies useful for treating e.g. arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse germline heavy chain variable (VH) region, V(H) 22.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                   /note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes, multiple sclerosis and psoriasis
                                                                                                              /note= "constant region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Fig 4; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                98GB-0009839.
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                                                                                                                                                                                                                                                                                                                                          99WO-GB01434.
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Matches 19; Conservative
                                                                          . 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLAX ) GLAXO GROUP LTD
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                                                                                                                                                                                            W09958679-A1
                                                                                                                                                                                                                                                                                                                                             07-MAY-1999;
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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglabulin of human origin. The manised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating thy infection. The proteins of the invention are useful for inhibiting or treating cleukocyte trafficing, for treating CCR2-mediated disorders such as their inhibiting restences; attended antibiding restences; attended disorders such as their for inhibiting restences; attended allocation of a medicament for treating CCR2-mediated disorders such as arthritis and multiple setences; attended allocation of a medicament for treating CCR2-mediated disorders cand in the manufacture of a medicament for treating allergy, anaphylaxis, and in the manufacture of a medicament for treating allergy, anaphylaxis, malignancy, chronic and acute inflammatory glomerulopathies, acquired increvention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neurointimal hyperplasia of a vessel in a mammal, and inhibiting neurointar intervention.

The present sequence is mouse germline heavy chain variable (VH)
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multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibroric disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neolintimal hyperplasia; VH; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                               O'Keefe T;
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                                                                                                                                                                                                                                                                                                                                                               Jones ST, O'Brien S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 152-153; 183pp; English.
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                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                  03-FEB-2000; 2000US-0497625.
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                                                                                                                                                                                                                                                                                                                                                               Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488888/53.
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Matches
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The present sequence may be used in the activation of new ketone prodrug compounds containing active agents. The ketone derivatives are useful as carriers for antitumour agents such as cytotoxic agents, where the antitumour agent is a microtubule stabilising agent such as paclitaxel, espointions or its therapeutically active analogue or an anthracycline antibiotic such as doxorubicin or its therapeutically active analogue. The inactive molecules in the ketone compounds are converted to active molecules by retro-Actable reaction. The antibody has bifunctional activity and specifically immunoreacts with cell surface antigen of a target cell. The active inspecifients can be mixed effectively with excipients as per desired amount along with the buffering agent to enhance the effectiveness and activity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                         New ketone compounds containing active agents useful as carriers for e.g. antitumor agents, antibiotics or fluorescent molecules -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                38C2; ketone compound; antitumour; cytotoxic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody, MAb; hybridoma; lung; adenocarcinoma; mammary; ovary; prostate; polymorphic epithelial mucin; PEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.9%; Score 95; DB 22; Length 29:
94.7%; Pred. No. 1.1e-07;
.....marches 0; Indels
                                                                                                                                                                                                                      Lerner RA;
                                                                                                                                                                                                                      m'
                                                                                                                                                                                                                      List
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR34018 standard; Protein, 115 AA.
                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 9; 45pp; English
                                                                                                                                                                                                                      Rader C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 EIRLRSDNYATHYAESVKG 223
                                                                                                                                        24-MAY-2000; 2000WO-US14366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91DE-4133791.
                                                                                                                                                                   99US-0318661.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 94.7 nes 18; Conservative
                                                                                                                                                                                            (SCRI ) SCRIPPS RES INST
              Mouse; antibody 38C2; 
targeted drug delivery
                                                                                                                                                                                                                      Shabat D,
                                                                                                                                                                                                                                                WPI; 2001-061339/07.
N-PSDB; AAC90471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 AA;
                                                                                 WO200071556-A1
                                                                                                                                                                   25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE4133791-A
                                                                                                             30-NOV-2000
                                                                                                                                                                                                                      Barbas CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BW 835 VH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR34018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                         Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Gaps

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Length 116;

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binding fragment of the SM3 antibody bound to a peptide recognised by the epitope binding site of SM3. The products and methods can be used to develop agants for the detection of tumour calls and for therapy against tumours. MUCl epitope minics can also be used to prevent or decrease immune response, e.g. in the therapy of diseases caused by autoimmune responses (such as arthritis, multiple solerosis, asthma or disbates), allergies, inflammatory disorders or transplant rejections such as graft versus host disease. The present sequence represents the amino acid sequence of a heavy chain variable region of SM3 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a synthetic branched mucin type glycolipid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Branched mucin type glycolipid; V region; heavy chain; antibody; cancer treatment; diagnosis.
                                                                                                                                                                                                                Score 93; DB 20; Length lire
Pred. No. 7.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW46958 standard; Protein; 119 AA.
                                                                                                                                                                                                                                   94.9%;
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Matches 18; Conservative
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                 50 EIRLKSNNYATHYAESVKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 AA;
                                                                                                                                                                                                  Sequence 116 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW46958;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a process for preparing a crystal using cadmium. Structure factors or structural coordinates obtained from the crystal of SM3 antibody bound to an epitope can be used to design mimics of the antibody or the epitope. The crystals—comprise at least an epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM3 antibody; epitope; mimic; crystal; tumour; MUC1 epitope; allergy; immune response; arthritis; multiple sclerosis; asthma; diabetes; inflammatory disorder; transplant rejection; graft versus host disease.
                                                                                                                                                                                                                                                                                              835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New SM3 antibody crystal structures - used to develop agents for treating e.g. tumors, autoimmune disorders, allergies, inflammatory disorders or transplant rejection
                                                                                                                                                                                                                                                                                          Monoclonal antibody BW 835 is produced by hybridoma cell line BW 8 The antibody strongly reacts with lung adenocarcinomas and human mammary-, overy- and prostate carcinomas. It additionally reacts with polymorphic epithelial mucin (PEM) but does not react with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sternberg MJE;
                                                                                                                                                                              New monoclonal antibody BW835 specific for tumour antigens useful for diagnosis and treatment of tumours affecting the breasts, ovaries, prostate and lungs
                                                                                                                                                                                                                                                                                                                                                                                                                                             94.9%; Score 93; DB 14; Length 115; 94.7%; Pred. No. 7.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 279-280; 316pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMCR ) IMPERIAL CANCER RES TECHNOLOGY
                                                                                        Seemann G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY03869 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                             Disclosure; Fig 1a; 24pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM3 heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EIRLKSDNYATHYAESVKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                        Bosslet K, Pfleiderer P,
                                                   (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-204650/17.
                                                                                                                           WPI; 1993-127068/16.
N-PSDB; AAQ40046.
                                                                                                                                                                                                                                                                                                                                                                           normal human tissue
                                                                                                                                                                                                                                                                                                                                                                                                              115 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-AUG-1998;
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                 11-OCT-1991;
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                                                                                                                                                                         The present sequence represents a branched mucin type synthetic glycolipid. A gene fragment encoding the V region of the heavy chain of an antibody recognising the present protein is claimed. The antibody gene fragment is useful for the development of cancer treatments and diagnosing agents.
Recognising branched mucin type synthetic glycolipid - using gene fragment of an antibody, useful in cancer treatment and diagnosis
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                                                                                                                     Disclosure; Pages 4-5; 6pp; Japanese.
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specific binding assay, affinity purification; drug targeting, toxin targeting, imaging; genetic; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1; 57pp; English.
                                                                                                                                                                  86US-0842476.
88US-0190778.
84US-0577976.
85US-0690750.
94US-0288981.
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                                                                                                                                        95US-0483749
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                                                                                                                                                                                                                                                                                                                               WPI; 2000-338508/29
                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 AA;
                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA38896
                                                                                                                                                                                                                                                                                                                                                                                                        treating cancer
                                                                                                                                                                    21-MAR-1986;
08-MAY-1988;
08-FEB-1984;
11-JAN-1985;
11-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-1988;
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                                                 Homo sapiens
                                                                                                                                        07-JUN-1995;
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                                                                              US6054561-A.
                                                                                                            25-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                 Ring DB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents the heavy chain variable region for monoclonal antibody (Nab) 488, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from mouse hybridoma cells. The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or meutralising the heavy metals in biological and inanimate systems. It can be used in such compositions as perfumes, commerciae, plarameceuticals, health care products, skin treatment products, pseticides, health care products, skin the products, pseticides, health care products and production of semi-conductor and integrated circuit components and production materials for electronic components. The products can provide for applications involving minute amounts of specific heavy metals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen binding site; immunoglobulin; cancer antigen; immunological; antibody; tumour; human; mucin; cancer; cytostatic; hybridoma;
                                                                                                                       Monoclonal antibody; Fd fragment, lead cation; perfume, cosmetic; pharmaceutical; health care; skin treatment; pesticide; herbicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy metals, such as lead cations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.9%; Score 93; DB 18; Length 120; 94.7%; Pred. No. 8.3e-08; ive 1; Mismatches 0; Indels
                                                                                         Lead binding MAb 4E8 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2G3 hybridoma VH domain SEQ ID NO:2. ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 81; 125pp; English.
AAW01589 standard; Protein, 120
                                                                                                                                                                                                                                                                                                                                                                                          Wylie DE;
                                                                                                                                                                                                                                                                                                            95US-0541373.
95US-0462798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 EIRLKSNNYATHYAESVKG 68
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                                                           22-AUG-1997 (first entry)
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Best Local Similarity 94.77
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                           (BION-) BIONEBRASKA INC.
                                                                                                                                                                                                                                                                                                                                                                                         Lopez O, Murray PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-043140/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT58263.
                                                                                                                                                                                                                                                                                05-JUN-1996;
                                                                                                                                                                                                                                                                                                            10-OCT-1995;
05-JUN-1995;
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                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                   WO9639518-A1
                                                                                                                                                        heavy metal.
                                                                                                                                                                                                                                               12-DEC-1996.
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                               AAW01589;
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AAY90812
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The present invention describes a monoclonal antibody (Mpb) (1) that binds to a human breast cancer antigen that is also bound by Mbb 454C11 and 52C29 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also described is a hybridoma that produces (1). (1) is useful in specific binding assays, affinity purification, drug or toxin targeting, imaging, and genetic or immunological therapeutics for various cancers. The present sequence represents a VH domain derived from a 2G3 hybridoma, which is used in the exemplification of the present invention.
Monoclonal antibody capable of binding to human breast cancer antigen useful for affinity purification, drug or toxin targeting, imaging, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric antibody; monoclonal antibody; Br-3; antibody engineering; tumour; antigen; breast carcinoma; colon carcinoma; ovary carcinoma; cancer; diagnosis; therapy; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW06212 standard; Protein; 142 AA.
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88US-0240624.
88US-0241744.
88US-0243739.
88US-0253002.
89US-0367641.
89US-0382768.
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06-JUN-1995; 95US-0466034.
                                                                                                                                                                                                                                                                                                                                                                       1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                     69 EIRLKSNNYATHYAESVKG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                           treatment of human cancer.
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                              Better MD, Chang CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1990-115825/15.
N-PSDB; AAQ08605.
                                                                   WPI; 1999-044574/04.
                                                                                                                                                                                                                                                                                                 142 AA;
                      (XOMA ) XOMA CORP
                                                                                 N-PSDB; AAV71155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-1988;
19-JUN-1989;
21-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ITGE-) INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Better MD,
                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR09423;
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR09423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ď
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                                                                                                                                                                                                                                      The heavy chain variable region (AAW06212) of mouse monoclonal antibody Br-3 is the product of a cDNA clone (AAP149437) isolated from a Br-3 hybridoma cDNA library. MAD Br-3 (IGG1) binds to an antigen that is expressed on the surface of human lung, breast, colon and ovary carcinomas, but not on most normal adult tissues. The heavy chain and light chain variable regions (see also AAW06211) of B38-1 can be linked to human constant regions and expressed in transformed host cells. Novel mouse-human chimeric antibodies (see also AAW06209-10 and AAW06213-18) can be produced that have specificity to human tumour antigens and can be used for the treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                             Chimeric mouse-human antibodies - recognise a human tumour antigen, used for the treatment and diagnosis of human cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heavy chain variable region; murine antibody Br-3; antibody ING-1; chimeric immunoglobulin; human tumour antigen; chimeric antibody; treatment; human cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

Best Local Similarity 94.7%; Pred. No. 1e-07;

Matches 18; Conservative 1; Mismatches 0: Indels
                                                                                                                     Robinson RR;
                                                                                                                      Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse Br-3 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ļ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW85059 standard; Protein; 142 AA.
                                                                                                                      Horwitz AH,
                                                                                                                                                                                                                  Example 3; Fig 15; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89WO-US03852.
88US-0240624.
88US-0241744.
88US-0243739.
88US-0253002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89US-0367641.
89US-0382768.
94US-0364001.
88US-0240624.
88US-0241744.
88US-0253002.
89US-0357641.
89US-038764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                              diagnosis of human cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 EIRLKSNNYATHYAESVKG
                                                                                                                      Better MD, Chang CP,
                                                                                                                                             WPI; 1997-011249/01.
                                                                                                                                                                                                                                                                                                                                                                                     142 AA;
                                                                                               (XOMA ) XOMA CORP.
                                                                                                                                                         N-PSDB; AAT43437
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21-JUL-1989;
27-DEC-1994;
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 06-SEP-1988;
08-SEP-1988;
13-SEP-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-1988
04-OCT-1988
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                                                19-JUN-1989
                                    04-0CT-1988
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW85059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric mouse-human antibodies - prepd. using genes coding for constant human region murine variable region, esp. to 3 tumour
                                                                                                                                                                              Chimeric antibody specific for human tumour antigen - useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 93; DB 20; Length 142; Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chang CP;
Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
Lei S,
                                                                                                                                                                                                                             immunoassay, imaging or antitumour agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR09423 standard; Protein; 143 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Br-3 Heavy Chain V Region (mouse).
Horwitz AH,
                                                                                                                                                                                                                                                                                               Example 3; Fig 15; 92pp; English.
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The invention relates to a multifunctional polypeptide comprising a domain with a blinding site that specifically recognises an extracellular group of the NKG2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multifunctional polypeptides comprising binding sites that specifically recognise extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating cancers and infectious diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kufer P, Riethmueller G, Lutterbuese R, Borschert K, Kischel R;
Mayer M, Hofmeister R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Fig 16; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2001; 2001WO-EP03414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAR-2000; 2000EP-0106467.
                                                                                                                                                                                                                                                                                                     26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                        P5-23 single chain Fv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-055119/07.
N-PSDB; AAS97144.
                                                                                                                                                        Local Similarity
es 18; Conserv
                                                                                                                               Sequence 143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KUFE/) KUFER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200171005-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001.
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polynucleotide are used for the preparation of a pharmaceutical composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, larynx, breast, ovary, uterus, cervix, prostate, Kidney, testis, thyroid, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, soctoaca or helmhiths. The autoimmune diseases, bacteria, fungi, sclerosis, Grave's disease, antklosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent diabetes mellitus, rhummatoid arthritis, pemphigus vulgaris and autoimmune hepatitis. Sequences AAU72820-AAAU72875 represent the NKGZD receptor and the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.77
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
         8888888888888
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                                                                                                              The sequence is used in the prodn. of a chimeric antibody mol. comprising two light chains and two heavy chains, each having a constant region (human) and a variable region (murine) having specificity to an antigen bound by murine monoclonal antibody (MAD) Br-3. The chimeric antibodies can be used for any purpose for which the oxiginal murine MADs can be used, with the advantage that they are more compatible with the human body. They are esp. used for the diagnosis and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.9%; Score 93; DB 11; Length 143; 94.7%; Pred. No. 1e-07; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                        Claim 13; Page 123 + Fig 15; 173pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 EIRLKSNNYATHYAESVKG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                   antigen
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Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahopatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; tetsis; thyroid; bladder; brain; melanoma; myeloma; Fv; sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytostatic; antimicrobial; immunomodulatory; llB2D10; 6H7E7; 8G7C10; ESSA7; 11B2D10; 47; 8G7C10x4-7; 8G5A7; 11B2D10; 6H7E7; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-13; P4-14; P5-3 tetramerisation domain; 3B10xP5-27; 3B10xP5-23. AAU72870 standard; Protein; 255 AA.

ö Gaps ö 94.9%; Score 93; DB 23; Length 255; 94.7%; Pred. No. 2e-07; ive 1; Mismatches 0; Indels Search completed: April 22, 2003, 12:51:16 Job time : 49.1786 secs 1 EIRLKSDNYATHYAESVKG 19 51 EIRLKSNNYATHYAESVKG 69

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RESULT 2
US-09-840-459-36
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Appl
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Sequence 36, Appl
Sequence 2, Appli
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                                                                                                                                                                                                                   April 22, 2003, 12:53:59 ; Search time 20.0179 Seconds (without alignments) 76.055 Million cell updates/sec
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Sequence 15,
Sequence 5, A
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Sequence 15,
Sequence 15,
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Sequence 5,
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Sequence 2
Sequence 3
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1: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpaa/USO8 \text{NEW PUB.pep:*} \\
2: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpaa/USO8 \text{NEW PUB.pep:*} \\
2: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpaa/USO6 \text{NEW PUB.pep:*} \\
4: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpaa/USO6 \text{NEW PUB.pep:*} \\
5: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpaa/USO6 \text{PUBCOMB.pep:*} \\
5: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpaa/USO8 \text{PUBCOMB.pep:*} \\
7: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpaa/USO9 \text{PUBCOMB.pep:*} \\
9: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpaa/USO9 \text{NEW PUB.pep:*} \\
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11: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpaa/USO1 \text{USOPUBCOMB.pep:*} \\
12: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpaa/USO1 \text{USOPUBCOMB.pep:*} \\
13: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpaa/USO1 \text{USOPUBCOMB.pep:*} \\
14: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpaa/USO3 \text{USOPUBCOMB.pep:*} \\
14: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpa/USO3 \text{USOPUBCOMB.pep:*} \\
14: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpa/USO3 \text{USOPUBCOMB.pep:*} \\
14: \( \cgn2 \frac{6}\) \perpendata/1\) \pubpa/USO3 \text{
                             GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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) US-09-840-459-36

US-09-810-459-36

US-09-564-329A-15

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
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        66.3
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        US-09-835-087-18
        Sequence 18, Appl 20

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        66.3
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        US-09-840-459-34
        Sequence 18, Appl 20

        23
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        117
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        US-09-835-087-10
        Sequence 10, Appl 20

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        117
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        US-09-835-087-11
        Sequence 11, Appl 20

        25
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        61.3
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        10
        US-09-835-087-12
        Sequence 11, Appl 20

        26
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        117
        10
        US-09-835-087-12
        Sequence 11, Appl 20

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        US-09-803-739-12
        Sequence 12, Appl 20

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        US-09-803-739-12
        Sequence 21, Appl 20

        30
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        US-09-803-739-21
        Sequence 21, Appl 20

        31
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        10
        US-09-803-739-21
        Sequence 21, Appl 20

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        66.3
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        US-09-803-739-21
        Sequenc
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### ALLGNMEN

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### Sequence 4, Application US/09883758

| Sequence 4, Application US/09883758
| Sequence 4, Application US/09883758
| Patent No. US20020058804A1
| GENERAL HYRORANTION:
| APPLICANT: Barbas ID. Carlos F. APPLICANT: Barbas ID. Carlos F. APPLICANT: Barbas Doron | APPLICANT: List, Banjani | APP
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GENERAL INFORMATION:

APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

APPLICANT: Witter, Owen N.

APPLICANT: Witter, Owen N.

APPLICANT: Witter, Owen N.

TITLE OF INVENTION: PECA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30435.54US14

CURRENT FILING DATE: 2000.05-14

CURRENT FILING DATE: 2000.05-14

FRIOR APPLICATION NUMBER: 09/564,329

PRIOR FILING DATE: 1099-07-20

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1998-01-12

PRIOR PLICATION NUMBER: 60/071,141

PRIOR FILING DATE: 1998-01-12

PRIOR FILING DATE: 1998-02-31

PRIOR FILING DATE: 1998-02-31

PRIOR PLING DATE: 1998-02-31
                                                                    APPLICANT: MITCH.
APPLICANT: MITCH.
APPLICANT: MITCH.
APPLICANT: GAIffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.4014
CURRENT APPLICATION NUMBER: US/09/564,329A
CURRENT FILING DATE: 1000-05-03
PRIOR PILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1998-01-12
PRIOR PELING DATE: 1998-01-12
PRIOR PELING DATE: 1998-02-33
PRIOR FILING DATE: 1998-02-33
PRIOR PELICATION NUMBER: 60/113,230
PRIOR PELING DATE: 1998-02-17
PRIOR PELING DATE: 1999-02-17
PRIOR PELING DATE: 1999-03-16
PRIOR PELICATION NUMBER: 60/124,658
PRIOR PELING DATE: 1999-03-16
PRIOR PELICATION NUMBER: 09/203,939
PRIOR PELING DATE: 1999-03-16
PRIOR PELING DATE: 1999-03-16
PRIOR PELING DATE: 1999-03-16
PRIOR PELING DATE: 1999-02-17
PRIOR PELING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
PURDER: PARCHAIN PERIOR PELING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
PURDER: PARCHAIN PERIOR PELING DATE: 1999-05-25
PRIOR PELING DATE: 1999-05-25
PRIOR PELING DATE: 1999-05-25
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89.5%; Pred. No. 3.8e-07;
iive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EIRLKSDNYATHYAESVKG 19
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Matches 17, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: SCID Mice
US-09-564-329A-15
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Sequence 2, Application US/09883758
Sequence 2, Application US/09883758
Sequence 2, Application US/09883758
Sex Control Carlos F.
APPLICANT: Barbas III, Carlos F.
APPLICANT: Babat, Doron
APPLICANT: List, Benjamin
APPLICANT: List, Benjamin
APPLICANT: Lerner, Richard A.
ITITLE OF INVENTION NUMBER: US/09/883,758
CURRENT PILING DATE: 2001-06-18
FRICK APPLICATION NUMBER: US/09/318,661*
PRIOR PILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 298
TYPE: PRI
CORGANISM: Mus musculus
US-09-883-758-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 95; DB 10; Length 298;
Pred. No. 1.9e-07;
1; Mismatches 0; Indels
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
TITLE OF INVENTION: HUMANISE ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANISE ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANER: US/09/840,459
CURRENT APPLICATION NUMBER: US/09/840,459
PRIOR PELING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR PILING DATE: 2000-02-03
PRIOR PILING DATE: 1999-07-23
PRIOR PILING DATE: 1999-07-23
PRIOR PILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PSELEED FOR WINDOWS VEISION 3.0
SOFTWARE: PSELEED FOR WINDOWS VEISION 3.0
LENGTH: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-36
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US-09-564-329A-15
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y GARDICANT Reiter, Robert E.

APPLICANT: Witte, Owen N.
TILLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/63,620
CURRENT FILING DATE: 2000-09-26
PRIOR FILING DATE: 1999-07-20
PRIOR PILING DATE: 1999-07-20
PRIOR PILING DATE: 1999-07-20
PRIOR PILING DATE: 1999-07-20
PRIOR PILING DATE: 1999-07-31
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-14
PRIOR FILING DATE: 1998-02-17
PRIOR PILING DATE: 1998-02-17
PRIOR PILING DATE: 1998-02-17
PRIOR FILING DATE: 1998-02-17
PRIOR FILING DATE: 1998-02-17
PRIOR FILING DATE: 1998-02-17
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-03-16
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                    PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR PILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR PILING DATE: 1999-02-17
PRIOR PILING DATE: 1999-02-17
PRIOR PILING DATE: 1999-02-17
PRIOR PELING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1998-03-16
PRIOR FILING DATE: 1998-03-17
PRIOR PILING DATE: 1998-03-07
PRIOR FILING DATE: 1998-03-07
PRIOR FILING DATE: 1998-03-07
PRIOR PILING DATE: 1998-03-07
PRIOR FILING DATE: 1999-05-05
PRIOR PILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-963-620-15; Sequence 15, Application US/09963620; Patent No. US20020141941A1; GENERAL INFORMATION:
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APPLICANT: Safftran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REPERENCE: 30435.540S14
CURRENT APPLICATION NUMBER: US/09/854,811
CURRENT APPLICATION NUMBER: 09/564,329
FRIOR FILING DATE: 2000-05-03
FRIOR FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 151
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APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
TITLE OF INVENTIOR PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REFERENCE: 30435.5403P
CURRENT APPLICATION NUMBER: US/09/934,773
CURRENT FILING DATE: 2001-08-21
PRIOR FILING DATE: 2000-05-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR PILING DATE: 1999-02-17
PRIOR PILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 15
LENGTH: 151
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Patent No. US20020136689A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09854811
Patent No. US20020119157A1
GENERAL INFORMATION:
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Matches 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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CORGANISM: SCID Mice
US-09-854-811-15
                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: SCID Mice
US-09-855-153-15
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US-09-854-811-15
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Sequence 5, Application US/09756301A

Sequence 5, Application US/09756301A

GENERAL INFORMATION:

APPLICANT: U-Junming

APPLICANT: Daddona, Peter

APPLICANT: Daddona, Peter

APPLICANT: Giegel, John

"APPLICANT: Giegel, John

"APPLICANT: Giegel, Scott

TITLE OF INVENTION: ALL-TNF Antibodies and Peptides of

TITLE OF INVENTION: Human Tumor Necrosis Factor

FILE PETERENCE: 0975.1005-008

CURRENT FILING DATE: 2001-01-08

FRIOR FILING DATE: 1998-08-12

PRIOR FILING DATE: 1998-08-12

PRIOR FILING DATE: 1998-08-14

PRIOR FILING DATE: 1994-10-18

PRIOR FILING DATE: 1994-02-04

PRIOR PLILING DATE: 1992-03-18

PRIOR FILING DATE: PACKEGO FOR WINDOWS VERSION 4.0

PRIOR FILING DATE: 1993-03-18

PRIOR 
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Sequence 5, Application US/09927703
GENERAL INFORMATION:
APPLICANT: Vilcek, Jan
APPLICANT: Maddona, Peter
APPLICANT: Knight, David M.
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Human Tumor Necrosis Factor
TITLE OF INVENTION: Human Tumor Necrosis Factor
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                                                    50 EIRSKSINSATHYAESVKG 68
        1 EIRLKSDNYATHYAESVKG 19
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US-09-756-301A-5
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US-09-927-703-5
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Sequence 5, Application US/10043432

Publication No. US20030054004A1

SERNEAL INFORMATION:
APPLICANT: Libror, Junming
APPLICANT: Daddon, John
APPLICANT: Might, David M.
APPLICANT: Sigel, Scott
TITLE OF INVENTION: Human Tumor Necrosis Factor
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILE REFERENCE: 0975-1005-013
CURRENT APPLICATION NUMBER: US-09/27,703

FRIOR APPLICATION NUMBER: US-09/133,119

FRIOR PILING DATE: 2001-01-08

FRIOR PILING DATE: 1994-10-18

FRIOR PILING DATE: 1994-02-04

FRIOR PILING DATE: 1993-03-03

FRIOR PILING DATE: 1993-03-04

FRIOR PILING DATE: 1991-03-18

FRIOR FILING DATE: 1991-03-18

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84.2%; Pred. No. 0.00014;
iive 0; Mismatches 3; Indels
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOCTWARE: PATENTIN Ver. 2.0
SEQ ID NO 15
LENGTH: 151
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Best, Local Similarity 84.2
Matches 16; Conservative
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; ORGANISM: Mus Balb/c
US-10-043-432-5
                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: SCID Mice
US-09-963-620-15
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APPLICANT: Vilcek, Jan
APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter
APPLICANT: Chight, David M.
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Anti-TVF Antibodies and Peptides of
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILE REFERENCE: 0975.1005-007
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Pred. No. 0.00014;
0; Mismatches 3;
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FILE KEKEKEKELS 1945.1003-00,
CURRENT FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: U.S. 09/133,119
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR PILING DATE: 1994-02-04
PRIOR PILING DATE: 1994-02-04
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-03
PRIOR FILING DATE: 1993-01-13
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-18
PRIOR FILING DATE: 1992-09-18
PRIOR FILING DATE: 1991-03-18
NUMBER: CERTING DATE: 1991-03-18
NUMBER: CERTING DATE: 1991-03-18
NUMBER: FEALSTON NUMBER: U.S. 07/670,827
PRIOR FILING DATE: 1991-03-18
NUMBER: FEALSTON NUMBER: U.S. 07/670,827
PRIOR FILING DATE: 1991-03-18
NUMBER: FEALSTON NUMBER: U.S. 07/670,827
PRIOR FILING DATE: 1991-03-18
NUMBER: FEALSTON NUMBER: U.S. 07/670,827
PRIOR FILING DATE: 1991-03-18
NUMBER: FEALSTON NUMBER: U.S. 07/670,827
PRIOR FILING DATE: 1991-03-18
NUMBER: FEALSTON NUMBER: U.S. 07/670,827
PRIOR PILING DATE: 1991-03-18
NUMBER: FEALSTON NUMBER: U.S. 07/670,827
PRIOR FILING DATE: 1991-03-18
                             PRIOR PELLING DATE: 1933-02-02
PRIOR FILING DATE: 1933-02-02
PRIOR FILING DATE: 1992-02
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-03-18
PRIOR PILING DATE: 1992-03-18
PRIOR PILING DATE: 1991-03-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PastSEQ for Windows Version 4.0
SOFTWARE: PastSEQ for Windows Version 4.0
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84.2%;
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Best Local Similarity 84.2
Matches 16; Conservative
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ORGANISM: Mus Balb/c
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ORGANISM: Mus Balb/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-756-161A-5
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GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: Wick, Jan
APPLICANT: Might, John
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott
ITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
ITLE OF INVENTION: Human Tumor Necrosis Factor
ITLE REFERENCE: 0975.1005-010
CURRENT APPLICATION NUMBER: US/09/766,535A
CURRENT FILING DATE: 2001-01-18
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PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1995-12-11
PRIOR APPLICATION NUMBER: U.S. 08/324,799
PRIOR FILING DATE: 1994-10-18
PRIOR PELICATION NUMBER: U.S. 08/192,102
PRIOR FILING DATE: 1994-02-04
                   CURRENT FILING DATE: 2001-08-10
PRIOR PLILING DATE: 2001-08-10
PRIOR PLILING DATE: 2001-08-10
PRIOR PLILING DATE: 2001-01-08
PRIOR PLILING DATE: 2001-01-08
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1992-09-11
PRIOR PILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-03-18
PRIOR FILING DATE: 1992-03-18
PRIOR FILING DATE: 1991-03-18
NUMBER OF SEQ ID NOS: 19
LENGTH: 119
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FILING DATE: 1994-02-04
APPLICATION NUMBER: U.S. 08/010,406
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FILE REFERENCE: 0975.1005-013
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Best Local Similarity 84.2
Matches 16; Conservative
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ORGANISM: Mus Balb/c
US-09-927-703-5
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US-09-766-535A-5
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Pred. No. 0.00014;
0; Mismatches 3; Indels
PRIOR APPLICATION NUMBER: U.S. 08/192,093
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-01-29
PRIOR PILING DATE: 1993-02
PRIOR PILING DATE: 1993-02
PRIOR PILING DATE: 1992-09-11
PRIOR PILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-18
PRIOR FILING DATE: 1991-03-18
PRIOR FILING DATE: 1991-03-18
PRIOR PILING DATE: 1991-03-18
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Job time : 20.0179 secs
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Best Local Similarity 84.2%; Pr
Matches 16; Conservative 0;
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; ORGANISM: Mus Balb/c
US-10-043-450-5
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Sequence 5, Application US/10043450

Patent No. US20020141996A1

GENERAL INFORMATION:

APPLICANT: Le, Junming

APPLICANT: Vilcek, Jan

APPLICANT: Daddona, Peter

APPLICANT: Siegel, Scott

TITLE OF INVENTION: Human Tumor Necrosis Factor

FILING DATE: 2002-01.10

PRIOR APPLICATION NUMBER: U.S. 09/756,398

PRIOR PILING DATE: 1998-08-12

PRIOR PILING DATE: 1998-08-12

PRIOR PILING DATE: 1998-10-18

PRIOR PILING DATE: 1994-10-18

PRIOR APPLICATION NUMBER: U.S. 08/192,102

PRIOR APPLICATION NUMBER: U.S. 08/192,861

PRIOR FILING DATE: 1994-02-04

PRIOR APPLICATION NUMBER: U.S. 08/192,861
                                                                                                                                                                                                                                                                                           Sequence 5, Application US/10010229

Patent No. US20020114805A1

GENERAL INFORMATION:

APPLICANT: Le', Junming

APPLICANT: Vilcek, Jan

APPLICANT: Daddona, Peter

APPLICANT: Siegel, John

APPLICANT: Siegel, Scott

TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of

TITLE OF INVENTION: Human Tumor Necrosis Factor

FILE REFERENCE: 0975.1005-013

CURRENT APPLICATION NUMBER: US/10/010,229

CURRENT FILING DATE: 2001-12-07

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 19

SEGTAARE: FactSEQ for Windows Version 4.0
         Best Local Similarity 84.2%; Pred. No. 0.00014;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                             50 EIRSKSINSATHYAESVKG 68
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; LENGTH: 119
; TYPE: PRT
; ORGANISM: Wus Balb/C
US-10-010-229-5
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US-10-010-229-5
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US-10-043-450-5
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OM protein - protein search, using sw model

April 22, 2003, 13:07:14 ; Search time 15 Seconds (without alignments) 102.543 Million cell updates/sec Run on:

US-09-674-716B-3 81 1 RSSKSLLYKDGKTYLN 16 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

2770 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	>	=	proteasome chain 1		inhibin beta-B cha	glyceraldehyde-3-p	very late antigen-	alpha-glucosidase	glucan 1,4-alpha-g	ulin, vasc		bable IMP d	c	topoisomerase I -	chemoattractant pr	lipoprotein lipase			ŭ			g heavy cl	Ig H chain V-D-J r	dihydropyrimidine	speci	protein P8 - curle	S-layer protein -	acidic proline-ric	NAD(+)-glycohydrol
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	101	732	082	733	736	344	018	240	202	101	914	373	311	146	279	501	PT0243	JQ2309	JQ2319	146512	JP0101	PH1314	PH1616	871396	C39509	E28027	A60476	A29806	8402
	a ;	4	809732	809082	809733	B24736	S54344	A28018	S21240	S21202	A44101	PH0914	PC2373	PH1311	A47146	A36279	B26501	PTO	J02	<b>J</b> 02	146	JPO	PH1	PH1	S71	623	E28	A60	A29	898
	BB	7	~	N	7	~	7	N	N	N	7	N	7	N	~	N	N	7	N	N	7	~	7	~	7	(7)	7	7	7	0
	Match Length	15	16	12	13	10	13	14	15	15	16	11	14	14	15	15	15	10	13	13	15	15	15	15	15	16	16	10	11	12
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Quer.	Mat	33	ო	32	c	27			27									~	~	~	N	N	7	N	~	ñ	7	7	7	χi
	Score	27	27	26	25	22	22	22	22	22	22	21	21	21	21	21	21	20	20	20	20	20	20	20	20	20	19.5	19	19	19
Result	No.	1	~	m	4	ß	v	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26		28	29

T-cell receptor be hypothetical prote	orf 61.1 - phage T thymic humoral fac	serum amyloid P-co inhibin beta-A cha	48K bile/gallbladd	translation elonga	microbial collagen T-cell antigen rec	alpha-conotoxin MI 214K excantigen (v	nitrogenase cofact	protein QF200022 -	I-cell receptor de
PH0930 G83988	G45681 A28719	B20569 S10926	G58501	B29806 PD0441	B26093 S47390	NTKNIM	832677	PA0058	G35141
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23.5	23.5	22.2	22.2	22.2	22.2	22	22.	22.2	22.2
19 19	19 18	18	18	18 18	18	18	18	18	178
30 31	332	3.4 4.5	36	37 38	39	4.4	4 4 4 6	44	45

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calmodulin, vasoactive intestinal peptide-binding protein, VIP binding protein, p18 - gu C;Species: Cavia porcellus (guinea pig)
C;Species: Cavia porcellus (guinea pig)
C;Abte: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: C44101
R;Stallwood, D; Brugger, C.H; Baggenstoss, B.A.; Stemmer, P.M.; Shiraga, H.; Landers, A;Title: Identity of a membrane-bound vasoactive intestinal peptide-binding protein with A;Reference number: A44101; MUID:92406918; PMID:1527080
                                                                                                                                                                                                                                                                                                                                                                 A;Accession: C44101
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <STA>
A;Experimental source: lung membranes
A;Note: sequence extracted from NCBI backbone (NCBIP:114109)
C;Keywords: intestine
```

Gaps ö Query Match 33.3%; Score 27; DB 2; Length 15; Best Local Similarity 50.0%; Pred. No. 3.8e+02; Matches 4; Conservative 2; Mismatches 2; Indels 9 KDGKTYLN 16 4 KDGNXYIS 11 RESULT 2 S09732 g ઠે

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photosystem I protein psad - spinach chloroplast (fragment)
C;Species: chloroplast Spinacia oleracea (spinach)
C;Species: chloroplast Spinacia oleracea (spinach)
C;Species: 12-reb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Feb-1997
C;Accession: S09732
R;IKeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.
R;IKeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.
R;IKeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.
A;Accession: S09732
A;Accession: S09732
A;Accession: S09732
A;Accession: S09732
A;Accession: Complexion
A;Residues: 1-16 cIKE>
A;Genetics:
A;Genetics: C, Keywords: chloroplast; photosynthesis; photosystem I; transmembrane protein

Gaps ., Score 27; DB 2; Length 16; Pred. No. 4.1e+02; 2; Mismatches 1; Indels Query Match 33.3%; Best Local Similarity 62.5%; Matches 5; Conservative

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9 KDGKTYLN 16 : | ||||: 2 RDFKTYLS 9 g ð

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alpha-glucosidase (EC 3.2.1.20) I - Bacillus "thermoamyloliquefaciens" (fragment)
C;Species: Bacillus "thermoamyloliquefaciens"
C;Species: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 21-Aug-1998
C;Accession: S21240
R;Suzuki, Y.; Yonezawa, K.; Hattori, M.; Takii, Y.
Eur. J. Biochem. 205, 249-256, 1992
A;Title: Assignment of Bacillus thermoamyloliquefaciens KP1071 alpha-glucosidase I to an nice and in structural parameters calculated from the amino acid composition.
A;Reference number: $21202; MUID:92209510; PMID:1555585
                                                                                                                                                                     Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - bovine (fragm CiSpecies: Bos primigenius taurus (cattle)
CiSpecies: D-oct-1995 #sequence_revision 30-Jan-1998 #text_change 03-Jun-2002
CiData, N. Jobta, N.H.; Inoue, S.; Hidaka, H.
RiOkazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
Biochem J. 306, 551-555, 1995
Biochem J. 300-beta is a target protein of neurocalcin delta, an abundant isoform in glia A;Reference number: S54343; MUID:95194333; PMID:7887910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.Alternate names: VLA-1 alpha chain - human (fragment)
N.Alternate names: VLA-1 alpha chain
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 12-May-1994
C;Accession: A28018
R;Takada, Y; Strominger, J.L.; Hemler, M.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3343, 1987
A;Title: The very late antigen family of heterodimers is part of a superfamily of molecu A;Reference number: A94151; MUID:87204112; PMID:3033641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.2%; Score 22; DB 2; Length 13; 50.0%; Pred. No. 2.2e+03; tive 3; Mismatches 0; Indels
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A;Wolecule type: procein
A;Residues: 1-15 <SU2>
A;Residuental source: strain KP1071
C;Superfamily: alpha-glucosidase; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 1-14 <TAK>
C;Keywords: duplication; heterodimer; membrane protein
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A, Molecule type: protein
A, Residues: 1-13 <OKA>
C, Keywords: oxidoreductase
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Matches 3; Conserv
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2 LEXDGRINL 10
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6 KDSMTFL 12
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7 LWRDGR 12
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                                                                                                           proteasome chain 1 - rat (fragment)
NyAlternate names: multicatalytic proteinase chain 1
NyAlternate names: multicatalytic proteinase chain 1
Species Rattus norvegicus (Norway rat)
C;Dectes Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
Spillley, K.S.; Davison, M.D.; Rivett, A.J.
FEBS Lett. 262, 327-329, 1990
A;Titles N-terminal sequence similarities between components of the multicatalytic prote
A;Reference number: S09082; MUID: 90242957; PMID: 2335214
A;Reference number: S09082; MUID: 90242957; PMID: 2335214
A;Residues: 1-12 < Lilb.
C;Superfamily: multicatalytic endopeptidase.complex chain C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     photosystem I protein psad - garden pea chloroplast (fragment)
C;Species: chloroplast Pieum sativum (garden pea)
C;Species: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Feb-1997
C;Accession: S09733
R;Ikeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.
FBES Lett. 263, 274-278, 1990
A;Title: Polypeptide composition of higher plant photosystem I complex. Identification (A;Reference number: S09730; MUID:90242987; PMID:2185953
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194736

194736

194736

195pecies: Sus scrofa domestica (domestic pig)

195pecies: Sus scrofa domestica (domestic pig)

195pecies: Sus scrofa domestica (domestic pig)

196pecies: Sus scrofa Sus revision 28-Sep-1987 #text_change 30-Sep-1993

197co. Natl. Acad. Sci. U.S.A. 82, 7217-7221, 1985

197Accession: B24736

197Accession: B24736

197Accession: B24736

197Accession: Dralminary

197Accession: preliminary

197Accession: Dralminary

197Accession: Dralminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 32.1%; Score 26; DB 2; Length 12; Similarity 66.7%; Pred. No. 4.4e+02; 4; Conservative 2; Mismatches 0; Indels
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Best Local Similarity 55.6°
Matche♪ 5; Conservative
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A, Residues: 1-13 <IKE>
C, Genetics:
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Best Local Similarity
Matches 4; Conserv
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2 RDLKTYL 8
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6 WYKDG 11
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Ig heavy chain DJ region (clone C68-101) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1311
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
A;Fitle: Predominance of fetal type DJH joining in young children with B precursor lymph A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-14 <MAS>
C;Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolog
C;Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                       [similarity] - Bacillus cereus (strain ts-4) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Bacillus cereus
C;Date: 20-Apr-2000 #text_change 02-Sep-2000
C;Accession: PC2373
R;Mateuno, K.; Myamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A;Title: Identification of DNA-binding proteins changed after induction of sporulation A;Reference number: PC2369; WUID:95218265; PMID:7766022
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C;Species: vaccinia virus
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 31-Oct-1997
C;Accession: A47148
F;Riemperer, N.; Traktman, P.
J. Biol. Chem. 268, 15887-15899, 1993
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A,Accession: PH0914
A;Molecule type: mkWA
A;Reddues: 1-11 <GOL>
A;Escidues: 1-11 <GOL>
A;Experimental source: myelin basic protein-immunized lymph node C;Keywords: T-cell receptor
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                                                                                                                                                         Score 21; DB 2; Length 11;
Pred. No. 2.8e+03;
1; Mismatches 2; Indels
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Similarity 50.0%; Pred. No. 3.5e+03;
4; Conservative 1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable IMP dehydrogenase (EC 1.1.1.205)
                                                                                                                                                              Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative 1
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Best Local Similarity 36.4'
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3 ESKFVKEGLTF 13
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A; Residues: 1-14 <WAS>
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                                                                                                                                                                                                                                                                                                                             3 SSDSLSYE 10
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PH1311
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0914
R;Gold, D.P.; Offiner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergine A;Reference number: PH0891; MUID:92078857; PMID:1836012
                                                                                                                                                                                                                                                                                                                                   C, Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 21-Aug-1990 (C, Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 21-Aug-1990 (C, Accession: S21202 R, Suzuki, Y.; Yonezawa, K.; Hattori, M.; Takii, Y. Eur. J. Biochem. 205, 249-256, 1992 A; Title: Assignment of Bacillus thermoamyloliquefaciens KP1071 alpha-glucosidase I to an nor and in structural parameters calculated from the amino acid composition. A; Reference number: S21202, MUID:92209510; PMID:1555585 A; Rocession: S21202 A; Rocession: S21202 A; Residues: 1-15 s0122 A; Residues: 1-15 s0122 A; Residues: 1-15 s0122 A; Residues: alpha-amylase core homology C; Superfamily: alpha-glucosidase; alpha-amylase core homology C; Superfamily: alpha-glucosidase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: A44101
R;Stallwood, D.; Brugger, C.H.; Baggenstoss, B.A.; Stemmer, P.M.; Shiraga, H.; Landers, B. Biol. Chem. 267, 19617-19621, 1992
A;Title: Identity of a membrane-bound vasoactive intestinal peptide-binding protein with A;Reference number: A44101; MUID:92406918; PMID:1527080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>،</u>
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                                                                                                                                                                                                                                                   - Bacillus stearothermophilus (fragment)
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Alternate names: exo-alpha-1-4-glucosidase I
Species: Bacillus stearothermophilus
Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 21-Aug-1998
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Pred. No. 2.7e+03;
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           Indels
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A; Residues: 1-16 <STA>
A; Experimental source: lung membranes
A; Douce: sequence extracted from NCBI backbone (NCBIP:114120)
C; Superfamily: calmodulin; calmodulin repeat homology
C; Reywords: EF hand; intestine
           2;
           Mismatches
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Best Local Similarity 36.4%
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RESULT 15
A36279
A36279
C; Demoattractant protein - earthworm (Lumbricus terrestris) (fragment)
C; Species: Lumbricus terrestris (common earthworm)
C; Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 30-Sep-1993
C; Date: 18-Jan-1991 #sequence_revision J.; Wang, D.; Halpern, M.
J. Biol. Chem. 265, 8736-8744, 1990
A; Title: Purification and characterization of a chemoattractant from electric shock-indu A; Reference number: A36279
A; Reference number: A36279
A; Reference number: A36279
A; Residues: Dreliminary
A; Residues: 1-15 < JIA>
A, Title: Biochemical analysis of mutant alleles of the vaccinia virus topoisomerase I cath R, Reference number: A47146; MUID:93340198; PMID:8393454
A, Accession: A47146
A, Status: preliminary; not compared with conceptual translation
A, Molecule type: DNA
A, Residuas: 1-15 KLEs
A, Residuas: 1-15 KLEs
C, Superfamily: vaccinia virus DNA topoisomerase
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                                                                                                                                                                                                                                                                              Query Match
25.9%; Score 21f DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.7e+03;
Matches 4; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                        Length 15;
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5 KDLRTY 10
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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sw model OM protein - protein search, using April 22, 2003, 12:55:49; Search time 24 Seconds (without alignments) 27.651 Million cell updates/sec Run on:

Title: Perfect score:

US-09-674-716B-3 81 1 RSSKSLLYKDGKTYLN 16 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

822 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# CITMMADIRG

	Description	P17229 pisum sativ		P81563 rattus norv			P49325 bacillus th	_		Q10997 halocynthia	conns	_	_				P56923 rana tempor			P08616 uperoleia r	P82006 white spot			P80526 fasciola he	-	_		P81096 brassica na		_	P80432 rattus norv	_	18 nicot	P01163 homo sapien
SUMMARIES	ΙD	PSAJ PEA	MALT BACTO	MM01_RAT	MY14 EISFO	FIBA ANAPL	SLAP_BACTG	SAMP_MUSCA	PPCK FASHE	SPI HALRO	CXA1 CONMA	EFTU CANFA	MCRZ METTM		GON1 PETMA		TEMK RANTE	UXA6_CHLTR	CSIS BACSU	TKN2 UPERU	V14K WSSV	LIGA_TRAVE	MY14 PHEVI	NEJ2 FASHE	UN07_CLOPA	ATP2_PINPS	C1QA_RAT	PC20 BRANA		MLB_SQUAC	COXO_RAT			MORN HUMAN
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de	Query Match	30.9	27.2	25.9	24.7	24.7	23.5	22.2										-	21.0			-				-	21.0						19.8	19.8
	Score	25	22	21	50.	20	19	18	18	18	18	18	18	18	17	17	17	11	17	17	17	17	17	17	17	17	17	17	17	17	16		16	
	Result No.		2	٣	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

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Score 25; DB 1; Length 13; Pred. No. 1.7e+02; 1; Mismatches 1; Indels

Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative

KDGKTYL 15 :| ||||| 2 RDLKTYL 8

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ð 셤 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
Maltase (EC 3.2.1.20) (Alpha-glucosidase I) (Fragment).
Bacillus thermoamyloliquefaciens.
Bacteria, Firmicutes, Bacillales; Bacillaceae; Bacillus.
17 TaxID-1425;

RESULT 2
MALT BACTO
ID MALT BACTO
DT 01-AUGDT 01-BCDT 01-BCD

15 AA.

PRT;

STANDARD;

MALT BACTO P80072;

[1] SEQUENCE.
STRAIN=KP1071 / FERM P8477;
MEDLINE=92209510; PubMed=1555585;
Suzuki Y., Yonezawa K., Hattori M., Takii Y.;

P56973 conus conso Q22093 pigeon pea P81037 oncorhynchu P42996 scyllorhinu P42999 squalus aca Q46464 campylobact P41490 locusta mig P81532 microplitis P01519 conus geogr P16651 canis famil P80659 physcomitre P80655 zea mays (m	ن	Photosystem I reaction center subunit IX (PSI-J) (Fragment). Photosystem I reaction center subunit IX (PSI-J) (Fragment). Photosystem I reaction center subunit IX (PSI-J) (Fragment). Photosystem strip (Streptophyta) Fubryophyta; Embryophyta; Embryophyta; Embryophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Vicieae; Pisum. NCBI_TaxID=3888; SEQUENCE.	notosystem I complex. products."; of the psaE and psaF. ; Transmembrane.
1 CXA1 CONCN 1 RAS19PWABP 1 MILT ONCKS 1 OXYA-SCYCK 1 OXYA-SCYCK 1 SYK CAMUP 1 LMT4 LOCMT 1 MP1 MCOC 1 CXA1 CONGS 1 FGFT CAMPA 1 FGFT CAMPA 1 FGFT CAMPA 1 UC19 MAIZE	ALIGNMENTS  D; PRT; 13 AA.  Created) Last sequence update)	Drocowstor (No. 11) (Fragm Ballocowstor) (Fragm Ballocowstor) (Fragm Ballocowstor) (Fragm Ballocowstor) (Fragm Ballocopiat.  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr. Spermatophyta; Magnoliophyta; eudicotyledons; core eudiencesida I; Fabales; Fabaceae; Papillonoideae; Vicieae; NCBI_TaxID=3888;	MEDLINE-90242987; PubMed-2185953; Ikeuchi M., Hitzano A., Hiyama T., Inoue Y.; Ikeuchi M., Hitzano A., Hiyama T., Inoue Y.; Polypeptide composition of higher plant photosystem I Identification of psal, psaJ and psaK gene products."; PEBS Lett. 263:274-278 (1990)!- FUNCTION: May help in the organization of the psaE subunits!- SMILARITY: BELONGS TO THE PSAJ FAMILY SMILARITY: BELONGS TO THE PSAJ FAMILY Chloroplast; Photosystem I; Photosynthesis; Transmembr TRANSMEM 7 >13 POTENTIAL SMON TER 13 13 SEQÜENCE 13 AA; 1516 MW; 9E2E45D11FDE3B41 CRC64;
16 19.8 16 19.8 16 19.8 15 19.8 15 18.5 18.5 18.5	T PEA STANDAR 229; AUG-1990 (Rel. 15, AUG-1990 (Rel. 15, TEM (Rel. 15,	Photosystem I reaction cen PSAJ. Plaum sativum (Garden pea) Chloroplast. Eukaryota, Viridiplantae; Spermatophyra, Magnoliophy eurosids I; Fabales; Fabac NCBI TaxID=3888;	MEDLINE=90242987; PubMed=2185953; Ikeuchi M., Hirano A., Hiyama T., Polypeptide composition of highe lidentification of psal, psal and FEBS Lett. 263:274-278(1990)!- FUNCTION: May help in the org subunits!- SIMILARITY: BELONGS TO THE PS PIR; S09733; S09733. Chloroplast; Photosystem I; Photo Chloroplast; Photosystem I; Photosystem I3 Photosyste
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         alpha-glucosidase I to an exo-alpha-1,4-glucosidase, and its striking similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence and in structural parameters calculated from the amino acid
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interstitial collagenase (EC 3.4.24.7) (Matrix metalloproteinase-1)
(MMP-1) (Fibroblast collagenase) (Myocardial collagenase) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                    Eur. J. Biochem. 205:249-256(1992).
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
linked D-glucose residues with release of D-glucose.
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
PIR; $21240; $21240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- PTM: THE N-TERMINAL IS BLOCKED.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
Hydrolase; Metalloprotease; Zinc; Calcium; Collagen degradation;
Extracellular matrix:
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                                                                                                                                                                 Score 22; DB 1; Length 15;
Pred. No. 6.6e+02;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.9%; Score 21; DB 1; Length 15; 40.0%; Pred. No. 9.8e+02; 1ve 3; Mismatches 3; Indels
 "Assignment of Bacillus thermoamyloliquefaciens KP1071
                                                                                                                                          15 AA; 1929 MW; 62B4CE501F2D3042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Heart;
MEDLINE-96201136; PubMed-8605638;
Tyagi S.C., Cleutjens J.P.M.;
"Myocardial collagenase: purification and structural characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 15
15 AA; 1787 MW; 15A57D24C0F6FD80 CRC64;
                                                                                                                                                                                                                                                                                            15 AA.
                                                                                                                                                                                        2; Mismatches
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                                                                                                                                                                   27.2%;
36.4%;
                                                                                                                                                                                           4; Conservative
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Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                      Hydrolase; Glycosidase.
                                                                                                                                                                                                                                    2 KKAWWKEGVVY 12
                                                                                                                                                                                                               4 KSLLYKDGKTY 14
                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                            composition.";
                                                                                                                                 NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                          MM01 RAT
P81563;
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NON TER
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                                                                                                                                                                  Query Match
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STREETER
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Sci. Sin., B, Chem. Biol. Agric. Med. Earth Sci. 28:31-35(1985).
-!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-!- MISCELLANBOUS: CONVERSION OF FIRSTNOGEN TO FIRSTNI IS TRIGGERED BY THROWBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                   Myoactive tetradecapeptide (ETP):
Stania foetida (Common brandling worm) (Common dung-worm).
Bukaryota; Metazoa; Amnelida; Clitellata; Oligochaeta; Haplotaxida;
Lumbricina; Lumbricidae; Eisenia
                                                                                                                                                                                                                                                     TISSUE=Gut;
MEDLINE=96087879; PubMed=8532604;
WREDLINE=96087879; PubMed=8532604;
Ukena K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
                                                                                                                                                                                                                                                                                                                                       "A novel gut tetradecapeptide isolated from the earthworm, Elsenia foetida.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIANE=85168193; PubMed=3983613;
Min Y., Ping Z., Yaoshi Z.;
"Purification and primary structures of duck fibrinopeptides A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anas platyrhynchos (Domestic duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
                                                                                                                                                                                                                                                                                                                                                                           Peptides 16:995-999(1995).
-1- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DB 1; Length 14;
Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIBRINOPEPTIDE A. PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMIDATION.
CC9ABEF941CD91AD CRC64;
                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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Neuropeptide; Amidation.
MOD RES
14
14
AMIDATION.
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75.0%;
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PEPTIDE 1 15
MOD_RES 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 75.0
Matches 3, Conservative
                        STANDARD;
                                                                                                                                                                                                                                         SEQUENCE, AND SYNTHESIS.
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                                                                                                                                                                                               NCBI_TaxID=6396;
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2 FKDG 5
MY14 EISFO
ID MY14 EISFO
AC P46979;
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FIBA ANAPL
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us-09-674-716b-3.closed.rsp

P49325; RESULT 6 SLAP BACTG ID SLAP BA

Matches

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Elochem. Biophys. Res. Commun. 213:169-174(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
MEDLINE=95366993; PubMed=7639732;
Tkalcevic J., Ashman K., Meeusen E.;
"Fasciola hepatica: rapid identification of newly excysted juvenile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Putative phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32)
Phosphoenolpyruvate carboxylase) (PEPCK) (Newly excysted juvenile protein 1) Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fasciola hepatica (Liver fluke).

Bukaryota, Metazoa, Platyhelminthes; Trematoda, Digenea;

Echinostomida, Echinostomata, Fascioloidea, Fasciolidae, Fasciola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
22.2%; Score 18; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                              Query Match 22.2%; Score 18; DB 1; Length 9; Best Local Similarity 60.0%; Pred. No. 1.1e+05; Matches 3; Conservative 2; Mismatches 0; Indels
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01-007-1996 (Rel. 34, Created)

10-00T-1998 (Rel. 37, Last sequence update)

15-DEC-1998 (Rel. 37, Last annotation update)

Serine proteinase inhibitor (Fragment).

Halocynthia roretzi (Sea squirt).

Bukaryota, Metazoa; Chordata; Urochordata; Ascidiacea;

Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000364; PEP carboxykin.
PROSITE; PS0505; PEPCK GTP; PARTIAL.
Lyase, Decarboxylase; GTP-binding.
NON TER
SEQUENCE 10 AA; 1069 MW; 8393A6187AA9C87A CRC64;
                       InterPro; IPR001759; Pentaxin.
PROSITE; PS00289; PENTAXIN; PARTIAL.
Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
Loomain 1 >9 PENTAXIN.
NON TER 9 9 SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA
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TISSUE=Hemolymph;
MEDLINE=96321313; PubMed=8759295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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PIR; B20569; B20569.
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Q10997;
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01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serum amyloid P-component (SAPP) (Fragment).
Mustclus canis (Smooth dogfish).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes;
Blasmobranchii, Galeomorphii, Galeoidea, Carcharhiiformes, Triakidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90078111; PubMed=2592346;
MEDLINE=90078111; PubMed=2592346;
Luckevich M.D., Beveridge T.J.;
Luckevich M.D., Beveridge T.J.;
J. Bacteriol. 171:6656-6667(1989).
-!- FUNCTION: THE S-LAYER IS A PARAYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH OBLIQUE (P2) SYMMETRY.
                                                                                                                                              Gaps
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                                                                                 Score 20, DB 1; Length 15;
Pred. No. 1.5e+03;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
S-layer protein (Surface layer protein) (Fragment).
Bacillus thuringiensis (subsp. galleriae).
Bacteria, Firmicutes; Bacillales, Bacillus.
NGBI_TaxID=29338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell wall; S-layer.

NON TER 10
SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;
                               D78A51FF88B40373 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AA
                                                                                                                                                                                                                                                                                                                                                                                               10 AA.
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MEDLINE=83160932; PubMed=6403520;
           15 15
15 AA; 1580 MW;
                                                                                    h 24.7%;
Similarity 36.4%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 75.0
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                                                                                                                                                                                                                                                         1 QDGKSSFQKEG 11
                                                                                          Query Match
Best Local Similarity
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GKTF 5
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ID SAMP_MUSCA
AC P19095;
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           NON TER
SEQUENCE
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Matches

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TISSUE=Heart;
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MCRZ_METTM
ID _MCRZ_METTM
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6 KTYV 9
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-1- TISSUE SPECIFICITY: Expressed by the venom duct.
-1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
                                                Comp. Biochem. Physiol. 1148:1-9(1996).
-!-FUNCTION: STRONGY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
-!- SUBUNIT: MONOMER.
-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
INTERPO: IRRO00215; Serpin.
PROSTEE; PS00204; SERPIN; PARTIAL.
Serpin; Serine proteage inhibitor; Glycoprotein; Plasma.
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-83073458; PubMed=7149738; MCIntosh J.M., Gray W.R., Olivera B.M.; "Isolation and structure of a peptide toxin from the marine snail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Shishikura F., Abe T., Ohtake S.-I., Tanaka K.; "Purification and characterization of a 58,000-Da proteinase inhibitor from the hemolymph of a solitary ascidian, Halocynthia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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-1- FUNCTION: ALPHA-CONOYCXINS ACT ON POSTSYRAPTIC MEMBRANES, BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND INHIBIT THEM.
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Mollusca, Gastropoda, Caenogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 1; Length 14;
Pred. No. 3e+03;
0; Mismatches 1; Indels
                                                                                                                                                                            22.2%; Score 18; DB 1; Length 10; 75.0%; Pred. No. 2.1e+03; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEEE91898BF5E5BD CRC64;
                                                                                                                                                    10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;
                                                                                                                                                                                                                                                                                                                              21-UL-1986 (Rel. 01, Created)
21-UL-1986 (Rel. 01, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Alpha-conotoxin MI (MI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A01784; NTKNIM.
HSSP; P56973; 1B45.
Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation.
3 8
                                                                                                                                                                                                                                                                                                                     14 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION
                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.2%;
Similarity 75.0%;
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 AA; 1499 MW;
                                                                                                                                                                                        Local Similarity 75.0
                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               Conus magus (Magus cone)
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conus magus.";
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1 | GKTY 14

9 GKNY 12
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Best Local {
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    STARRAGE
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MEDLINE=91099370; PubMed=2269306;

REDPET S., Linder D., Ellermann J., Thauer R.K.;

Rospert S., Linder D., Ellermann J., Thauer R.K.;

Rospert S., Linder D., Ellermann J., Thauer R.K.;

Reductionly distinct methyl-coenzyme M reductases in Methanobacterium thermoautotrophicum strain Marburg and delta H.";

Bur. J. Bloochem. 194:871-877(1990)

-I- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio) ethanesulfonic acid) with 7-mercaptoheptanoylthreonine phosphate to methans and an hetezodisulfide.

-I- CATALYITC ACTIVITY: CH(3)-S-COM + H-S-HTP = CH(4) + COM-S-S-HTP.

-I- COFACTOR: THE ENZYME COMPLEX BINDS TICHTLY (BUT NOT COVALENTLY)

TO TWO MOLECULES OF COENZYME F430. F430 IS A YELLOW NICKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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-! SUBCELLULAR LOCATION; Mitochondrial.
-!- SUBCELLULAR LOCATION; Mitochondrial.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EP-TU/EP-1A SUBFAMILY.
EP-TU/EP-1A SUBFAMILY.
Interpro; IPRO00795; EF GTPDind.
PROSITE; PS00301; EFACTOR GTP; PARTIAL.
PROSITE; Psotein biosynthesis; Mitochondrion; GTP-binding. NON TER
NON TER
SEQÜENCE 14 AA; 1600 MW; 8CAPOBGAE7CCDE41 CRC64;
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SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO GAMMA CHAINS.
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last amnotation update)
Methyl-coenzyme M reductase II gamma subunit (EC 1.8.-.-) (MCR II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE=88163340, PubMed=9504812;
Dunn M.J., Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2133).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dog heart proteins.";
Electrophoresis 18:2795-2802(1997).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
-AMINOACYL-TENA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanobacterium thermoautotrophicum (strain Marburg / DSM 2. Achaea; Buryarchaeota; Methanobacteriales; Methanobacteriales; Methanobacteriacee; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 14;
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                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-DEC-1998 (Rel. 37, Last annotation update)
Elongation factor Tu, mitochondrial (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 AA.
    14 AA.
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    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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STANDARD;
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STRAIN=DM-7;
Schreiner S.J.;
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              SLLYKD 10
                              |::| |
2 SVIYLD 7
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                                                                                                        GON1_PETMA
P04378;
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                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD RES
                                                                                                                                                                                                                                                                                                                                           brain."
                                                                                RESULT 14
GON1 PETMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SP34_DICMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- MISCELLANDROUS: BELONGS TO THE NIFT GENE CLUSTER WHICH IS EXPRESSED IN HETEROCYSTS UNDER ANARDOSIC AND AEROBIC CONDITIONS.
-!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES. NIFS/ISCS SUBFAMILY.
cyanobacterium.";
Proc. Natl. Acad. sci. U.S.A. 92:9358-9362(1995).
-!- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR ATOMS FROM
-!- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR ATOMS FROM
CYSTEINE TO PRODUCE ALANINE. SEEMS TO PARTICIPATE IN THE
BIOSYNTHESIS OF THE NITROGENASE METALLOCLUSTERS BY PROVIDING THE
INORGANIC SULFUR REQUIRED FOR THE FE-S CORE FORMATION (BY
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PCC 7937 / ATCC 29413;
MEDLINE=96016168; PubMed=7568132;
Thiel T., Lyons E.M., Erker J.C., Ernst A.;
"A second nitrogenase in vegetative cells of a heterocyst-forming
                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Cysteine desulfurase 1 (EC 4.4.1.-) (Nitrogenase metalloclusters biosynthesis protein nifSl) (Fragment).
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena
NCBI_TaxID=1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.2%; Score 18; DB 1; Length 15; ilarity 50.0%; Pred. No. 3.3e+03; Conservative 2; Mismatches 1; Indels
                                                                                                            Score 18; DB 1; Length 14;
Pred. No. 3e+03;
                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=PCC 7937 / ATCC 29413;
Monnerighn U., Boehme H.;
Submitted (DC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AA; 1684 MW; 08B8F106DE65547D CRC64;
                                                                    14 14 14
14 AA; 1557 MW; 97E9439C4223B871 CRC64;
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PROSITE; PS00595; AA TRANSFER CLASS 5; PARTIAL.
Nitrogen fixation; Lyase; Pyridoxal phosphate.
                                                                                                                                                                                                                                                              15 AA.
                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                PRT;
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                                                                                                            22.2%;
                                                                                               Guery Match
Beet Local Similarity 37.55,
                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                          Anabaena variabilis.
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Matches 3; Conserv
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SEQUENCE
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NIS1_ANAVA
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Gaps

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MEDLINE-86168192; PubMed=3514603;
Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;
"Primary structure of gonadotropin-releasing hormone from lamprey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of a surface protein in macrocysts of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mucoroides.";
Submitted (NOV-1998) to the SWISS-PROT data bank.
-!- FUNCTION: THIS PROTEIN IS PRESENT IN THE MACROCYST PRIMARY WALL
WHICH IS PRODUCED BY AMORBAE DURING THE ONSET OF SEXUAL
                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata, Vertebrata, Hyperoartia, Perromyzontiformes; Petromyzontidae; Petromyzon. NCBL_TaxID=7757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 261:4812-4819(1986).
-!- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND FOLLICLE-STIMULATING HORMONES.
                                                                                               Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17; DB 1; Length 10;
Pred. No. 3.1e+03;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium mucoroides (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=31287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION.
1E4B36237B1735AB CRC64;
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                                      20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
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10 AA.
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-!- SIMILARITY: BELONGS TO THE GNRH FAMILY.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00446; GnRH; 1.
PROSITE; PS00473; GNRH; 1.
Hormone; Amidation; Hypothalamus.
                                                                                                                       (Luliberin I).
Petromyzon marinus (Sea lamprey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Surface protein P34 (Fragment)
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SEQUENCE 10 AA; 1244 MW;
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57.1%;
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InterPro; IPR002012; GnRH.
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STANDARD;
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Best Local Similarity
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                                            Query Match 21.0%; Score 17; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 3.1e+03; Matches 3; Conservative 0; Mismatches 0; Indels
FT NON TER 10 10 SQUENCE 10 AA; 1190 MW; 1B6A707AA3345B50 CRC64;
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Search completed: April 22, 2003, 13:13:03 Job time : 25 secs

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7 GKTYL 11
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SEQUENCE
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Matches
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ID PE
AC PE
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Q94750 homo sapien
Q9476 mus musculu
Q95476 mus musculu
Q1641 homo sapien
Q95519 bacillus st
Q9518 bacillus st
Q95618 homo sapien
P81468 spinacia ol
P82468 pseudomonas
Q950702 homo sapien
Q91477 bacillus ce
Q91477 bacillus ce
Q91478 burgia paha
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Q9ud47 homo sapien
                                                                                                                                        (without alignments)
117.741 Million cell updates/sec
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                                                                                                                       April 22, 2003, 13:10:19 ; Search time 28 Seconds
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
5: sp_invertebrate:*
5: sp_mamman!*
5: sp_mammal!*
6: sp_nammal!*
7: sp_nammal!*

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Q9UD47
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P82207
Q9UJ50
Q9X7K1
Q91YF5
Q16141
Q9R5L9
Q9TWR6
Q16183
P82164
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Q9L4F7
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sp_bacteriap:*
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Match Length DB
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Maximum DB seq length: 16
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                                                                                                                                                                                                                                                    Sequence:
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17 20 24.7 16 4 Q9UCI8 Q9uci8 homo sapien 19 23.5 1 1 5 P83321 Q9wa2 gallus gall 20 19 23.5 11 13 Q9WA2 GAPPE Q9wa2 gallus gall 20 19 23.5 11 13 Q9WA2 Q9WA2 Q9Wa2 gallus gall 21 19 23.5 11 10 Q9AFPZ Q9Wa2 gallus gall 22 19 23.5 14 10 Q9AFPZ Q9WA2 Q9AFBZ cicer ariet Q882V1 24 19 23.5 15 16 Q9TRT3 Q9ETT G982V1 CAPPE GAPPE CICERACMYC Q9TRT3 GAPPE GA
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## ALIGNMENTS

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STRAINEBLOS;
Leimkuchler S., Klipp W.;
Leimkuchler S., Klipp W.;
Leimkuchler S., Klipp W.;
The molybdenum coffactor biosynthesis protein MobA from Rhodobacter capsulatus is required for the activity of molybdenum enzymes binding MGD, but not for xanthine dehydrogenase harbouring the MPT cofactor.";
FEBS Lett. 174:239-246(1999).
EMBL, AJ131528; CAB43542.1;
NON_TER
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                                                                                                                                                                                                                            Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
Rhodobacter.
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Pred. No. 3.5e+03;
0; Mismatches 1; Indels
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                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Molybdopterin cofactor biosynthesis protein C C-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 AA; 1692 MW; 1DFB0534394788F8 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Mutant DNA polymerase beta (Fragment).
Homo saplens (Hunan).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GM3 synthase protein (Fragment).
GM3 Synthase.
Mus musculus (Mouse).
            16 AA.
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27.2%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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STRAIN-ICR; TISSUE-BRAIN;
Shuichi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1061;
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                                                                                                                                                                                    (Fragment).
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ID Q161-
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DT 01-N
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                                                                                                            Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
NCBI _TaxID=7091;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                 "Protein database for several tissues derived from five instar of slikworm.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=20225451; PubMed=10760572;
White G.R.M., Varley J.M., Heighway J.;
"Genomic structure and expression profile of LPHH1, a 7TM gene variably expressed in breast cancer cell lines.";
Blochim. Biophys. Acta 1491:75-92(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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White G.R.W., Varley J.M., Hedbhway J.;
"Isolation and characterisation of a human homologue of the
latrophilin gene from a region of 1p31.1 implicated in breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h
Similarity 57.1%; Pred. No. 6.5e+02;
8; Conservative 1; Mismatches
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                                                                                                                                                                                                                                                                                                                   STRAIN=XINHANG X KEMING; TISSUE=BODY WALL, AND FAT BODY; MEDLINE=21177481; Pubmed=11280994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 15
15 AA; 1877 MW; 580F6BD4703CA70C CRC64;
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Unknown protein from 2D-page (Fragment)
Bombyx mori (Silk moth)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Latrophilin-2 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chuan Hsueh Pao 28:217-224(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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1 YEDNKPFI 8
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5 EEGRUYL 11
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MEDLINE=92209510; PubMed=1555585;
Suzuki Y., Yonozawa K., Hattori M., Takii Y.;
Suzuki Y., Yonozawa K., Hattori M., Takii Y.;
Assignment of Bacillue Hermoamyloliquefaciens KP1071 alpha-
glucosidase I to an exo-alpha-1,4-glucosidase, and its striking
similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence
and in structural parameters calculated from the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                       Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                        MEDINE=94220089; PubMed=7545922;
Sadakane Y., Maeda K., Kuroda Y., Hori K.;
"Identification of mutations in DNA polymerase beta mRNAs from
                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Geobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Mollusca, Gastropoda, Caenogastropoda,
Neogastropoda, Muricoidea, Muricidae, Rapana.
NCBI_TaxID=29165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94007762; PubMed=8403854;
Idakieva K., Severov S., Svendsen I., Genov N., Stoeva S.,
Beltramini M., Tognon G., Di Muro P., Salvato B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB 2; Length 15;
Pred. No. 4.4e+03;
2; Mismatches 5; Indels
                                                                                                                                                             Score 22; DB 4; Length 13;
Pred. No. 3.8e+03;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 AA; 1931 MW; 62B4CE40013D3042 CRC64;
                                                                                                                                          SEQUENCE 13 AA; 1568 MW; D88C62798C9542CD CRC64;
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                                                                                                                                                                                                                                                                                                                 01-WAY-2000 (TrEMBLrel. 13, Created)
1-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
EXO-alpha-1,4-glucosidase (EC 3.2.1.20) (Fragment).
                                                                                           patients with Werner syndrome.";
Blochem. Blophys. Res. Commun. 200:219-225(1994)
EMBL; S69873; AAD14051.1; -.
NON TER. 1
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Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
                                               SEQUENCE FROM N.A.
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                        NCBI_TaxID=9606;
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Q9TWR6
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MEDLINE=94378189; PubMed=7916494;
Kalb K., Santoso S., Unkelbach K., Kiefel V., Mueller-Eckhardt C.;
Kalb K., Santoso S., Unkelbach K., Kiefel V., Mueller-Eckhardt C.;
Ilocalization of the Br polymorphism on a 144 bp exon of the GPIa gene and its application in platelet DNA typing.";
Thromb. Haemost. 71:651-654(1994).
EMBL: $72155; AD14096.1; -.
NON TER 1
SEQÜENCE 16 AA; 1968 MW; B31EFE05E038C26A CRC64;
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NCBI_TaxID=3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
"Structural properties of Rapana thomasiana grosse hemocyanin: isolation, characterization and N-terminal amino acid sequence different dissociation products.";
Comp. Biochem. Physiol. 106B:53-59(1993).
NOW TER 1 1 1
NON TER 15 15
SEQÜENCE 15 AA; 1735 MW; 78985413C9E90B6B CRC64;
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Pred. No. 4.8e+03;
3; Mismatches 1; Indels
                                                                                                                                                                                                    Score 22; DB 5; Length 15;
Pred, No. 4.4e+03;
                                                                                                                                                                                                                                                        2; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DTN-2001 (TrEMBLrel. 17, Last annotation update)
Chloroplast 30s ribosomal protein S14 beta (Fragment).
Spinacia oleracea (Spinach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 AA
                                                                                                                                                                                                                                                        2, Mismatches
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                                                                                                                                                                                                         Query Match 27.2%;
Best Local Similarity 55.6%;
Matches 5; Conservative
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SEQUENCE FROM N.A.
STRAIN=ATCC 14579 TYPE STRAIN;
STRAIN=ATCC 14579 TYPE STRAIN;
MEDLINE=20055637; Dubmed=10589720;
OKEtad O., Gominet M., Purnelle B., Rose M., Lereclus D., Kolsto A.B.;
OKEtad O., Gominet M., Purnelle B., Rose M., Lereclus D., Kolsto A.B.;
Sequence analysis of three Bacillus cereus loci under PICR-regulated
genes encoding degradative enzymes and enterotoxin.";
Microbiology 145:3129-3138 (1999).

EMBL; AJZ43711; CAB69804.1; -.

NON_TER 11

SEQUENCE 11 AA; 1335 MW; 4277A30E20572333 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                    Gaps
   "Major histocompatibility complex class I presentation of exogenous and endogenous protein-derived peptides by a transfected human monocyte cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brugia pahangi.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1396,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Emes R.D., Thompson F., Devaney E.;
"A novel mRNA up-regulated in mammalian-derived microfilaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DB 2; Length 11;
Pred. No. 6.7e+03;
2; Mismatches 2; Indels
                                                                                                                                                Score 21, DB 7; Length 15;
Pred. No. 6.5e+03;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brugia.";
Submitted (MAX-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ277990; CAB93515.1; -.
                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2011 (TrEMBLrel. 16, Last annotation update)
Phosphatidylinositol-specific phospholipase C (PI-PLC)
                                                                                                                    15 AA; 1838 MW; 98DCDCC01F8F7E15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel, 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Mmc1 protein (Fragment).
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50.0%;
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Similarity 44.4%;
4; Conservative
                                                     Immunology 86:606-611(1995)
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Best Local Similarity
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les 4; Conserv
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SEQUENCE FROM N.A.
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3 YGVARTYLD 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus cereus.
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Q9NFK8
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C -1 - SUBCELLULAR LOCATION: CHLOROPLAST.

-1 TISSUB SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.

-1 MISCELLANEOUS: S14 ALPHA AND BETA FORMS DIFFER IN PI. S14 ALPHA AND SEAS SPECTECOTY.

-1 MASS SPECTENOMETRY: NW=11745.9; METHOD=ELECTROSPRAY.

-1 MASS SPECTROMETRY: NW=11747; METHOD=ELECTROSPRAY.

-1 MASS SPECTROMETRY: NW=11747; METHOD=MALDI.

-1 MISCELLANEOUS: ON THE 2D-GEL ITS NW IS: 14 KDA.

-1 MISCELLANEOUS: ON THE 2D-GEL ITS NW IS: 14 KDA.

-1 MISCELLANEOUS: ON THE 2D-GEL ITS WA IS: 14 KDA.

-1 MISCELLANEOUS: ON THE 2D-GEL ITS WA IS: 14 KDA.

R PROFERS: SPECTROMETRY: BELOGORAL S14; MATHAL.

R PÉGM: PROSONAL PROSONAL S14; PARTIAL.

R RADAG SPOOTS: RIBOSONAL S18; PARTIAL.

R RIDOSOMAL S18; PARTIAL.

R RIDOSOMAL S18; PARTIAL.

R RIDOSOMAL S18; PARTIAL.
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Submitted (APR-2000) to the SWISS-PROT data bank.
-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: LYS-|-XAA, INCLUDING
LYS-|-PRO.
-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY S5 (SERINE PROTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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P82466;
01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Lysyl endopoptidase (EC 3.4.21.50) (Fragment).
Pseudomonas aeruginosa.
Bacteria, proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Fraction 60=HLA BC locus class I-bound peptide (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21, DB 2; Length 15;
Pred. No. 6.5e+03;
1; Mismatches 0; Indels
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Pred. No. 5.1e+03;
3; Mismatches 2; Indels
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MEDLINE=96165039; PubMed=8567028;
Harris P.E., Colovai A.I., Maffei A., Liu Z., Foca N.S.;
                                                                                                                                                                                                                         NON TER 12 12
SEQUENCE 12 AA; 1513 MW; 5E84D3F10116D057 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AA; 1483 MW; 3F42C5E66C4F76DD CRC64;
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                                                                                                                                                                                                                                                                     25.9%;
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Local Similarity 75.0%;
les 3; Conservative
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NON TER 15 15
SEQUENCE 15 AA; 1483 MW;
                                                                                                                                                                                                                                                                                     Local Similarity 44.4
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MEDLINE=9404990; PubMed=8401609;
Andrawis A., Solomon M., Delmer D.P.;
"Cotton fiber annexins: a potential role in the regulation of callose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                Query Match
24.7%; Score 20; DB 5; Length 14;
Best Local Similarity 45.5%; Pred. No. 8.8e+03;
Matches 5; Conservative 2; Mismatches 4; Indels
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Plant J. 3:763-772(1993).
SRQUENCE 15 AA; 1689 MW; 1087950BAC4F69F9 CRC64;
1 1
14 14
14 AA; .1602 MW; 5C4C62C55AB89397 CRC64;
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3 SATSLMMKQMK 13
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Q9S8R5;
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April 22, 2003, 12:54:59 ; Search time 73 Seconds (without alignments) 29.206 Million cell updates/sec
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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1 RSSKSLLYKDGKTYLN 16
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Maximum DB seq length: 16
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
1	81	1	16	21	AAY32254	Light chain CDR L1
10	77		16	19	AAW39818	Light chain CDR1 o
m	75		16	19	AAW39815	Light chain CDR1 o
4	75		16	13	AAW39824	Light chain CDR1 o
'n	69	85.2	16	13	AAW39875	Light chain CDR1 o
9	9		16	19	AAW39839	Light chain CDR1 o
7	62.5		15	19	AAW39821	Light chain CDR1 o
60	61		16	23		Human Kappa II lig
o	9		16	20		Peptide CDR-L1 der
10	59		16	22		Murine derived ant

(GLAX ) GLAXO GROUP LTD.

Murine monoclonal		CZ4Z:II MAD Kappa				Anti-human Fas mon	Q1 ·	u	Murine 13H10 light	CDR1 of the light		Mouse antibody 13G	Murine anti-PI-3,4	Mouse Kappa II lig	₽	VL sequence of ant	n	Murine CD4/CD34 re	CDR1 of the light	Anti-platelet glyc	Murine antibody S2	6D9 antibody light	Mouse 6D9 catalyti	L27eY catalytic an	Sequence of light	lementarity	3HIS catalytic ant	Mouse antibody Act	MHC-Clas	talytic	MAb 3B9 light chai	I-Fas MA	E the light	Light chain CDR fo
22	7	2 14	25	2	5 18	9	2	9	9	16 19 AAW70926	9	16 21 AAB21364	6 22	6 23	61 9	6 16 .	6 19	9	6 19	6 21	6 2	16 15 AAR59420	22	N	14	ď		23		22		15 19 AAW83027		
7	2 57 70.	67.	67	55 67	53 65	7 53 65	9 53 65	53 65	0 52 64	1 51 63	2 49 60	49	4 49 60	5 48 5	6 47 5	7 46 5	8 46 5	46 5	0 45 5	u,	45	43 5	43 53	4	40 45	40 4	39 4	39 48.	36 44.	34 42	32.5 40	5 40.	32.5 4	2.5 40.

## ALIGNMENTS

CD23; FCERII; IgB receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; urfilammatory bowel disease; ulcerative collitis; Crohn's disease; Sjograft-versus-host disease; asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy. Light chain CDR L1 of mouse anti-CD23 MAb C11. AAY32254 standard; Peptide; 16 AA. 99WO-GB01434. 98GB-0009839. 15-FEB-2000 (first entry) 07-MAY-1999; 09-MAY-1998; WO9958679-A1 Mus musculus 18-NOV-1999. AAY32254; RESULT 1 AAY32254 

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in far smaller doses than antibodies that antagonise cocaine by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 80; 147pp; English.
                                      Claim 13; Page 81; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       AAW39815 standard, peptide; 16 AA.
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                                                                                                                                                                                                                                                                       Local Similarity 93.8
                                                                                                                                                                                                                                                                                                                1 RSSKSLLYKDGKTYLN 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overdose; addiction.
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                                                                                                                                                                                                                                   16 AA;
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                                                                                                                                  This bequence represents comprementative determined of the light chain of murine anti-CD23 (FCERII) monoclonal antibody Cl1 (see also AAY32262). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of Cl1 light and heavy chain CDS (see AAY3224-59) to render them capable of binding to the CD23 (type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowed lalesage, ulocarative colitis, Crohn's disease, Sogren's syndrome, allergies allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, cathma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, particularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction
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                                                              Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required
                                                                                                                            This sequence represents complementarity determinating region 1 (CDR L1) of the light chain of murine anti-CD23 (FCERII) monocle
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                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 81; DB 21; Length 16; 100.0%; Pred. No. 5e-07; ive 0; Mismatches 0; Indels
 Shearin J;
 Rapson NT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Light chain CDR1 of catalytic antibody 6A12.
 Ellis JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW39818 standard; peptide; 16 AA.
                                                                                                   Claim 1; Page 40; 81pp; English
                                                                                                                                                                                                                                                                                                                                                    determining the binding agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RSSKSLLYKDGKTYLN 16
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 Bonnefoy JMP, Crowe SJ,
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                           WPI; 2000-053101/04.
                                                                                                                                                                                                                                                                                                                                                                              16 AA;
                                     N-PSDB: AAZ34739
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AAW39818-20 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 6A12, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic caid from 3H-phenyl occaine. The 6A12 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoceter transition state analogue. Antibody 6A12 has a per minute KCat of 0.072. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They concentration that can be achieved).
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AAW39824-26 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 12H1, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified using TSA2, and has a per minute Kcat of 0.16. The antibodies particularly for the treatment of an subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be
identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of occaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Variable domain; lambda light chain; catalytic antibody; degradation; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
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                                                                                                                                                                 Length 16;
                                                                                                                                                           Score 75; DB 19; Length 16
Pred. No. 5.2e-06;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain CDR1 of catalytic antibody 12H1.
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                                                                                                                                                                                                                                                                                                                                                            AAW39824 standard; peptide; 16 AA.
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                                                                                                                                                               Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative
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AAW39975-77 represent the sequences of the light chain complementarity determining regions (CDRs) of a catalytic antibody which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. These antibodies were found to have CDRs of the present sequence. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
                                                                                                                                                                                                                      Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                                                                                                                                                                              Light chain CDR1 of a catalytic antibody capable of degrading cocaine.
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Pred. No. 5.4e-05;
0; Mismatches 2; Indels
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                                                                                                        AAW39875 standard; peptide; 16 AA.
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                 1 RSSRSLLYRDGKTYLN 16
RSSKSLLYKDGKTYLN
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Score 75; DB 19; Length 16; Pred. No. 5.2e-06; 2; Mismatches 0; Indels

ch 1 Similarity 87.5%; 14; Conservative

Query Match Best Local Similarity Matches 14; Conserv

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Best Local Similarity

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02-MAY-2000; 2000US-0563222
overdose; addiction.
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                                                                                                                               Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction
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Pred. No. 5.4e-05;
2; Mismatches 1; Indels
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                                                                                                      Light chain CDR1 of catalytic antibody 8G4E
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              AAW39839 standard; peptide; 16
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81.2%;
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Best Local Similarity
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                                            AAW39839;
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Matches
 AAW39839
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AAW39821-23 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 2AlO, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The 2AlO antibody was identified using TSAl, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2AlO has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo
                                                                                                                                                                                                                                                                                                                                                        New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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87.5%; Pred. No. 0.00064;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU70328 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Page 82; 147pp; English.
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                                                                                                                                               (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2001; 2001WO-US14349.
97WO-US10965.
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                                                                                                                                                                                                                                                                                          WPI; 1998-077166/07.
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Neutralized antibody partial peptide derived from hepatitis C virus - useful for inhibiting Hepatitis C Virus (HCV) serine protease activity
                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 14; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY14404 standard; peptide; 16 AA.
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                         (EPIC-) EPICYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 75.0
Matches 12, Conservative
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                                                                                                                                         WPI; 2002-055482/07
                                                                                    Hein MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 AA;
                                                                                                                                                                                                                                                                                               preparing array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention.
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                                                                                    Hiatt AC,
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Greiner Claim 1; Page 9; 18pp; German. (MUEL/) MUELLER-HERMELINK H K. 74.1%; 80.0%; 99DE-1062583. 99DE-1062583 13-SEP-2001 (first entry) Local Similarity 80.0 les 12; Conservative 1 RSSKSLLYKDGKTYL 15 1 RSSKSLLHSDGNTYL 15 Mueller-Hermelink HK, WPI; 2001-426596/46. (GREI/) GREINER A. 16 AA; DE19962583-A1. 23-DEC-1999; 23-DEC-1999; 28-JUN-2001. AAB86292; activity. Sequence Query Match gb. Best Loca Matches RESULT 10 Mus AAB86292 ð 셤 The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides calls), comprising using a library of two different polynucleotides to encoding different immunoglobulin binding protein (IRBP) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transfected cells, to generate an IBBP that binds to a ligand, and transformed plant cells are selected, and at least 75% sequence identity to a framework region (RR) of a native IGM, IGG, IGA, IGD, IGE, IGY, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammalian cells). The CHBP is useful for discovery of e.g. screening assays of IGBPs having desired characteristics. The present sequence is a mammalian immunoglobulin derived peptide that may be incorporated into an IGBP of ö Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for Gaps Complementarity determining region, CDR; monoclonal antibody; MAb; hepatitis C virus; HCV; protease; binding site. ö Peptide CDR-L1 derived from anti-HCV Ser/Thr protease MAb 8D4. Score 61; DB 23; Length 16; Pred. No. 0.0012; 2; Mismatches 2; Indels 75.3%; 97JP-0297451 97JP-0297451

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rhis invention describes novel antibodies (Ab) in which the variable region (VR) of at least one chain and/or the VR of at least one heavy chain includes at least one of 7 specified sequences, or fragments of these sequences, or contain at least one light chain and/or heavy chain encoded by specific nucleic acid sequences (I) and (II), reproduced, or their fragments. The products of the invention have antitumor and immunomodulatory activity. Ab, or other antibodies that recognize the same antigen, are used: (1) to identify cognate antigens, comparation, e.g. in an extracorporeal system; (iii) for generating additional antibodies able to label PC; and (iv) for treating autoimmune diseases and/or tumores, e.g. multiple myeloma, lymphoma and/or plastocytoma. Ab are specific for mature PC, i.e. they do not recognize plastocytoma. Ab are specific for mature PC, i.e. they do not recognize plastocytoma. Ab are specific for mature productions as immunogens. Cherospeutic agents, they should show fewer side effects than conventional chemotherapeutic agents. This sequence represents the Wue-1 antibody
                                                                                                                                                                                                                                                                                  ö
                                               This sequence represents a peptide derived for the sequence of the light chain variable region complementarity determining region (CDR)-1 of the anti-hepatitis C virus (HCV) Ser/Thr protease monoclonal antibody (MAb) 8D4 protein. The invention relates to the use of partial peptides (AAY14348-Y14353) from the MAb 8D4 for inhibiting HCV serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody; Wue-1; variable region; light chain; heavy chain; antitumor; immunomodulatory; cognate antigen identification; autoimmune disease; tumor; multiple myeloma; lymphoma; plastocytoma; CDR-1.
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibodies specific for plasma cells, useful for treatment and diagnosis of autoimmune diseases and plasma cell tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine derived antibody Wue-1 light chain variable region CDR-1.
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                                                                                                                                                                                                                                         Length 16;
                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                       Score 60; DB 20;
Pred. No. 0.0018;
1; Mismatches 2,
                 Example 1; Page 13; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB86292 standard; peptide; 16 AA.
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Sequences AAB73652-AAB73654 represent, respectively, CDRs 1-3 of the light chain variable region (LH) of antibody IOR C5.
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                                                              16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                                                      AAR24704;
                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iwasa S,
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                                                                                                                                                                                                                                                                                     RESULT 12
AAR24704
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    ន្តដ្ឋនូ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a chimeric antibody, or an Fv-type single-chain fragment, derived from the murine monoclonal antibody or single-chain fragment, derived from the murine monoclonal antibody in CRS expressed by hybridoma ECCC 97061101. It contrains the CDRS (complementarity determining regions) of IOR CS and human constant regions, in both heavy and light chains. The IOR CS antibody specifically binds to the IOR C2 antigen which is expressed on malignant and normal coloractal cells. The invention also encompasses a cell line which expresses the humanised IOR C5 antibody; host cells which expresses the coloractal cells. The invention also encomposition for treatment, location or in vivo identification of malignant tymours of colon and rectum, including their metastases and recurrences, containing the humanised antibody or the Fv fragment thereof, plus an excipient; and a method antibody or the Fv fragment thereof, plus an excipient, and method antibody or the fragment and including their metastases or recurrences, and for in vivo diagnosis of tumours of reat malignant tumours of the colon or rectum, including their metastases or recurrences, and for in vivo diagnosis, (imaging) of tumours, particularly when radiolabelled.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant antibody, or single-chain fragment, derived from murine monoclonal IOR C5, useful for treatment and diagnosis of colo-rectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody IOR C5; hybridoma BCCC 97061101; mouse; humanised; IOR C2 antigen; colorectal cancer; tumour; metastasis; therapy; drug targetting; imaging; diagnosis; extostatic; VL; light chain variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mateo De Acosta Del Rio CM, Roque Navarro LT, Morales Morales A;
Perez Rodríguez R, Ayala Avila M, Gavilondo Cowley JV;
Duenas Porto M, Bell García H, Rengifo Calzado E, Iznaga Escobar N;
Ramos Zuzarte M;
                                                                                                                                               Gaps
  variable region light chain complementarity determining region CDR1 fragment described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine monoclonal antibody IOR C5 light chain variable region CDR1
                                                                                                                                             ö
                                                                                                   Score 59, DB 22; Length 16;
Pred. No. 0.0027;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                               AAB73652 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 24; 30pp; Spanish.
                                                                                                      72.8%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                             Query Match
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                    1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                                                                            1 KSQSLLDSDGKTYLN 16
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                                                                 16 AA;
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Synthetic.
                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                    AAB73652;
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                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric monoclonal antibodies - contain anti-human fibrin antibody light and heavy chain variable and constant for treating thrombotic conditions e.g. myocardial infarction
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                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of an anti-human fibrin antibody light chain variable
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     Length 16
                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric monoclonal antibody, anti-fibrin antibody, antithrombotic agent, myocardial infarction therapy
Score 59; DB 22;
Pred. No. 0.0027;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tada H;
                                                                                                                                                                                                                                                                                                                AAR24704 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 49; 87pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region chain designated 'A'.
  72.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91EP-0121591
                                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-1992 (first entry)
  Query Match 72.8
Best Local Similarity 75.0
Matches 12; Conservative
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                                                                                                                 1 RSSKSLLYKDGKTYLN 16
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Tsurushita

Paul SM,

Bales KR,

2000US-0184601

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New humanised antibody for the treatment of Alzheimer's comprises the inhibition and reduction of the formation of amyloid plagues
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                                                                                              08-DEC-2000; 2000US-0254465.
                                                            26-FEB-2001; 2001WO-US06191.
                                                                                                                                                                    Holtzman DM, Demattos R,
                                                                                                                                 (UNIW ) UNIV WASHINGTON
                                                                                                                                            ELIL ) LILLY & CO ELI
                                                                                                                                                                                                       WPI; 2001-550087/61.
              WO200162801-A2
                                                                                    24-FEB-2000;
                                    30-AUG-2001
                                                                                                                                                                                Vasquez M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA014984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
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ID AAO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complementarity determining region; CDR1; Hu266; nootropic; neuroprotective; Abeta peptide; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; antibody; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               The sequences given in AAR30448-50 represent the kappa chain and AAR30451-53 the heavy chain complementarity determining regions (CDR of a monoclonal antibody (MAD), C242:II. G242:II is a monoclonal murine Ab of IgG class produced when culturing in an appropriate medium a hybridoma cell line obtained by fusing spleen cells from a mouse, which has been immunised with a human colonic adenocarcinoma cell line, with the murine myeloma cell line Sp2/0. C242:II when bound to a cell surface antigen is capable of being endocytosed or
                                                                                                       Kappa; chain; heavy; complementarity determining region; CDR; MAb; monoclonal antibody; C242:II; murine; IgG; hybridoma; cell line; spleen; human; colonic; adenocarcinoma; myeloma; Sp2/0; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody reacting with CA-242 antigen - obtd. by culturing hybridoma cell line C242:11 or mutants, useful for diagnosis and therapy of pancreatic or colorectal cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human light chain complementarity determining region, CDR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55; DB 14; Length 16;
Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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             AAR30448 standard; peptide; 16 AA
                                                                                                                                                                                                                                                                                                              Lind P, Lindholm L;
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 11; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.9%;
73.3%;
                                                                                  C242:11 MAb kappa chain CDR1
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                                                           (first entry)
                                                                                                                                                                                                                                                                                      (KABI ) KABI PHARMACIA AB.
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Best Local Similarity 73.3
Matches 11, Conservative
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Synthetic.
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                                                           06-MAY-1993
                                                                                                                                                                                                                                                                                                               Holmgren J,
                                                                                                                                             endocytosis
                                                                                                                                                                                                                  07-JAN-1993
                                                                                                                                                                                          EP521842-A.
                                                                                                                                                                   Synthetic.
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                                    AAR30448;
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AAR30448
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The invention relates a humanised antibody that specifically binds an epitope contained within positions 13-28 of amyloid beta peptide, beta. The antibody is useful to inhibit and reduce the formation of amyloid plaques or the effects of toxic soluble Abeta species in humans their fragments are used for the manufacture of a medicant. This includes their fragments are used for the manufacture of a medicant. This includes tissues for the treatment of clinical/pre-clinical Alzheimer's disease, Down's syndrome or pre clinical cerebral amyloid angiopathy. Specifically, the antibody is used to sequester Abeta into plasma, brain or cerebrospinal fluid to prevent/reverse accumulation of the Abeta peptide within the brain thereby improving cognition. The present sequence is human light chain CDR1 (complementarity determining region 1) used to humanise the mouse monoclonal antibody 266 to produce Hu266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; graft rejection; CC chemokine receptor 2 antagonist; CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant; lung transplant; pancreas transplant; bowel transplant; heart-transplant; graft versus host disease; chronic graft rejection; antibody light chain; mAb 1D9; CDR1; complementarity determining region 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse mAb 1D9 antibody light chain complementarity determining region 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55; DB 22; Length 16;
Pred. No. 0.013;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                   67.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 62.5
les 10; Conservative
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Inhibiting graft rejection, graft versus host disease or chronic rejection of a transplanted graft, involves administering a CCR2 antagonist -
                                                                                     Claim 25; Page 12; 16pp; English.
                  (MILL-) MILLENNIUM PHARM INC
     14-APR-2000; 2000US-0549448.
                                            WPI; 2002-351265/38.
                                Hancock WW;
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The invention comprises a method of inhibiting graft rejection, graft versus host disease or chronic rejection of a transplanted graft. The wethod involves administering an antagonist of CC chemokine receptor 2 (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may be an anti-CCR2 antibody (i.e. containing light and heavy chain complementarity determining regions from various non-human origins). CCR2 is known to be involved in the rejection of transplanted grafts. The method of the invention is useful for inhibiting graft rejection particularly allografts such as kidney, liver, lung, heart-lung, particularly and heart. The method of the invention is also useful for inhibiting graft versus host disease and for inhibiting chronic rejection of a transplanted graft. The present amino acid sequence represents a mouse made in the chain complementarity determining region 1

Sequence 16 AA;

Gaps ; Score 55; DB 23; Length 16; Pred. No. 0.013; 3; Mismatches 2; Indels 67.9%; 68.8%; Query Match
Best Local Similarity 68.8
Matches 11; Conservative

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Search completed: April 22, 2003, 13:12:32 Job time : 74 secs

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Sequence 2, Appli
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Sequence 4, Appli
Sequence 9, Appli
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Sequence 183, Appli
Sequence 692, Appli
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                                                                                                        April 22, 2003, 13:13:30 ; Search time 41 Seconds (without alignments) 31.270 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/DCT NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-217-268B-29
US-09-217-268B-29
US-09-13-4
US-10-091-236-14
US-10-091-236-4
US-09-879-461-16
US-09-879-461-16
US-09-879-461-16
US-09-879-461-16
US-09-879-461-16
US-09-879-948-343
US-09-809-638-693
US-10-084-813-693
US-10-084-813-694
US-10-084-813-694
US-10-084-813-694
US-10-084-813-694
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US-09-809-638-622
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                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                           301932 seqs, 80129803 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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                                                                                                                                                                                                                     1 RSSKSLLYKDGKTYLN 16
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Match Length
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20 26 32.1 12 10 US-09-850-351A-61 Sequence 61, Appl 22 26 32.1 14 10 US-09-736-968A-18 Sequence 18, Appl 23 23 26 32.1 14 10 US-09-736-968A-18 Sequence 18, Appl 24 26 32.1 14 10 US-09-736-960-18 Sequence 18, Appl 25 30.9 10 10 US-09-876-904A-344 Sequence 344, Appl 25 30.9 10 10 US-09-876-053-070 Sequence 3, Appl 26 25 30.9 10 10 US-09-969-037-1 Sequence 1, Appl 28 30.9 11 9 US-09-969-037-2 Sequence 2, Appl 30 25 30.9 12 9 US-09-969-037-1 Sequence 3, Appl 31 25 30.9 12 9 US-09-969-037-2 Sequence 2, Appl 32 25 30.9 15 9 US-09-969-037-2 Sequence 2, Appl 33 25 30.9 15 9 US-09-969-037-2 Sequence 2, Appl 33 25 30.9 15 9 US-09-969-037-1 Sequence 2, Appl 34 24 29.6 12 9 US-09-969-03-26 Sequence 2, Appl 34 29.6 12 9 US-09-96-288-25 Sequence 2, Appl 36 24 29.6 15 9 US-09-96-288-25 Sequence 2, Appl 37 24 29.6 15 9 US-09-96-288-25 Sequence 2, Appl 37 24 29.6 16 9 US-09-96-288-25 Sequence 2, Appl 40 24 29.6 16 9 US-09-96-288-25 Sequence 2, Appl 40 23.5 29.0 11 10 US-09-96-288-27 Sequence 10.6, Appl 41 23.5 29.0 11 10 US-09-96-2813 Sequence 113, Appl 44 23.5 29.0 11 10 US-09-913-41 Sequence 113, Appl 44 23.5 29.0 11 10 US-09-913-41 Sequence 12, Appl 44 23.5 29.0 11 10 US-09-913-41 Sequence 12, Appl 42 23.5 29.0 11 10 US-09-913-41 Sequence 26, Appl 42 23.5 29.0 11 10 US-09-913-41 Sequence 26, Appl 44 23.5 29.0 11 10 US-09-913-41 Sequence 26, Appl 44 23.5 29.0 11 10 US-09-913-41 Sequence 26, Appl 44 23.5 29.0 11 10 US-09-913-41 Sequence 26, Appl 44 23.5 29.0 11 10 US-09-913-41 Sequence 26, Appl 44 23.5 29.0 11 10 US-09-913-41 Sequence 26, Appl 44 23.5 29.0 11 10 US-09-913-41 Sequence 26, Appl 44 23.5 29.0 11 10 US-09-913-41 Sequence 26, Appl 44 23.5 29.0 11 10 US-09-913-41 Sequence 26, Appl 56 28 29.0 11 10 US-09-913-41 Sequence 27, Appl 56 28 29.0 11 10 US-09-913-41 Sequence 27, Appl 56 28 29.0 11 10 US-09-913-41 Sequence 27, Appl 56 28 29.0 11 10 US-09-913-41 Sequence 27, Appl 56 29.0 11 10
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## ALIGNMENTS

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US.09-835-087-14

Sequence 14, Application US/09835087

Sequence 14, Application US/09835087

Sequence 14, Application US/09835087

Sequence 14, Application US/09835087

SEPTIME NO USZ0020042370A1

TITLE OF INVENTION: Method of Treating Graft Rejection Using TITLE OF INVENTION: Method of Treating Graft Rejection Using TITLE OF INVENTION: Method of Treating Graft Rejection Using TITLE OF INVENTION: Thibitors of CCR2 Function

CURRENT FILING DATE: 2001-09-34

PRIOR FILING DATE: 2001-09-44

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FRATURE: RESEQ for Windows Version 4.0

SEQ ID NO 14

IENGTH: 16

TYPE: PRT

ORGANISM: MAS MUSCULUS

FRATURE:

NAME/KEY: DOMAIN

UCATION: (1)...(16)

COATION: (1)...(16)

COATION: (1)...(16)

COATION: (1)...(16)

MACKEY: DOMAIN

US-09-813--097-14

Guery Match

Graft Reserrative 3; Mismatches 2; Indels 0; Gaps

OY 1 RSSKSLINTGCKTYIN 16

I KSSQSLIDSDGKTFLN 16

Sequence 8, Application US/09518737

Sequence 8, Application US/09518737

Sequence 8, Application US/09518737

Sequence 8, Application US/09518737

APPLICANT: RNGAM, RNGAM, RAUCHI
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Sequence 4, Application US/10091313

Fublication No. US20030044406A1

GENERAL INFORMATION:

APPLICANT: DINGIVAN, CHRISTINE

TITLE OF INVENTION: BISORDERS BY ADMINISTERING CD2 ANTAGONISTS IN COMBINATION WITH O TITLE OF INVENTION: PROPHYLACTIC OR THERAPEUTIC AGENTS

TITLE OF INVENTION: PROPHYLACTIC OR THERAPEUTIC AGENTS

FILE REPERBACE: 10271-063

TITLE OF INVENTION: PROPHYLACTIC OR THERAPEUTIC AGENTS

FILE REPERBACE: 10271-063

CURRENT APPLICATION NUMBER: US 60/273,098

PRIOR APPLICATION NUMBER: US 60/273,098

PRIOR APPLICATION NUMBER: US 60/346,918

PRIOR FILING DATE: 2001-03-02

PRIOR FILING DATE: 2001-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/10091236
Patent No. US2020168360A1
Patent No. US2020168360A1
Patent No. US2020168360A1

PAPLICANT: DINGIVAN, CHRISTINE A.
TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING INFLAMMATORY OR AUTOIMMUNE
TITLE OF INVENTION: DISORDERS BY ADMINISTERING INTEGRIN ALPHA-V-BETA-3 ANTAGONISTS
TITLE OF INVENTION: COMBINATION WITH OTHER PROPHYLACTIC OR THERAPEUTIC AGENTS
FILE REFERRINCE: 10271-053-999
CURRENT APPLICATION NUMBER: US/10/091,236
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: US 60/273,098
PRIOR PLING DATE: 2001-03-02
PRIOR PAPLICATION NUMBER: US 60/216,321
PRIOR PLING DATE: 2001-08-31
PRIOR PLING DATE: 2001-08-31
PRIOR PLING DATE: 2001-08-31
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Pred. No. 2.1;
6; Mismatches 2; Indels
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                                 CURRENT APPLICATION NUMBER: US/09/796,744
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: UP 2000-59508
PRIOR PILING DATE: 2000-03-03
PRIOR PLING DATE: 2000-13-28
PRIOR PILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 8
TYPE: PRT
TYPE: PRT
ORGANISM: Mus musculus
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Best Local Similarity 46.7%;
Matches 7; Conservative 6
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
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Best Local Similarity 61...
8; Conservative
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ORGANISM: Mus
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Sequence 29, Application US/09217268B
Patent No. US20020065398A1
GENERAL INFORMATION:
APPLICANT: Mateo de Acosta del Rio, Christina M
APPLICANT: Rodriquez, Rolando P
APPLICANT: Rodriquez, Rolando P
APPLICANT: Frias, Ernesto M
TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use FILE REFERENCE: 2720.1US
CURRENT APPLICATION NUMBER: US/09/217,268B
CURRENT PILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 15
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APPLICANT: SHOJI, EMI
APPLICANT: SHOJI, EMI
APPLICANT: SAKUNDA, MIKKIKO
APPLICANT: FURUYA, AKIKO
APPLICANT: FURUYA, KAZUYASU
APPLICANT: NIWA, KINPEI
APPLICANT: SHIBATA, KENJI
APPLICANT: SHIBATA, KENJI
APPLICANT: YAMASAKI, MOTOO
TITLE OF INVENTION: GENE RECOMBINANT ANTIBODY AND ANTIBODY FRAGMENT THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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APPLICANT: SAITO, NAOAKI
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3,4-DIPHOSPHATE
FILE REPERENCE: 1965/49618
CURRENT APPLICATION NUMBER: US/09/518,737
CURRENT FILING DATE: 2000-03-03
PRIOR PLING DATE: 1999-09-03
PRIOR PLING DATE: 1999-09-03
SOFTWARE: PACENTIN VOX: 10
SOFTWARE: PACENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.1%; Score 43; DB 10; Length 15; Best Local Similarity 46:7%; Pred. No. 0.62; Matches 7; Conservative 6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 9; Length 16;
Pred. No. 0.068;
5; Mismatches 2; Indels
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OTHER INFORMATION: CDR of murine R3 antibody
US-09-217-268B-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09796744
Patent No. US20020098527A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 56.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSSKSLLYKDGKTYLN 16
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ORGANISM: Mus musculus
US-09-518-737-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Murine
FEATURE:
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US-09-217-268B-29
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ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Holmes, Stephen D.
APPLICANT: Holmes, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUMPLAIL 1996
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAT APPLICATION DATE: 12-Jun-2001
CIASSIFICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CIASSIFICATION: CUNKNOWN>
PRIOR APPLICATION OWNER: 08/612,929
FILING DATE: CUNKNOWN>
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: US 08/136,783
FILING DATE: US 08/136,783
ATTORNAY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15
                                                         Length 16;
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                                                                                                 5; Indels
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                                                         DB 10;
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Pred. No. 33;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                         Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
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US-10-205-150-4
; Sequence 4, Application US/10205150
                                                                                                                                                                                                                                                              US-09-879-461-16;
; Sequence 16, Application US/09879461;
; Publication No. US20020193575A1;
; GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.1%;
                                                       Query Match
Best Local Similarity 56.2%;
Matches 9; Conservative
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(215) 27
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Best Local Similarity 43.8
Matches 7; Conservative
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                                                                                                                                         1 RSSKSLLYKDGKTYLN 16
; OTHER INFORMATION: LDP-02
US-09-748-960-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-879-461-16
                                                                                                                                                                                                                                             RESULT 9
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; Sequence 4, Application US/20030068320A1
; Publication No. US20030068320A1
; CENERAL INFORMATION:
    APPLICANT: DINGIVAN, CHRISTINE
; TITLE OF INVENTION: METHODS OF ADMINISTERING/DOSING CD2 ANTAGONISTS FOR THE PREVENTIC
; TITLE OF INVENTION: MD TREATMENT OF AUTOIMMUNE DISORDERS OR INFLAMMATORY DISORDERS
; FILE REFERENCE: 10271-054-999
; CURRENT APPLICATION NUMBER: US 60/273,098
; PRIOR APPLICATION NUMBER: US 60/273,098
; PRIOR FILING DATE: 2001-03-02
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
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LOCATION: (1)...(16)
OTHER INFORMATION: CDR1 of the light chain of antibodies Act-1 and
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Patent No. US20010046496A1

GENERAL INFORMATION:
APPLICANT: Bretten. Lee R.
APPLICANT: Poxt, Judith A.
APPLICANT: Allison, David Edward
TITLE OF INVENTION: Method of Administering an Antibody
FILE REFERENCE: 1855.2007-001
CURRENT APPLICATION NUMBER: US/09/748,960
CURRENT APPLICATION NUMBER: US 09/550,082
PRIOR APPLICATION NUMBER: US 09/550,082
PRIOR PILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9; Length 16;
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                                                                                                                                                               DB 9; Length 16;
                                                                                                                                                                                                       3; Indels
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2; Mismatches
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Pred. No.
                                                                                                                                                                 Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.1%;
  NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
                                                                                                                                                               48.1%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                               Query Match
Best Local Similarity 61.5
Matches 8; Conservative
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                                                                                  ; TYPE: PRT
; ORGANISM: Mus sp.
US-10-091-313-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mus sp.
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                                                             LENGTH: 16
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Sequence 928, Application US/10084813
Sequence 928, Application US/10084813
Publication No. US20030068615A1
GENERAL INFORMATION:
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
CURRENT PILING DATE: 2059-20-27
PRIOR FILING DATE: 2000-08-25
PRIOR PILING DATE: 1099-08-27
NUMBER OF SEQ ID NOS: 1242
SOUTHARD: PARCHELING DATE: 1299-08-27
SOUTHARD: PARCHELING DATE: 1399-08-27
SOUTHARD: PARCHELING DATE: 1399-08-27
SOUTHARD: PARCHELING DATE: 1399-08-27
SOUTHARD: BENCH PARCHELING DATE: 1399-08-27
SOUTHARD: PARCHEL
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Publication No. US20030068615A1
GENERAL INFORMATION:
APPLICANT: SAXINGER, CARL
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
FILE REFERENCE: 215875
CURRENT APPLICATION NUMBER: US/10/084,813
CURRENT FILING DATE: 2002-02-27
PRIOR PLICALION NUMBER: PCT/US00/23505
PRIOR PLICALION DATE: 200-08-25
PRIOR PLICALION NUMBER: US 60/151,270
PRIOR PLILING DATE: 1999-08-27
PRIOR PLILING DATE: 1999-08-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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         ## APPLICANT: Arthur B. Raitano
| APPLICANT: Aya Jakobovits |
| TITLE OF INVENTION: 125F5C8: A TISSUE SPECIFIC PROTEIN |
| TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS |
| FILE REFERENCE: 129.35U501 |
| CURRENT APPLICATION NUMBER: US/09/809,638 |
| CURRENT APPLICATION NUMBER: 2001-03-14 |
| NUMBER OF SEQ ID NOS: 746 |
| SOTHWARE: PASELSEQ for Windows Version 4.0 |
| SEQ ID NO 497 |
| TITLE OF THE OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.3%; Score 27; DB 9; Length 12; Best Local Similarity 41.7%; Pred, No. 2.1e+02; Matches 5; Conservative 3; Mismatches 4; Indels
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55.6%; Pred. No. 81;
ative 1; Mismatches
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-09-809-638-497
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                                                                        APPLICANT: LINGAND:
APPLICANT: OF VACCINES COMPRISING AN ANTIGEN AND AN IMMUNOGENIC OLIGODECOXYN
TITLE OF INVENTION: AND A POLYCATIONIC POLYMER AS ADJUVANTS
FILE REFERENCE: SONN:018US
CURRENT APPLICATION NUMBER: US/10/205,150
FRICH REPTENCE: 2002-07-25
PRICH REPTENCE: 2001-01-05
NUMBER: POT/EPD1/00087
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 4
LENGTH: 9
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US-09-876-904A-343

Sequence 343, Application US/09876904A

Fublication No. US20030072794A1

Sequence 343, Application US/09876904A

Fublication No. US20030072794A1

SEREMATION: APPLICANT: BOULIKAS, TENI

TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

TITLE OF INVENTION: CONUGATES INTO TARGETED LIPOSOME COMPLEXES

TITLE OF INVENTION: UNMBER: US/09/876,904A

CURRENT FILING DATE: 2001-06-08

PRIOR PILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 629

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 343

LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Peptide US-10-205-150-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Ser/Thr protein kinase US-09-876-904A-343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 497, Application US/09809638
Publication No. US20030059895A1
GENERAL INFORMATION:
APPLICANT: Mary Faris
APPLICANT: Pia M. Challita-Eid
APPLICANT: Steve Chappell Mitchell
APPLICANT: Daniel E.H. Afar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
Publication No. US20020197269A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity
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6 YRDHKTHLH 14
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Sequence 693, Application US/10084813
| Publication No. US2003068615A1
| Publication No. US2003068615A1
| GENERAL INPORMATION:
| APPLICANT: SAXINGER, CARL
| TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
| TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
| FILE REPRENCE: 21895
| CURRENT APPLICATION NUMBER: US/10/084,813
| CURRENT PAPLICATION NUMBER: PCT/US00/23505
| PRIOR APPLICATION NUMBER: US 60/151,270
| PRIOR FILING DATE: 1999-08-27
| NUMBER OF SEQ ID NOS: 1242
| SOFTWARE: Patentin Version 3.1
| SEQ ID NO 693
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                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FRATURE:
COTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: binding peptide US-10-084-813-693
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Job time : 41 secs
NUMBER OF SEQ ID NOS: 1242
SOFTWARE: Patentin version 3.1
SEQ ID NO 692
LENGTH: 15
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ORGANISM: Artificial Sequence
FEATURE:
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4 KNLKIEDSDTYI 15
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                                                                                                                                                                                                       April 22, 2003, 13:11:19 ; Search time 14 Seconds (without alignments) 33.626 Million cell updates/sec
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Sequence 25,
Sequence 22,
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Sequence 3
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1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
                                 GenCore version 5.1.4_D5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-672-345C-25
US-09-214-095D-22
US-09-214-095D-22
US-09-214-095D-19
US-08-672-345C-19
US-08-672-345C-79
US-09-214-095D-19
US-09-214-095D-19
US-09-214-095D-19
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US-08-672-345C-79
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US-08-123-18
US-08-123-18
US-08-123-18
US-08-123-30B-30
US-08-123-30B-30
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US-08-123-30B-68
US-08-123-30B-68
US-08-50-55BE-29
US-08-50-55BE-29
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 RSSKSLLYKDGKTYLN 16
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Match Length
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1122 B
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116 B
117 B
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Sequence 1
Patent No.
Sequence 1
Sequence 2
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Sequence 1
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SOFTWARE: Petentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN 1996
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPERBONE-JOCKET NUMBER: 0575/51400
TELECOMUNICATION INFORMATION:
SEQUENCE CLASSIFICS:
SEQUENCE CLASSIFICS:
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; Patent No. 5948658
; GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
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Pred. No. 1.3e-06;
1; Mismatches 0;
US-08-159-339A-133
US-08-36-125-23
US-08-36-125-23
US-09-017-628-23
US-08-45-36-23
US-08-477-960-18
5443956-15
US-08-159-339A-219
US-08-159-339A-219
US-08-159-339A-219
US-08-159-331-615A-16
US-08-159-331-615A-16
US-08-165-38-3
PCT-US95-08441-3
US-07-620-669-16
US-07-98-361-16
US-07-98-361-16
US-07-98-361-16
US-07-98-361-16
US-07-98-361-16
US-07-98-361-16
US-07-98-361-16
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STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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93.8%;
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 93.8
Matches 15; Conservative
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Pred. No. 1.3e-06;
1; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk Computible COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: BATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/672,345C FILIND DATA: A-TORNEY/AGENT INFORMATION: A-35 ATTORNEY/AGENT INFORMATION: NAME: White, John P. REGISTRATION NUMBER: 28,678 REGISTRATION NUMBER: 0575/51400 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION FOR SEQ 1D NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
                                                                                                                        GENERAL INC. 0.20130/
GENERAL INCOMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPRENCE: 51400-A-PCT-US
CURRENT FILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
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Best Local Similarity 87.5%; Pred. No. 2.8e-06;
Matches 14; Conservative 2; Mismatches 0;
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STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                           ; Sequence 25, Application US/09214095D ; Patent No. 6280987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.1%;
93.8%;
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amino acid
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Best Local Similarity 93.8'
Matches 15; Conservative
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LENGTH: 16 amino acide
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                                                                    US-09-214-095D-25
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LENGTH: 16
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Pred. No. 1.3e-06;
1; Mismatches 0; Indels
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Sequence 22, Application US/09214095D
Fatent No. 6280987
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT APPLICATION NUMBER: US/09/214,095D
NUMBER OF SEQ ID NOS:
SOFTWARE:
SEQ ID NOS:
SEQ ID NO 22
LENGTH: 16
                                                                                                                                                                                                                                                                                                       ZIP: 10036
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. 28,678
REFERENCE/DOCKET NUMBER: 05/5/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ. 100:
TELECOMMUNICATION OF SEC.
                                                                                   APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
US-08-672-345C-25
; Sequence 25, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.1%;
93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
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ORGANISM: Murinae gen. 8p.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 15; Conserv
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STATE: New York
COUNTRY: USA
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Score 75; DB 4; Length 16;
Pred. No. 2.8e-06;
2; Mismatches 0; Indels
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GRENRAL INFORMATION:
APPLICANT: Landry, Donald; TITLE OF INVENTION:
FILE REFERENCE: 51400-A-PCT-US; CURRENT APPLICATION NUMBER: US/09/214,095D; CURRENT FILING DATE: 1999-01-19; NUMBER OF SEQ ID NOS: 121; SOFTWARE: Patentin version 3.0; SEQ ID NO 28; LENGTH: 16
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 0575/51400

TELEPHONE: 212-278-0400

TELEPHONE: 212-391-0525

INFORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 43, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
Pred. No. 2.8e-06;
2; Mismatches 0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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   87.58;
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Best Local Similarity 87.5
Matches 14; Conservative
      Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Murinae gen. sp. US-09-214-095D-28
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                             1 RSSRSLLYRDGKTYLN 16
                                                                                        1 RSSKSLLYKDGKTYLN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
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US-09-214-095D-28
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GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INFORMATION:
ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATOS: 121
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 92.6%;
Best Local Similarity 87.5%;
Matches 14; Conservative
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                                              RSSKSLLYKDGKTYLN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                         RESULT 6
US-08-672-345C-28
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Gaps 0;

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Gaps
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                                                                                                                                           ô
                                                                                                Score 69; DB 4; Length 16;
Pred. No. 2.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.2%; Score 69; DB 4; Length 16; 87.5%; Pred. No. 2.7e-05; Live 0; Mismatches 2; Indels
                                                                                                                                           1, Indels
                                                                                                                                                                                                                                                                                                                      Sequence 79, Application US/09214095D;
Patent No. 6280987;
GENERAL INFORMATION:
APPLICANT: Landry, Donald;
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/214,095D;
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SEQ ID NO 79
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-438-123-1

Sequence 1, Application US/08438123

Patent No. 5552930

GENERAL INFORMATION:

APPLICANT: Lindholm et al

TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lowe, Price, Leblanc & Becker

SEQUENCES:

ADDRESSEE: Lowe, Price, Leblanc & Becker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSER: Lowe, Price, Leblanc & Becker STREET: Suite 300, 99 Canal Center Plaza CITY: Alexandria STATE: Virginia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/906,350
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
WEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                Query Match 85.2%;
Best Local Similarity 81.2%;
Matches 13; Conservative
                 ; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                      1 RSSKSLLYKDGKTYLN 16
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ORGANISM: Murinae gen.
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US-09-214-095D-79
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Pred. No. 2.7e-05;
0; Mismatches 2; Indels
                                      Score 69; DB 2; Length 16;
Pred. No. 2.7e-05;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                         Sequence 79, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
    APPLICANT: Landry Donald, W.
    APPLICANT: Copper and Dunham LLP
    ADDRESSE: Cooper and Dunham LLP
    STREET: 1185 Avenue of the Americas
    CITY: New York
    STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
FILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPRENCE: S1400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF, SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036
COMPUTER: ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENDABLE FORM:
COMPUTER: ENDABLE FORM:
COMPUTER: ENDABLE FORM:
COMPUTER: DEAFTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION NUMBER: 26,678
ATORNEY/AGENT INVERFATION:
NAME: White, John P.
REDISTRATION NUMBER: 26,678
REDISTRATION NUMBER: 26,678
TELEPHONE: 212-279-0400
TELEPHONE: 212-291-0525
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
TENGTH FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                   Query Match
Best Local Similarity 81.2%;
Matches 13; Conservative
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                                                                                                                                                  1 KSSQSLLYSDGKTYLN 16
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STRANDEDNESS: single
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 14; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New YC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-09-214-095D-43
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US-08-672-345C-43
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Search completed: April 22, 2003, 13:14:20 Job time : 15 secs
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56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 16 amino acids
amino acid
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Best Local Similarity 56.2.
The 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
       Washington
                           D. C.
                                                            20004
                         STATE: D. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-244-626-4
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US-08-244-626-4
; Sequence 4, Application US/08244626
; Sequence 4, Application US/08244626
; Patent No. 5502167
; GENERAL INFORMATION:
; APPLICANT: Walsh, Louise
; APPLICANT: Walsh, Louise
; APPLICANT: Lewis, Alam Peter:
; TITLE OF INVENTION: CDR GRAFTED HUMANISED CHIMERIC T-CELL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 4; Length 16;
Pred. No. 0.018;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                    Score 55; DB 1; Length 16;
Pred. No. 0.0056;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B: Rothwell, Figg, Ernst & Kurz, p.c.
555 Thirteenth Street, N. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/09406532A Frence 18, Application US/09406532A Frence 18, Application US/09406532A Frence 18, APPLICANT: Connie L. Erickson-Miller APPLICANT: Connie L. Erickson-Miller APPLICANT: James D. Winkler TILE OF INVENTION: TIEZ Agonist Antibodies FILE REFERENCE: P50843 CURRENT APPLICATION NUMBER: US/09/406,532A CURRENT APPLICATION NUMBER: 06/102,098 FRIOR FILING DATE: 1998-09-28 NUMBER OF SEQ ID NOS: 21 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 18
NAME: J.G. Mullins
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 149-011
TELECOMMUNICATION INFORMATION:
INFORMATION: 703 684 1111
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: SITE
; LOCATION: (1)...(16)
; OTHER INFORMATION: light chain CDR 1
US-09-406-532-18
                                                                                                                     LENGTH: 16

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Polypeptide
US-08-438-123-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.2%;
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 73.3%;
Matches 11; Conservative
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Best Local Similarity 66.7
Matches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-406-532-18
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CALP: 20004
CADDUTER: ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/24,626
FILING DATE: July 15, 1994
CLASSIFICATION NUMBER: PCT/GB92/02251
FILING DATE: December 4, 1992
CLASSIFICATION NUMBER: PCT/GB92/02251
FILING DATE: December 4, 1992
CLASSIFICATION STATE
ATORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION NUMBER: 30, 377
REFERENCE/DOCKET NUMBER: 1808-153A
TELECOMMULCATION: 1808-153A
TELECOMMULCATION: 1808-153A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
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GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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OM protein - protein search, using sw model

Run on:

April 22, 2003, 13:20:30 ; Search time 43 Seconds (without alignments) 15.650 Million cell updates/sec

US-09-674-716B-5 31 1 LMSTRAS 7 Title: Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

456

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pirl:* 3: pir2:* 4: pir4:* PIR 73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	dene p20K protein	pyruvate kinase (E			T-cell receptor be	20K pro	34.5K structural p		serrawettin W2 - S	aggrecan - bovine	hypoxanthine phosp	Ig heavy chain CRD	T-cell receptor be	-cell	T-cell receptor be	surface protein te	hypothetical prote	н	σ	Fc epsilon RIIb -	acetylcholinestera	hypothetical prote		ų	ಕ	primage - Citrobac	pap fimbrial regul	thetical	u
Ð	150412	σ	I40469	I51434	PT0518	B31836	H44817	F44817	A58728	842620	A37114	PT0295	PT0577	PT0565	PT0700	869237	A37765	S14159	B26206	A46474	A34026	B33541	155382	178890	870154	140702	B37325	T14910	PT0686
DB	m	~	7	7	7	N	~	N	4	~	~	N	7	N	~	~	~	7	N	0	~	~	4	ო	N	~	N	N	0
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Query	45.2	41.9	38.7	38.7	38.7	35.5	35.5				32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	•	32.3	32.3	29.0	29.0	29.0	29.0	29.0	29.0
Score	14	13	12	12	12	11	11	11	11	11	10	10	10	. 10	10	10	10	10	10	10		10	10	σ	თ	σ	σ	σ	σ
No.	1	7	m	4	ഗ	9	7	œ	თ	10	1	12	13	14				18	13	20	21	22	23	24	25	56	27		29

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Gaps

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11arity 100.0%; Pred. No. 2.8e+05; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 3; Conserva

3 RAS 5

5 RAS 7

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T-cell receptor be dnaA protein - Pse	hypothetical 6 pro D-SP2.5 region - m T-cell recentor be	T-cell receptor ga laminin Bl - weste	orf 3 rara 5'-regi microcin C7 - Esch pilE protein - Esc	mabinlin II chain seed protein ws-5 myomodulin - Calif	neuromodulatory pe neuromodulatory pe neuromodulatory pe
0.0	6 2 PC4127 6 2 I49808 6 2 PT0643	100	6 4 S15596 7 2 S45311 7 2 S25266	7 2 S38516 7 2 E61491 7 2 A28340	7 2 833244 7 2 833245 7 2 833246
9 29.0 9 29.0	9 29.0	2000	9 29.0 29.0	9 29.0 9 29.0 9 29.0	9 29.0 29.0 29.0
30 31	332 34	300	8 338 39	4 4 4 4 4 4 2 4 2 4 2 4 2 4 2 4 2 4 2 4	4 4 4 5 4 5

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pyruvate kinase (EC 2.7.1.40) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Os-Unr-1987 #sequence_revision 05-Jun-1987 #text_change 03-Mar-1995
C;Accession: Al1490
R;Hjelmquist, G.; Andersson, J.; Edlund, B.; Engstrom, L.
Biochem. Biophys. Res. Commun. 61, 559-563, 1974
A;Title: Amino acid sequence of a (32-P)phosphopeptide from pig liver pyruvate kinase ph. A;Reference number: Al1490; MUID:75127438; PMID:4375989
A;Accession: Al1490
A;Molecula type: protein
A;Residues: 1-6 c4DE>
A;Residues: 1-6 c4DE>
A;Residues: 1-6 c4DE>
A;Residues: Jocotysis; phosphotransferase
Growth protein - chicken (fragment)

Growth gallus (chicken)

Growth gallus (gallus (chicken)

Growth gallus (gallus gallus)

Growth gallus (gallus)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Residues; 1-3 <MAO>
A;Cross-references: GB:L02537; NID:g212616; PID:g212617 C;Genetics: A;Gene: p20K
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1 MST 3
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20K protein - Rickettsia rickettsii (fragment)
C.Species: Rickettsia rickettsii
C.Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
C.Accession: B31836
R.Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
Bacteriol. 10, 4493-4500, 1988
A;Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia ricke
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34.55K structural protein - Leuconostoc oenos phage P32 (fragment)
G.Species: Leuconostoc oenos phage P32
C.Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C.Accession: H44817
J. Gen. Microbiol. 137, 2135-2139, 1991
A.Fitle: Lysogeny in Leuconostoc oenos.
A.Reference number: A44817; MUID:92085033; PMID:1748868
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C;Species: Leuconostoc oenos phage P54
C;Species: Leuconostoc oenos phage P54
C;Accession: F44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
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Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0;
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A, Molecule type: DNA
A, Residues: 1-5 <AND>
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J. Exp. Med. 174, 115-124, 1991 A;Feener and the sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT6509; MUID:91277601; PMID:1711558
                                  dhazz-like protein - Bacillus subtilis (fragment)

(jSpecies: Bacillus subtilis

(jSpecies: Bacillus subtilis

(jSpecies: Bacillus subtilis

(jAccession: 14046)

Ristruck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.

Mol. Gen. Genet. 215, 478-482, 1999

A.Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.

A.Reference number: 140469; MUID:89218958; PMID:2468993

A.Reference number: translated from GB/EMBL/DDBJ

A.Residue: preliminary; translated from GB/EMBL/DDBJ

A.Residues: 1-5 cRES.

A.Gonetics: EMBL:X14796; NID:940130; PIDN:CAA32902.1; PID:94376204
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C;Species: Xenopus laavis (African clawed frog)

C;Species: 25-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C;Date: 15-1434

Nucleic Acids Res. 15-1494

A;Title: Are there major developmentally regulated H4 gene classes in Xenopus?.

A;Accession: 151434
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Pred. No. 2.8e+05;
1; Mismatches 1; Indels
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A;Molecule type: mRNA
A;Residues: 1-6 <WOO>
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A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor
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60.0%; Pred. No. ...
1; Mismatches
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Best Local Similarity
Matches 3; Conserv
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C;Keywords: glycosyltransferase; pentosyltransferase
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A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
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A, Status: translation not shown
A, Molecule type: mRNA
A, Residues: 1-5 < FE2>
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                                                                                                                                                                         Species: Serratia marcescens
C;Species: Serratia marcescens
C;Species: Serratia marcescens
C;Date: 10-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 12-Feb-1998
C;Accession: A58728
R;Matsuyama, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.
J. Bacteriol. 174, 1769-1776, 1992
A;Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent and A;Reference number: A58728; MUID: 92193260; PMID: 1548227
A;Accession: A58728
A;Status: unencoded polypeptide
A;Rocession: A58728
A;Status: unencoded polypeptide
A;Residues: 1-5 < ANT>
A;Experimental source: strain NS 25
C;Comment: A surfactant lipopeptide promoting flagellum-independent surface translocatic C;Comment: A surfactant lipopeptide promoting flagellum-independent surface translocatic C;Comment: A surfactant lipopeptide strain NS 25
C;Comment: A surfactant lipopeptide carboxyl end; D-amino acid; lipoprotein; unencode F;1/Modified site: D-leucine (Leu) #status experimental
F;4/Modified site: D-phenylalanine (Phe) #status experimental
F;4/Modified site: D-phenylalanine (Phe) #status experimental
F;1-5/Cross-link: 3-hydroxydecanoyl amino pad, ester carboxyl end (Leu-Ile) #status experimental
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Cypecies: Schistosoma mansoni
Cypecies: Schistosoma mansoni
Cypecies: Seletosoma mansoni
Rytuan, L.; Craig, S.P.; McKerrow, J.H.; Wang, C.C.
A; Title: The hypoxanthine-granine phosphoribosyltransferase of Schistosoma mansoni. Furt
A; Reference number: A37114; MUID:90337955; PMID:2199439
A; Status: preliminary
A; Status: preliminary
A; Residues: 1-5 < YUA>
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C;Species: Bos primigenius taurus (cattle)
C;Accession: S42620
R;Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.
Matrix Biol. 14, 171-179, 1994
A;Title: Aggrecan in bovine tendon.
A;Reference number: S42620; MUID:94340214; PMID:7520336
A;Accession: S42620
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35.5%; Score 11; DB 4; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels
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A;Residues: 1-7 <VOG>
A;Rxperimental source: flexor tendon
C;Reywords: cartilage
                                                                                                                                                                - Serratia marcescens
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Best Local Similarity 40.0°
Matches 2; Conservative
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R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PP0295
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
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J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0295
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C;Species: Mns musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0577; PT0574
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Cispecies: Mus musculus (house mouse)
Cjbate: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
CjAccession: PT0565
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.larity 66.7%; Pred. No. 2.8e+05;
Conservative 1; Mismatches 0
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R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Rectus: translation not shown
A;Retus: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 cFES
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PT0700
C;Accession: PT0700
R;Reeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Theference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0700
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0700
A;Retus: translation not shown
A;Mesidues: 1-5 < PEE>
A;Especimental source: newborn thymus, strain BALB/C
C;Reywords: T-cell receptor
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MEDLINE=89006280; PubMed=2971595;
NCBI_TaxID=546;
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TISSUE=Liver;
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P42561 hirudo medi
P58707 anthopleura
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P58706 anthopleura
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P82072 litoria rub
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                                                                                                                                                         April 22, 2003, 13:14:25 ; Search time 11 Seconds (without alignments) 26:394 Million cell updates/sec
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                         GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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-!- FUNCTION: MEDIATES TETRAHYDROBIOPTERIN INHIBITION OF GTP
CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
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01-JAN-1990 (Rel. 13, Last sequence update)
01-DAN-1990 (Rel. 40, Last annotation update)
Adenosylmethionine-8-amino-7-oxonomanoate aminotransferase
(EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
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15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
17-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation update)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
NCBI_TaxID=10090;
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Bacteria; Froteobacteria; gamma subdivision; Enterobacteriaceae;
Citrobacter.
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P25154
P13736
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-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
SWISS-12DPAGE; P99025; MOUSE.
INIT MET
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                                    UF01_MOUSE
ACPH_RABIT
CIP1_MYTED
CIP2_MYTED
BI01_LITRU
FARP_MONEX
LOK1_LOCMI
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Conservative
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les 2; Conserv
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P23210;
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                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae, PACC clade,
Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
"The malze two dimensional gel protein database: towards an integrated
                                                                                                                                                              Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli,
Citrobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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-1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.0, ITS MW IS: 30.0 kDa.
Maize-2DPAGE; P80630; COLEOPTILE.
MaizeDB; 123956; -.
                                                                                                                                         oxononanoate = 8-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 447)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.5%; Score 11; DB 1; Length 5; 66.7%; Pred. No. 1.1e+05; tive 1; Mismatches 0; Indels
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InderPro; IPR000954; Aminotran 3.
PROSITE: PS00600; AA TRANSFER CLASS 3; FARTIAL.
Blotin blosynthesis; Transferaes; Aminotransferaes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 5 AA; 582 MW; 6AAABIBIA6F00000 CRC64;
                                                                                                           -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 AA.
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Theor. Appl. Genet 92.007
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                                                                                                                                                                                                                                                                                                        AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyridoxal phosphate.
NON TER 5
SEQUENCE 5 AA; 582
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Best Local Similarity
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1 MTT 3
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P80630;
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10 24 MAIZE
10 25 MAIZE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Wistar; TISSUE-Heart;
Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Sallkov J.,
Jungblut P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus,
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P56376; (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jungblut P.R.;
Submitted (SEP-1998) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 8.5, ITS MW IS: 42 kDa.
THOSTER
2 OR A.
                              01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
Capsid assembly and DNA maturation protein (Virion protein UL38)
(Capsid protein VP19C) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                 Herpes simplex virus (type 1 / strain KOS)
Viruses, dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 AA; 703 MW; 67376451A336F000 CRC64;
6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses, dsDNA viruses, no RNA st
Alphaherpesvirinae, Simplexvirus
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UH11 RAT
AC P56576;
DT 15-DEC-195
DT 11-DEC-195
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WWA1 ACHFU

Matches

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SEQUENCE.
MEDILINE=87005252; PubMed=3093276;
Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
White B.A., An F.Y., Clewell D.B., Suzuki A.;
"Isolation and structure of the Streptococcus faecalis sex pheromone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1-07-1989 (Rel. 12, Created)
01-07-1989 (Rel. 12, Last sequence update)
01-07-1989 (Rel. 12, Last sequence update)
01-FB-1991 (Rel. 17, Last annotation update)
Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora; Achatinacea; Achatinidae; Achatina
                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Ganglion;
MEDILINE-932565912; PubMed=8495720;
MEDILINE-93265912; PubMed=8495720;
Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
"Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snall, Achatina fulica.";
PEBS Lett. 323:104-108(1993).
PIR; S33244; S33244.
Neuropeptide; Amidation.
SEQÜENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIRES Lett. 206:69-72 (1986).
-!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
HARBORING PAM373.
-!- MISCELLANBOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
SPECIFICITY OF PHEROMONES TO PLASMIDS.
-!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
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                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.0%; Score 9; DB 1; Length 7; ilarity 100.0%; Pred. No. 1.1e+05; Conservative 0; Mismatches 0; Indels
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llarity 100.0%; Pred. No. 1.1e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
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                                                                                                                                                                                 7 AA.
                                                                                                                                                                                                                                                                                           Achatina fulica (Giant African snail).
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hes 2; Conserv
Best Local Similarity
Matches 2, Conserv
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P35921;
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SEQUENCE
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P11932;
                                                  2 MS 3
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| MS 5
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FEBS Let
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Achatinacea; Achatinidae; Achatina.
NCBI_TaxID=6530;
                                                                                                                                                                                                                                                                                                                                                                    Achatina fulica (Giant African snail).
Bukaryota, Metazoa, Mollusca, Gastropoda, Pulmonata, Stylommatophora,
Achatinacea, Achatinidae, Achatina.
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                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.; "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica."; FEBS Lett. 323:104-108 [1993].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minakata H., Ikeda T., Munecka Y., Kobayashi M., Nomoto K.;
"Wwamide-1, -2 and -3: novel neuromodilatory peptides isolated from ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108 [1933].
-1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
PIR; $33245; $33245.

MOD_RES MIDATION.
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                                                     29.0%; Score 9; DB 1; Length 7; 66.7%; Pred. No. 1.1e+05; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 7 AMIDATION.
7 AA; 993 MW; 7362D5B69B041310 CRC64;
   7 7 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
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Achatina fulica (Giant African snail)
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TISSUE-Ganglion;
MEDLINE-93265912; PubMed=8495720;
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MEDLINE=93265912; PubMed=8495720;
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                                                                                              Conservative
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Best Local Similarity
Matches 2; Conservat
                                                                       Local Similarity
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WWA2 ACHFU

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Best Local Similarity
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Matches 1; Conserv
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DCMS_PSECH
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-I. MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE CELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE MEMBRANE RELEASES THE ACTIVE PEPTIDE TUTTSIN FROM THE GAMMA CTAIN. TUTTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avigad G., Markus Z.;
"Identification of a peptide inhibitor of galactose oxidase from Dactylium dendroides.";
Fed. Proc. 31:447-447(1972).
-!- FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE STALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY BINDING TO ITS PROSTHETIC COPPER GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.; "The characteristics, isolation and synthesis of the phagocytosis stimulating peptide tuftsin."; Biochem. Biophys. Res. Commun. 47:172-179(1972).
                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-JAN-1988 (Rel. 06, Last sequence update)
01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Galactose oxidase inhibitor.
Dactylium dendroides (Cladobotryum dendroides).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Hypocreaceae; Hypomyces.
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                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phagocytosis-stimulating peptide (Tuftsin)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
MEDLINE=72187087; PubMed=4112769;
                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
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MIM; 191150; -.
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P06294;
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Matches
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-!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
-!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92028852; PubMed=1681803;
Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
"Isolation of L.-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a
novel neuropeptide from sea anemones.";
Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas carboxydohydrogena.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anthopleura elegantissima (Sea anemone).
Bukaryota, Metazoa, Chidaria, Anthozoa, Zoantharia, Actiniaria,
Nynantheae, Actiniidae, Anthopleura.
NCBI_TaxID=6110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dioxide.
-!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
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01-FEB-1991 (Rel. 17, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase small chain (EC 1.2.99.2)
dehydrogenase subunit S) (CO-DH S) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.4%; Score 6; DB 1; Length 4; 50.0%; Pred. No. 1.1e+05; tive 1; Mismatches 0; Indele
                                                                  DB 1; Length 7;
1.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AA; 420 MW; 6DD33DD6F000000 CRC64;
Copper; Metalloenzyme inhibitor.
SEQUENCE 7 AA; 706 MW; 75BB01A456D97DB0 CRC64;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                  22.6%; Score 7; DB 1
llarity 25.0%; Pred. No. 1.1e
Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                         PRT;
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Oxidoreductase; Iron-sulfur.
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MEDLINE=89006280; PubMed=2971595;
Shiuan D., Campbell A.;
"Iranscriptional regulation and gene arrangement of Escherichia coli,
"Iranscriptional regulation and gene arrangement of Escherichia coli,
Girobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
                                McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P., "The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-Khamide and Antho-Khamide.", Peroc. R. Soc. Lond., B. Biol. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron-specific.
                                                                                                                                                                                                                                 Gaps
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Citrobacter.
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01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Biotin synthase (BC 2.8.1.6) (Biotin synthetase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.4%; Score 6; DB 1; Length 5;
llarity 50.0%; Pred. No. 1.1e+05;
Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                      19.4%; Score 6; DB 1; Length 4; 50.0%; Pred. No. 1.1e+05;
                                                                                                                                                                   4 4 4 AMIDATION.
4 AA; 512 MW; 6DD339C9A0000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AA; 532 MW; 75A5B1EDD6F00000 CRC64;
                                                                                                                                                        L-3-PHENYLLACTYL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M21922; -; NOT ANNOTATED CDS.
Biotin biosynthesis; Iron-sulfur; Transferase.
                                                                                                                                                                                                                                                                                                                                        5 AA.
                                                                                                                                                                                                                              1; Mismatches
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                       MEDLINE=93391436; PubMed=8397415;
                                                                                                                                                                                                                              1; Conservative
                                                                                                                                             Neuropeptide; Amidation.
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                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 1; Conserva
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Best Local Similarity
Matches 1; Conserv
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SEQUENCE
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Bukaryota, Medazoa, Arthropoda, Mandibulata; Pancrustacea, Hexapoda, Ilnsecta, Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria, Blattoidea, Blattidae, Periplaneta.

NCBI_TaxID=6978, 6850, 6759;
                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=P.americana;
MEDLINE=76074708; PubMed=576;
Starratt A.N., Brown B.E.;
"Structure of the pentapeptide proctolin, a proposed neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stangler J., Diroksen H., Keller R.,
"Identification and immunocytochemical localization of proctolin in
pericardial organs of the shore crab, Carcinus meenas.";
Peptides 7:67-72(1986).
-!- FUNCTION: STIMULATES CARDIAC OUTFUT AND HINDGUT MOTILITY,
MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
-!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
THE CRAB PERICARDIAL ORGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=P.americana;
MBDLINE=81225865; PubMed=6113690;
O'Shea M., Adams M.E.;
"Pentapoptide (proctolin) associated with an identified neuron.";
Science 213:567-569(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).
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MEDLINE=90287800; PubMed=2356151;
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
Shabanowitz J.;
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                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
     5 AA.
                                                                                                                                                                         Periplaneta americana (American cockroach)
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Job time : 12 secs
  PRT;
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MEDLINE=86232789; PubMed=2872661;
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  STANDARD;
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PIR; A60411; A60411.
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SEQUENCE 5
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Matches
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Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 22, 2003, 13:20:00 ; Search time 81 Seconds (without alignments) 17.807 Million cell updates/sec Run on:

US-09-674-716B-5 31

1 LMSTRAS 7 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched: Total number of hits satisfying chosen parameters:

28

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL 21:*

sp_archea:*
sp_bacteria:*
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sp_iungi:*
sp_invertebrate:*
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sp_mhc:*
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sp_rodent:*
sp_vortebrate:*
sp_vortebrate:* 9: 111: 112: 114: 116:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

2			Description	P82541 spinacia ol	Q65578 bovine herp	Q47505 escherichia	P70804 azotobacter	Q95945 saccharomyc	P93233 lycopersico	Q99007 hordeum vul	P82181 spinacia ol	P82182 spinacia ol	Q47029 enterobacte	O34028 sphingomona	P83073 bacillus ce	Q15897 homo sapien	Q15903 homo sapien	O99182 gnatholebia	O63668 rattus norv
2011			a a	P82541	Q65578	047505	P70804	095945	P93233	099007	P82181	P82182	047029	034028	P83073	Q15897	Q15903	099182	063668
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## ALIGNMENTS

RESULT 1

								eophyta;	.03							proteins in			RNA.					S19 BETA			COTEINS.						
	Α.		update)	n update)	(Fragment).			Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	ceae; Spinacia.					n A.R.;	"The plastid ribosomal proteins. Identification of all the proteins	the small subunit of an organelle ribosome (chloroplast).";		FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.		LANT TISSUES.	ELECTROSPRAY.		IS DIFFER IN PI.		: 12 KDA.	SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.					. iig.	63333735A411C000 CRC64;
	e AA.	_	quence	notation	19 beta			yta; Em	otyledo	nopodia		OMETRY.			ramania	entific	ibosome		RECTLY	ST.	N ALL P	METHOD=	THOD=MA	TA FORM		SIMMIS	FAMILY		AL.	IAL.	KTIAL.	A-Dingi	A411C00
Ë	PKI;	Created)	Last se	Last an	otein S			reptoph	1; eudic	les; che		S SPECTR	SAF;	374039;	K., Sub	eins. Id	anelle r	55 (2000)	SINDS DI	HLOROPLA	RESSED I	0477.0;	0495; ME	A AND BE	FORM.	O-GEL IT	THE S19F	nal_S19.	S19; PARTIAL.	19; PART	S19; PARTIAL.	ast; rkn	63333735
	PRELIMINARY;	(TrEMBLrel. 15,		(TrEMBLrel. 17,	30S ribosomal protein S19 beta (Fragment).	Spinacia oleracea (Spinach).		iridiplantae; St	a, Magnoliophyta	Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia. MCBI Tarin-1662.	1	SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.	STRAIN=CV. ALWARO; TISSUE=LEAF;	MEDLINE=20435797; PubMed=10874039;	Yamaguchi K., von Knoblauch K., Subramanian A.R.;	ribosomal prote	bunit of an orga	J. Biol. Chem. 37:28455-28465(2000).	: THIS PROTEIN E	SUBCELLULAR LOCATION: CHLOROPLAST.	TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.	MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY	MASS SPECTROMETRY: MW=10495; METHOD=MALDI	MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN	FORM IS THE MINOR BASIC FORM.	MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.	TY: BELONGS TO	InterPro, IPR002222; Ribosomal	Pfam; PF00203; Ribosomal S1	PRINTS; PR00975; RIBOSOMALS19; PARTIAL.	PROSITE; PS00323; RIBOSOMAL	Ribosomai protein; chioropiast; rkwa-binding. Now TRP	, 732 MW;
	P82541	2000		01-JUN-2001	Chloroplast 3	Spinacia ole	Chloroplast.	Eukaryota; V:	Spermatophyta	Caryophyllidae;	[1]	SEQUENCE, FUI	STRAIN=CV. A	MEDLINE=2043	Yamaguchi K.	"The plastid	the small su	J. Biol. Che	- 1 - FUNCTION	- 1 - SUBCELLU	-i- TISSUE S	-!- MASS SPE	-!- MASS SPE	-!- MISCELLA	FORM IS	-!- MISCELLA	-!- SIMILARI	InterPro; IP	Pfam; PF0020	PRINTS; PR00	PROSITE; PSO	Kibosomai pr	ω
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Rehm B.H.A., Ercesvag H., Valla S.,
"A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is
part of an alg gene clueter physically organized in a manner similar
to that in Pseudomonas aeruginosa.",
J. Bacteriol. 178:5884-5889(1996).
NON TER 1
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MEDLINE=81069885; PubMed=6254986;
Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
"Assembly of the mitochondrial membrane system: Structure and nucleotide sequence of the gene coding for subunit 1 of yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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01-FEB-1997 (TYEMBLrel. 02, Created)
01-FEB-1997 (TYEMBLrel. 02, Last sequence update)
01-07B-2002 (TYEMBLrel. 21, Last annotation update)
Inside intron 5 (Fragment).
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Last annotation update)
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Mitochondrion.
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J. Biol. Chem. 255:11927-11941(1980)
EMBL; V00694; CAA24066.1; -.
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MEDLINE=96427318; PubMed=8830682;
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01-FEB-1997 (TrEMBLrel. 02, C;
01-FEB-1997 (TrEMBLrel. 02, Ls
01-DEC-2001 (TrEMBLrel. 19, Ls
AlgT protein (Fragment).
ALGT.
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Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
Escherichia.
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Score 11, DB 10; Length 6;
Pred. No. 6.7e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 0.8 kDa protein (Fragment).
Niveses deDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
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                                                                                                                                                                                                                                                                                                                                          7 7 AA.
      35.5%;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
MccA protein.
      Query Match 35.5
Best Local Similarity 66.7
Matches 2, Conservative
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                                                                                                                                                                                       1 TRS 3
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5 AA; 600 MW; 61E3344DD6F00000 CRC64;

SEQUENCE

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X54643; CAA38455.1; -.
Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
Calcium; Multigene family.
NON_TER 5 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=HIMALAYA; TISSUE=ALBURONE LAYER;
MEDLINE=91329704, PubMed=1831055;
Jacobsen J.V., Close T.J.;
"Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley
                                                                                                                                                       Lycopersicon esculentum (Tomato). Babryophyta; Tracheophyta; Streptophyta; Streptophyta; Babryophyta; Core eudicots; Spermatophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                      Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.; "Differential induction of seven 1-aminocyclopropane-1-carboxylate synthase genes by elicitor in suspension cultures of tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aleurone layers.";
-i- Catalytic Activity: EndoHydrolysis OF 1,4-Alpha-Giucosidic Linkages in Oligosaccharides And Polyasaccharides.
-i- Copacyor: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
-i- COPACYOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
-i- MISCELLANBOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.0%; Score 9; DB 10; Length 7; 50.0%; Pred. No. 6.7e+05; ative 1; Mismatches 1; Indels
                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                            7 AA.
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                                                                                                                                                                                                                                                                                                                                    (iycopersicon esculentum).";
Plant Mol. Biol. 34:275-286(1997).
EMBL; U75692; AAC49682.1; -.
                                                                                                                                                                                                                                                                         MEDLINE=97351561; PubMed=9207843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
Alpha-amylase (EC 3.2.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                            PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                      NCBI_TaxID=4081;
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4 LVRT 7
                                                                                                                          (Fragment).
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RESULT 6
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MEDLINE=2043=798; Pubmed=10874046;
Yamaguchi K., Subramanian A.R.;
"The plastid ribosomal proteins. Identification of all the proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 20, Last annotation update)
Chloroplast 50s ribosomal protein L10 gamma (Fragment).
Spinacia oleracea (Spinach).
Spinacia oleracea (Spinach).
Spermatophyta, Viridiplantea, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, eudicotyledons, core eudicots;
Carryophyllidae, Carryophyllales, Chenopodiaceae; Spinacia.
                                                                                                                                                                                          Spinacia oleracea (Spinach).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Caryophyllidae, Caryophyllales; Chenopodiaceae; Spinacia.

NCBI_TaxID=3562;
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                      1; Indels
 Length 5;
                                                                                                                                                 01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2002 (TrEMBLrel. 20, Last sentention update)
Chloroplast 50S ribosomal protein L10 beta (Fragment).
25.8%; Score 8; DB 10; I
25.0%; Pred. No. 6.7e+05;
tive 2; Mismatches 1;
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                                                                                                                             6 AA.
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                         Conservative
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             Local Similarity
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01-JUN-2000
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1 MANK 4
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5 TK 6
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  Query Match
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P82182
ID P8218
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Matches
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5 VNT 7
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P83073
AC P83073;
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DT 01-0CT-2
DE 88 KDA FO FO
C BACIllus
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Q15897
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MEDLINE-94079349; PubMed=8257126;
Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;
"Analysis of the and (3)-VIa gene encoding a novel 3-N-
acetyltransferase.";
Antimicrob. Agents Chemother. 37:2074-2079(1993).
EMBL; M88012; AAA16193.1; -.
NON_TER. 1
the 50 S subunit of an organelle ribosome (chloroplast).";
J. Biol. Chem. 275:28466-28483(2000).

- I. FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
- I. SUBCELLULAR LOCATION: CHLOROPLAST.
- I TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
- I. MISCELLANEOUS: ON THE 2D-CEL ITS MM IS: 16.5 KDA.
- I. MISCELLANEOUS: ON THE 1.10P FAMILY OF RIBOSOMAL PROTEINS.
R INTERPRO; IPRO01790; Ribosomal L10P.
R Pfam; PF00466; Ribosomal L10P; PARTIAL.
R PROSITE; PS01109; RIBOSOWAL L10; PARTIAL.
R RIBOSOMAL L10; PARTIAL.
R RIBOSOMAL L10; PARTIAL.
R RIBOSOMAL SOUTH CHICOPLAST; RNA-binding.
C 6 AA; 675 MW; 6321B415B05DB000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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047029 047029 PRELIMINARY; PRT; 7 AA.
04702916 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 03, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Ad Al protein (Fragment).
AD Al.
Britchbacter cloacae.
Britchbacter cloacae.
Britchbacter.
Britchbacter.
Britchbacter.
Britchbacter.
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Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae; Sphingomonas.
NCBI_TAXID=56193;
SEQUENCE FROM N.A.
STRAIN=DJ77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.6%; Score 7; DB 2; Length 7; llarity 50.0%; Pred. No. 6.7e+05; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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034028
AC 034028;
DT 01-43N-1)
DT 01-45N-1)
DT 01-DEC-2
DE CATECHOO
OC Sphingon

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047029
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RESULE
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TISSUB-FIACENTA,

Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,

Leo C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,

Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay B.A., Zhao Z.-Y.,

Caskey C.T.H.,

"Isolation of chromosome-specific genes by reciprocal probing of

arrayed cDNAs and cosmid libraries.";

Hum. Mol. Genet. 0:0-0(1995).

EMBI. 132077; AAA73887.1; -.

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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(clone XP6A11A) (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
88 kDa protein (Fragment).
8acillus cereus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
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                                                                                                                                                                                                                                                0; Indels
Kim Y.-C.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U88298; AAB66311.1; -.
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                                                                                                                                                                                       Query Match 22.6%; Score 7; DB 2; Length 7; Best Local Similarity 33.3%; Pred. No. 6.7e+05; Matches 1; Conservative 2; Mismatches 0; Indel
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                                                                                   Dioxygenase.

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SEQUENCE 7 AA; 868 MW; 71A452D1A699D460 CRC64;
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Browne N., Dowds B.C.A.;
Submitted (JUL-2001) to the SWISS-PROT data bank,
NON TER 5
SRQUENCE 5 AA; 623 Mw.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 AA
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Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
Caskey C.T.H.,
"Isolation of chromosome-specific genes by reciprocal probing of
arrayed cDNAs and cosmid libraries.";
Hum. Mol. Genet. 0:0-0(1995).

EMBL: L32082; AAA73893.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=20072928; PubMed=10603257;
Murphy W.J., Thomerson J.E., Collier G.E.;
"Phylogeny of the Neotropical killifish family Rivulidae
(Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mitochondrion.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cytochrome oxidase I (Fragment).
                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(clone XP7R7B) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 AA; 849 MW; 6B040339CDD33DB0 CRC64;
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7 AA; 899 MW; 672721F6CB572030 CRC64;
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Pred. No. 6.7e+
1; Mismatches
1; Mismatches
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EMBL; AF002591; AAD01074.1; -.
                                                                                                                                    PRT;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps

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Search completed: April 22, 2003, 13:23:41
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Peptide fused to i MAb 55.1 light cha Hepatitis C virus

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Anti-platelet glyc Anti-progesterone MAD NFS2 light cha MAD NFS2 light cha MAD NFS2 light cha Humanised anti-HIV G-protein coupled Anti-IL-5 MAD ligh MAD MCPC603 VI CDR MAD MCPC603 VI

Human CD4 protein G-CSF agonist anti Anti-SAF-1 antibod CDR2 VL peptide. Human Kappa IV lig Mouse Kappa IV ligh Chromogenic substr Peptide used to de Human matriptase s Enzyme inhibitor p Enzyme inhibitor p

Enzyme inhibitor p Prostate tumour as

Human elastase var Synthetic peptide CDR2 of the light

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Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Light chain CDR2 of catalytic antibody 6A12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                 AAY08713
AAB079523
AAY95234
AAY3227
AAY3227
AAU81257
AAU70347
AAB35205
AAR46961
AAR76083
                                                AAYOSO16
AAY95223
AAX95226
AAX30157
AAX57964
AAX57964
AAX57317
AAX54108
AAX94108
AAX9485
AAX9485485
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                                       AAW31179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW39819 standard; peptide; 7 AA
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  16-JUN-1998 (first entry)
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 25-JUN-1997;
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  AAW39819;
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| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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                GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                       of hits satisfying chosen parameters:
                                                                                                                                                                                                                              908470 seqs, 133250620 residues
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AAW39876
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Listing first 45 summaries
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                                                                   protein search, using
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identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
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100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                               100.0%; Score 31; DB 19;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Light chain CDR2 of catalytic antibody 12H1.
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                                                                                                                                                                                                                                  Local Similarity
nes 7; Conserv
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Matches
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                                                                                                                 AAW39818-20 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 6A12, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of release 3H-benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoseter transition state analogue. Antibody 6A12 has a per minute Kcat of 0.072. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
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in far smaller doses than antibodies that antagonise cocaine by simply binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7;
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100.0%; Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                             Claim 13; Page 81; 147pp; English.
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1es 7; Conservative
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This sequence represents complementarity determinating region 2
(CDR L2) of the light chain of murine anti-CD23 (FCERII) monoclonal
antibody Cl1 (see also ANY32262). The invention provides altered
antibodies, such as chimeric or humanised antibodies, which comprise
Sufficient of the amino acid sequences of Cl1 light and heavy chain
CDRs (see ANY32254-59) to render them capable of binding to the CD23
CDRs (see ANY32254-59) to render them capable of binding to the CD23
CDRs (see ANY32254-59) to render them capable of binding to the CD23
CDRs (see ANY32254-59) to render them capable of binding to the CD23
CDRs (see CDRS soluble CD23 formation for treatment of arthritis,
lupus erythematorsus, Hashimoto's thyroiditis, multiple sclerosis,
clubus erythematorsus, Hashimoto's thyroiditis, unitiant nephrotic
syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
collits, Crohn's disease, Sjogren's syndrome, allergies, allergic
cathma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
eczema, graft-versus-host disease, CODD, insulltis, bronchitis
(particularly chronic bronchitis) or diabetes (particularly type 1
for studying interactions between CD23 and various ligands and
chermining the binding agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                  CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; vietis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; slogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy.
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                                                                                                                                         AAY32255 standard; Peptide; 7 AA.
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Best Local Similarity
Matches 7; Conserv
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AAW39815-17 represent the sequences of the light chain complementarity determining regions (CDRs) of the catalytic antibody 3B9, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl occaine. The 3B9 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that
                                                                                                                                                                                                                        Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
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Pred. No. 7.8e+05;
                                                                                                                                                                                           Light chain CDR2 of catalytic antibody 3B9.
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                                                                                                    AAW39816 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                       overdose; addiction
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LMSTRAS 7
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AAW39876
ID AAW3
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AC AAW3
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WO200183806-A1.
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                                                               Light chain CDR2 of a catalytic antibody capable of degrading cocaine
                                                                                                     Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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85.7%; Pred. No. 7.8e+05;
ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                      /note= "not specified"
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 5; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU70329 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Kappa II light chain CDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0672345.
                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US10965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                    16-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                       overdose; addiction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-077166/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA;
                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LMSTRAS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LMSTRXS
                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                 WO9749800-A1
                                                                                                                                                                                                                                                                                                                                                                                            31-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Landry DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU70329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                    Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides encoding different immunoslobulin binding protein (198P) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transformed cells, to generate an IgBP that binds to a ligand, and transformed plant cells are selected, and at least 75% sequence identity to a framework region (FR) of a native in IgB, IgB, IgB, kappa or lambda immunoslobulin molecule. The method is useful for preparing an immunoslobulin binding protein. The method is useful for preparing an immunoslobulin binding protein. Carray, preferably heavy chain binding protein (CHBP) array in eukaryotic cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammalian cells). The CHBP is useful for discovery of e.g. screening assays of IgBPs having desired characteristics. The present sequence is a mammalian can IgBP of immunoslobulin derived peptide that may be incorporated into an IgBP of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acids encoded by 5' portion of pTugAS vector SacI-HindIII region.
                                                                                                                                                                                                                                                                                                                                                                                                         Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22; DB 23; Length 7; Pred. No. 7.8e+05; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prugAS vector; Cellulomonas fimi; endoglucanase C; CBD; cellulose binding domain; polysaccharide binding peptide; fusion protein; recombinant protein; cell separation; affinity phase separation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 14; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY81430 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.0%;
71.4%;
                                                                 02-MAY-2001; 2001WO-US14349
                                                                                                                                      02-MAY-2000; 2000US-0563222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Juery Match
Best Local Similarity 71.**,
S. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                            (EPIC-) EPICYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                               WPI; 2002-055482/07.
                                                                                                                                                                                                                                                                                 Hein MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preparing array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LMSTRAS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention.
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08-NOV-2001
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                                                                                                                                                                                                                                                                                 Hiatt AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY81430;
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AntiHBs; monoclonal antibody; Epstein Barr virus; EBV; adr type; human; HBs antigen; hepatitis C.

Homo sapiens

Peptide Seg ID No:6 of JP11089576.

25-JUN-1999 (first entry)

AAY06840;

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The invention relates to a novel two-phase partition system for affinity which comprises a phase-forming oligosaccharide polymer to which a polyaccharide binding peptide (FBP) binds, and a phase to which a polyaccharide binding peptide (FBP) binds, and a phase to sparation inducing agent. The system may be used for the separation and purification of recombinant proteins from cheal cultures. The protein of interest is expressed in the host cell as a fusion protein with a conformation system. The fusion protein partitions into the polyaccharide binding peptide, and the cell lysate or fermentation of conformation system. The fusion protein partitions into the coligosaccharide bolymer phase, and can then be isolated e.g., via the case of a solution with a low ionic strength, high pl or containing a chaotropic agent, or by the use of chemical cleavage agents such as chaotropic agent, or by the use of chemical cleavage agents such as chaotropic agent, or by the use of chemical cleavage agents such as chaotropic agent, or by the use of chemical cleavage agents such as chaotropic agent, or by the use of chemical cleavage agents such as chaotropic agent, or by the use of chemical cleavage agents such as chaotropic agent, or by the use of chemical cleavage agents such as chaotropic agent, or by the use of creaming the protein can be cleaved from the PBP and the invention include a wide variety of medically and industrially important proteins e.g., interleving the method of the invention include a wide variety of medically and industrially impuring that receptor can be used for cell separation and/or enrichment of a ligan of a particular receptor can be used to isolate cells comprising that receptor can be used to isolate cells comprising that receptor can be used to isolate cells compressed polymer makes it suitable fellulosic substrates offer a new, cost-effective, highly flaxible affinity partition systems continuous purification. Selective binding of EPP from the collapsaccharide polymer makes it suitable for purifica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Two-phase partition affinity separation system useful for separating and purifying proteins comprises a phase-forming oligosaccharide polymer and a phase-separation agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ļ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 3A; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Kilburn DG
                                                                                                                                                                                                                                                                                                                                       (UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                   92US-0865095.
90US-0603987.
94US-0249037.
                                                                                                                                                                                                                                                   95US-0505860
    96US-0685808
                                                                               88US-0216794
                                                                                                                                                                                                                                                                                                                                                                                                                       Tomme P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-328038/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 AA;
24-JUL-1996;
                                                                                                                            08-APR-1992;
                                                                                                                                                                                                                                                   24-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                            наупев СА,
                                                                                                                                                                                                                24-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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The invention relates to an antiHBs monoclonal antibody having the following properties: (A) CDR-3 of H chain variable region; (B) it contains no Epstein Barr virus (EBV); (C) it binds at least one adr type among human HBs antigens. The antiHBs monoclonal antibody is high in antibody titer and has low risk of EBV contamination. It can be used to prevent hepatitis C.

Anti-HBs monoclonal antibody - produced without the risk of Epstein

97JP-0255705. 97JP-0255705.

19-SEP-1997; 19-SEP-1997;

06-APR-1999.

(NISN ) NISSHINBO IND INC.

WPI; 1999-281053/24.

Claim 4; Page 7; 12pp; Japanese.

Barr virus contamination

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Gaps

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Length 7; Indels

61.3%; Score 19; DB 20; 80.0%; Pred. No. 7.8e+05; iive 1; Mismatches 0;

Conservative

Local Similarity nes 4; Conserv

Matches

3 STRAS

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7 AA;

Sequence Query Match

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Tumour antigen; antibody; CDR; complementarity determining region; binding molecule identification; tumour-specific binding polypeptide; cancer therapy; light chain.
                                                                                                 Tumour antigen antibody light chain CDR2 clone F14.
                                             AAY05015 standard; peptide; 7 AA.
                                                                                                                                                                                                                             97US-0905825.
97US-1112222.
                                                                                                                                                                                                            98WO-US16280
                                                                                                                                                                                                                                                        (IXSY-) IXSYS INC.
                                                                                 16-JUN-1999
                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                           04-AUG-1998;
                                                                                                                                                                                                                             04-AUG-1997;
04-AUG-1997;
                                                                                                                                                                        WO9906834-A2
                                                                                                                                                                                           11-FEB-1999,
3 STRAT
                                                                AAY05015;
                              RESULT 10
                                       AAY0501
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61.3%; Score 19; DB 21; Length 4; 100.0%; Pred. No. 7.88+05; rive 0; Mismatches 0; Indels

Conservative

Query Match Best Local Similarity Matches 4; Conserv

MSTR 5

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AAY06840 standard; peptide; 7 AA.

AAY06840 ID AAY0 XX RESULT 9

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The present invention describes a method for detecting a retroviral genetic recombinant having agg and pol functions, involving a cell suspected of having a recombinant and propagating the recombinant in the presence of any necessary helper functions. This is useful as it enables the detection of vectors which are able to replicate in the host cell, and allows the production of vectors suitable for gene therapy. The present sequence is a peptide fragment used to demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence may be fused to the haemagglutinin 2 (HA2) fragment (amino acids 66-222) of influenza A and the resulting fusion protein used in a vaccine. The purpose of this particular sequence is not given in the specification although such additional peptides to the virus antigen may contain another influenza antigen or other antigen or confer some advantage upon expression of the HA2 peptide. Alternatively the fusion peptide may comprise a sequence which is selectively cleavable by a proteolytic enzyme or upon exposure to a
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide; influenza; vaccine; virus; antigen; expression; cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine compsn. for immunising against influenza A - comprises portion of a haemagglutinin 2 sub unit peptide of an influenza
                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide fused to influenza A polypeptide for use in vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.1%; Score 18; DB 15; Length 7; ilarity 66.7%; Pred. No. 7.8e+05; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                            Score 18; DB 22; Length 6;
Pred. No. 7.8e+05;
0; Mismatches 2; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shatzman A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scott MO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 45; 58pp; English.
Example 5; Fig 14; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR46961 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                              58.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92WO-US07312
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                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-118165/14.
                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                        6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion protein.
                                                                                                                                                                                                                                                                                                                                          2 MSTRAS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                 1 MGARAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dillon SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR46961;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                             This sequence represents a light chain complementarity determining region (CDR) from a tumour antigen specific antibody.

The invention relates to a method for identifying a binding molecule having selective affinity for a ligand comprising; a) selectively immobilising a diverse population of binding molecules to a solid support, (b) simultaneously contacting the diverse population immobilised on the solid support with 2 or more Ifgands; and (c) determining at least one binding molecule which selectively binds to one or more of the identification of binding molecules which selective afficient methods for the identification of binding molecules which exhibit selective affinity for one or more ligands of interest. They are used particularly for identifying tumour-specific binding polypeptides which can be used as targeting agents for cancer therapy that minimises impact on non-tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retroviral recombination assays, systems and cells, useful for evaluating the risk of producing a replication-competent retrovirus from a retroviral-based vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Retroviral recombination assay; gene therapy vector; viral vector; gag; pol; replication; HIV.
                                                                         Identifying binding molecules for ligands, particularly tumour antigens - by selectively immobilising a population of binding molecules to a solid support and screening for binding to two or more ligands
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Retroviral recombination assay peptide fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB35205 standard; Peptide; 6 AA.
                                                                                                                                                                              Claim 15; Page 57; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cappes JC, Wu X, Wakeield J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.3%;
80.0%;
Wu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0143015.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
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Huse WD, Watkins JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANZYME INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                    WPI; 1999-153951/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-091927/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200104360-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 STRAS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 STRAT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB35205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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AAR76083;

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Tumour antigen, antibody, CDR, complementarity determining region; binding molecule identification; tumour-specific binding polypeptide; cancer therapy; light chain.
                                                                                                                                                                                                                                                                                                                                                     AAW31170-W31181 are peptides derived from various gentoypes of hepatitis C virus. The peptides were used for the production of PCR (polymerase chain reaction) primers used for discrimination between hepatitis C virus (HCV) genotypes. Classification of the genotype of HCV can be achieved precisely and simply according to the international Standardisation of Classification. The primers can be used to distinguish between HCV genotypes la, lb, 2a, 2b, 3a, 3b, 4, 5a, 6a and 6b.
                                                                                                                                                                                                                                                                          Primers used for determining hepatitis C virus genotype - provide a rapid and accurate method of hepatitis C virus genotyping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 18; Lengtn /, Pred. No. 7.8e+05;
   3b; 4; 5a; 6a; 6b; diagnosis; amplification; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour antigen antibody light chain CDR2 clone F15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                         Example 1; Page 18; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY05016 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n 58.1%;
Similarity 57.1%;
4; Conservative 1
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                                                                                                                                96JP-0038875.
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97US-1112222
                                                                                                                                                              95JP-0352511
95JP-0035997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-153951/13.
N-PSDB; AAX28193.
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                                  Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA;
                                                                                                                                                                                                            (SRLS-) SRL KK.
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1 LLSPRGS
                                                                JP09234072-A.
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04-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9906834-A2
                                                                                                                                01-FEB-1996;
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01-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An antigen binding structure is based on the CDRs (given in AAR76078-84) of the heavy and light chains of MAD 55.1 (ECACC 93081901), which recognises the colorectal tumor-associated antigen CAS5.1. It is optionally humanized and in the form F(ab')2, F(ab)', FV, SCFV or V-min, and is produced in transgenic animals or plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                     Antigen binding structure; complementarity determining region; CDR; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monoclonal antibody; MAb; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering; humanized antibody; immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus; HCV; genotype determination; la; lb; 2a; 2b; 3a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen binding structures containing CDRs recognising the CA55.1 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 16; Length 7;
Pred. No. 7.8e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus genotype 5a peptide, OMM25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hall SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 97; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW31179 standard; peptide; 7 AA.
                                                                                                            AAR76083 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copley CG,
                                                                                                                                                                                                                                                                                                      humanīzed antibody; immunotoxin
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llarity 80.0%;
Conservative (
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                                                                                                                                                                           (first entry)
                                                                                                                                                                                                       MAb 55.1 light chain CDR2.
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Rose MS, Wright AF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-215262/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                   | |||:
LTSTRS 7
LMSTRA 6
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03-DEC-1993;
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Sequence

Best Loca Matches

ઠે ద AAW31179;

RESULT 14 AAW31179

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Gaps

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This sequence represents a light chain complementarity determining region (CDR) from a tumour antigen specific antibody.

The invention relates to a method for identifying a binding molecule having selective affinity for a ligand comprising; (a) selectively immobilising a diverse population of binding molecules to a solid immobilising a diverse population of binding molecules to a solid on the solid support with 2 or more ligands; and (c) determining at least one binding molecule which selectively binds to one or more of the ligands. The method allows for the rapid and efficient methods for the identification of binding molecules which exhibit selective affinity for one or more ligands of interest. They are used particularly for identifying tumour-specific binding polypeptides which can be used as transeting agents for cancer therapy that minimises impact on non-tumour
                   Identifying binding molecules for ligands, particularly tumour antigens - by selectively immobilising a population of binding molecules to a solid support and screening for binding to two or more ligands
                                                                                                                                                   Claim 15; Page 57; 80pp; English.
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Gaps ö Query Match
Best Local Similarity 80.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 7 AA; Sequence

tissues.

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Search completed: April 22, 2003, 13:21:55 Job time : 35 secs

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Sequence 32, April Sequence 10, Appil Sequence 11, Appil Sequence 43, Appil Sequence 64, Appil Sequence 11, Appil Sequence 11, Appil Sequence 53, Appil Sequence 53, Appil Sequence 62, Appil Sequence 62, Appil Sequence 75, Appil Sequence 47, Appil Sequence 48, 
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Sequence 32, Appl
Sequence 10, Appl
Sequence 18, Appl
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                                                                                                                                                                                                                                          April 22, 2003, 13:23:45; Search time 15 Seconds (without alignments) 37.394 Million cell updates/sec
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1: /cgn2_6/prodata/1/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/prodata/1/pubpaa/PUT.NW PUB.pep:*
4: /cgn2_6/prodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/prodata/1/pubpaa/USO6_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubpaa/USO6_PUBGOMB.pep:*
7: /cgn2_6/prodata/1/pubpaa/USO7_PUBGOMB.pep:*
6: /cgn2_6/prodata/1/pubpaa/USO7_PUBGOMB.pep:*
7: /cgn2_6/prodata/1/pubpaa/USO7_PUBGOMB.pep:*
9: /cgn2_6/prodata/1/pubpaa/USO9_NEW_PUB.pep:*
10: /cgn2_6/prodata/1/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/prodata/1/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/prodata/1/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/prodata/1/pubpaa/USO9_NEW_PUB.pep:*
13: /cgn2_6/prodata/1/pubpaa/USO0_NEW_PUB.pep:*
14: /cgn2_6/prodata/1/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-09-977-797A-30
US-09-977-797A-30
US-09-10-146-644-11
US-10-144-644-11
US-10-144-644-11
US-09-828-708-43
US-09-947-137-8
US-10-078-458-11
US-09-995-973-53
US-10-1014-774-19
US-09-995-973-53
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US-09-995-973-53
US-09-995-973-53
US-09-995-973-53
US-09-995-973-53
US-09-9850-351A-75
US-09-828-708-45
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
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Maximum DB
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20	15	48.4	7	10	US-09-828-708-49	Sequence 49, Appl
21	14	45.2	e	10	US-09-982-172-82	82,
22	14	45.2	Ω.	2	US-09-800-433-7	7,
23	14	45.2	2	10	US-09-976-165-63	63
24	14	45.2	9	σ	US-09-858-852A-66	9
25	14	45.2	9	σ	US-09-925-179-35	
26	14	45.2	9	10	US-09-802-077-35	ù.
27	14	45.2	9	10	US-09-802-096-35	35,
28	14	45.2	9	2	US-09-736-959A-22	Sequence 22, Appl
29	14	45.2	9	10	US-09-990-762-66	99
30	14	45.2	7	6	US-09-977-797A-82	Sequence 82, Appl
31	14	45.2	7	6	US-09-967-237-107	Sequence 107, App
32	14	45.2	7	6	US-10-217-957-3	Sequence 3, Appli
33	14	45.2	7	σ	US-10-217-957-4	Sequence 4, Appli
34	14		7	10	US-09-765-086-71	-
35	14	45.2	7	10	US-09-253-794-21	21,
36	14	45.2	7	10	US-09-947-137-29	29,
	13	41.9	4	10	US-09-220-920-71	71,
38	13	41.9	4	10	US-09-839-447A-78	78
39	13	41.9	4	10	US-09-782-980-102	102,
40	13	41.9	4	10	US-09-405-499-3	3,
41	13	41.9	4	9	US-09-872-349-1	
42	13	41.9	4	10	US-09-982-172-87	87,
43	13	41.9	4	10	US-09-751-100B-15	15
44	13	41.9	ហ	6	US-09-933-999A-30	
45	13		ഗ	10	8-0	٠,
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					ALIGNMENTS	
RESULT 1	•					
US-09-977-797A-30	-797A-	30				
; Sequenc	e 30,	Sequence 30, Application US/09977797A	ion US,	660	77797A	
; Publication No. USZ:	TNFOR	PUDIICACION NO. USZUUJUU4477ZAI GENERAI INFORMATION:	300447	ZAI		

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GENERAL INFORMATION:
APPLICANT: Watkins, Jeffrey D.
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
FILE REFERENCE: AME-06805
CURRENT APPLICATION NUMBER: US/09/977,797A
FRIOR APPLICATION NUMBER: 08/905,825
PRIOR FILING DATE: 1998-08-04
PRIOR FILING DATE: 1997-08-04
PRIOR FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 136
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Watkins, Jeffrey D. APPLICANT: Watkins, Jeffrey D. APPLICANT: Huse, William D. APPLICANT: Wu, Herren TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 9; Length 7; Pred. No. 2.7e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 32, Application US/09977797A; Publication No. US20030044772A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                61.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: CDR2 of humanized

OTHER INFORMATION: murine anti-human B7-2 light chain
US-09-249-011A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Ames, Robert S.

APPLICANT: Appelbaum, Edward R.

APPLICANT: Cook, Richard M.

APPLICANT: Cook, Richard M.

APPLICANT: Gross, Mitchell S.

APPLICANT: Gross, Mitchell S.

APPLICANT: Gross, Thomes, Esphen D.

APPLICANT: Theisen, Timothy W.

TITLE OF INVENTION: Treatment of IL5 Mediated Disorders

NUMBER OF SQUENCES: 76

CORRESPEDINGENCE ADDRESS:

ADDRESSEE: MithKilme Beecham Corp

STREET: P.O. Box 1539-UM2220

CITY: King of Prussia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19406-0359

COMPUTER: READBLE FORM:

MEDIUM TYPE: Rloppy disk

COMPUTER: Enabable FORM:

MEDIUM TYPE: Bloppy disk

COMPUTER: Enabable FORM:

MEDIUM TYPE: Bloppy disk

COMPUTER: Enabable FORM:

MEDIUM TYPE: Bloppy disk

COMPUTER: STEMP PC Compatible

OPERATING SYSTEM: PC-DS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/470110

FILING DATE: 06-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/363131

FILING DATE: 06-JUN-1995

PRIOR APPLICATION NUMBER: US 08/363131

FILING DATE: 13-DEC-1994

ATTORNEY/AGRAT INFORMATION: INFORMATION:

NAME: CHARLY AFFAIRM TINFORMATION:

NAME: CHARLY AFFAIRM TINFORMATION:
                                                                                                                                                                                                                                                                                                                    Score 17; DB 9; Length 7; Pred. No. 2.7e+05; 0; Mismatches 1; Indels
    CURRENT APPLICATION NUMBER: US/09/249,011A
CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 11, Application US/10144644; Publication No. US20030059429A1; GENERAL INFORMATION:
                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 7 amino acids
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Patent No. US2002013035A1
GENERAL INFORMATION:
APPLICANT: VURAN CORPORATION
TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
TITLE OF INVENTION: S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME
FILE REFERENCE: OV17440
CURRENT APPLICATION NUMBER: US/10/146,305
CURRENT PILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: KR 10-2001-26634
PRIOR PILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: KOPATENTI I.71
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APPLICANT: VELDMAN, GEERTRUIDA M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
FILE REFERENCE: 08702.0081-00000
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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80.0%; Pred. No. 2.7e+05;
Live 0; Mismatches 1;
FILE REFERENCE: AME-06805
CURRENT APPLICATION NUMBER: US/09/977,797A
CURRENT FILING DATE: 2002-06-25
FRIOR APPLICATION NUMBER: 09/129,026
PRIOR APPLICATION NUMBER: 09/129,026
PRIOR APPLICATION NUMBER: 08/905,825
PRIOR FILING DATE: 1997-08-04
FRIOR FILING DATE: 1997-08-04
SOFTWARE: Patentin version 3.1
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/09249011A Patent No. US20020176855A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
APPLICANT: CARRENO, BEATRIZ
APPLICANT: CELNIKER, ABBIE CHERYL
APPLICANT: COLLINS, MARY
APPLICANT: GOLDMAN, SAMUEL
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
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KNIGHT, ANDREA
O'HARA, DENISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Escherichia coli
US-10-146-305-10
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Matches 4; Conservative
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; ORGANISM: Homo sapiens
US-09-977-797A-32
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US-10-146-305-10
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APPLICANT:
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US-10-078-458-11
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                                                                                                                   Sequence 8, Application US/09947137
Sequence 8, Application US/09947137
GENERAL INFORMATION:
APPLICANT: Samith, Bruce F.
APPLICANT: Samoilova, Tatiana
TITLE OF INVENTION: Compounds to Muscle
FILE REFERENCE: 5721-8
CURRENT APPLICATION NUMBER: US/09/947,137
CURRENT FILING DATE: 1998-05-25
FRIOR PILING DATE: 1998-05-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.6%; Score 16; DB 10; Length 7; 60.0%; Pred. No. 2.7e+05; trive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Phage display library peptides US-09-947-137-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-10-078-458-11
Sequence 11, Application US/10078458
Publication No. US20020187934A1
GENERAL INFORMATION:
APPLICANT: LUKE, Richard William Arthur
APPLICANT: COTYON, Ronald
TITLE OF INVENTION: PEPTIDE DERIVATIVES
CURRENT APPLICATION NUMBER: US/10/078,458
CURRENT APPLICATION NUMBER: US/10/078,458
CURRENT PELING DATE: 1999-05-17
PRIOR FILING DATE: 1999-05-17
PRIOR PILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: CT/GB97/03199
PRIOR FILING DATE: 1997-11-21
PRIOR PILING DATE: 1997-11-27
SEQUENTWARE: PatentIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.01
Matches 3; Conservative
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1 MSTQS 5
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Sequence 46, Application US/09828708
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: autocimmune disease
FILE REFERENCE: 1361.005U31
CURRENT APPLICATION NUMBER: US/09/828, 708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Mindows Version 4.0
SEQ ID NO 46
LENGTH: 7
L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Button, D.
APPLICANT: Button, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
TITLE OF INVENTION: autoimmune disease
TITLE REFERENCE: 136.1005913
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 43
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                                                                                                                                                                                54.8%; Score 17; DB 9; Length 7; 80.0%; Pred. Nov. 2.7e+05; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 43, Application US/09828708
Patent No. US20020146753A1
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                             Best Local Similarity 80.0 Matches 4; Conservative
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                      STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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US-09-828-708-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
TYPE: amino acid
                                                                                                                                                                                                                                                                                                          3 STRAS 7
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                                                                                                ; MOLECULE TY
US-10-144-644-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-09-828-708-43
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                                                                                                                                                                                   Query Match
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Gaps

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RESULT 13
US-10-116-25-58

Sequence 58, Application US/10116255

Publication No. US2003003646A1

GENERAL INFORMATION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
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Sequence 62, Application US/09913238

Publication No. US2030049251A1

FUBLICANT: Barbas, Carlos F.

APPLICANT: Steinberger, Peter

TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR

TITLE OF INVENTION: INHIBITING CCR5-DEPENDENT INFECTION OF CELLS BY HIV-1

FILE REFERENCE: TSRI 728.1

CURRENT APPLICATION NUMBER: US/09/913,238
                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: zinc finger; OTHER INFORMATION: binding domain US-09-995-973-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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48.4%; Score 15; DB 9; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 1; Mismatches 1; Indels
         CURRENT APPLICATION NUMBER: US/09/995,973
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 53
LENGTH: 7
                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-116-255-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LMSTR 5
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US-09-800-433-8
; Sequence 8, Application US/09800433
; Sequence 8, Application US/09800433
; Patent No. US20020106378A1
; GENERAL INFORMATION:
; APPLICANT: O'Hare and Elliott
; TITLE OF INVENTION: Materials and methods for intracellular transport and
; TITLE OF INVENTION: their uses
; TITLE OF INVENTION UNMER: US/09/800,433
; CURRENT APPLICATION NUMBER: US/09/800,433
; CURRENT PILING DATE: 1999-09-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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APPLICANT: D'Azzo, Alessandra
APPLICANT: Bonglovanni, Antonella
APPLICANT: Nastasai, Tommaso
TITLE OF INVENTION: Protein Specific for Cardiac and Skeletal Muscle
FILE REFERENCE: 2427/1F509-USI
CURRENT APPLICATION NUMBER: US/10/014,774
CURRENT PILING DATE: 2001-00-29
PRIOR PILING DATE: 2000-04-28
PRIOR PLING DATE: 10999-04-29
PRIOR PLING DATE: 10999-04-29
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 19
LENGTH: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 48.4%; Score 15; DB 10; Length 6; Best Local Similarity 75.0%; Pred. No. 2.7e+05; Matches 3; Conservative 1; Mismatches 0; Indels
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48.4%; Score 15; DB 12; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels
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Publication No. US20030024006A1
GENERAL INFORMATION:
APPLICANT: CHOO, Yen
APPLICANT: ULLMAN, Christopher G.
TITLE OF, INVENTION: GENE SWITCHES
FILE REFERENCE: 8325-2003 / G7-USI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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CORGANISM: Homo sapiens
US-10-014-774-19
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US-10-014-774-19
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Score 15; DB 10; Length 7; Pred. No. 2.7e+05; 1; Mismatches 0; Indels
                                                                 TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-09-850-351A-75
                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: April 22, 2003, 13:29:09 Job time : 16 secs
                                                 TYPE: amino acid
STRANDEDNESS: single
    SEQUENCE CHARACTERISTICS
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Best Local Similarity 75.0%;
Matches 3; Conservative
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Muller-Cohn, Judy
Stamp, Lisa
Morill, George
TITLE OF INVENTION: No. US2020100080Alel Pesticidal Toxins and Nucleotide
Sequences Which Encode These Toxins
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COUNTRY: US

ZIP: 32606-669

COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERNIT SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PATENTIN RC-DOS/MS-DOS
SOFTWARRE: PATENTIN RC-DOS/MS-DOS
SOFTWARRE: PATENTIN DATA:
APPLICATION NUMBER: US/09/850,351A
FILING DATE: 07-MAY-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                         Query Match 48.4%; Score 15; DB 9; Length 7; Best Local Similarity 60.0%; Pred. No. 2.7e+05; Matches 3; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
ADDRESSEE: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/073,898
FILING DATE: 06-MAY-1998
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-0CT-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: 39,355
TELECOMMUNICATION INFORMATION:
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: PCT/EPO 0/12419
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 85
SOFUR PROSE SEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 62
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Feitelson, Jerald S. Schnepf, H. Brnest Narva, Kenneth B. Stockhoff, Brian A. Schmeits, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 75, Application US/09850351A Patent No. US20020100080A1 GENERAL INFORMATION:
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TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 75:
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OTHER INFORMATION: Synchesized
US-09-913-238-62
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                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                3 STRAS 7
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/51400

TELERHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23, Application US/08672345C
Patent No. 5948658
GENERAL INFOATION:
APPLICANT: Landary Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
CORRESPONDESS:
ADDRESSEE: Cooper and Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 100.0%; Score 31; DB 2; L. Similarity 100.0%; Pred. No. 1.9e+05; 7; Conservative 0; Mismatches 0;
PCT-US93-08435-24
PCT-US93-08435-37
PCT-US93-08435-41
PCT-US93-08435-41
US-08-53-065-14
US-08-53-065-14
US-08-340-233-90
US-09-084-605B-8
US-09-084-605B-8
PCT-US96-11495-14
US-09-082-358B-47
US-09-082-358B-47
US-09-082-358B-47
US-09-082-358B-47
US-09-082-358B-47
US-09-082-358B-47
US-09-082-358B-47
US-09-082-358B-47
US-08-084-111C-10
US-08-084-111C-10
US-08-084-111C-10
US-08-08-1122-7
US-08-08-1122-7
US-08-09-012-126-8
US-09-012-126-8
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1185 Avenue of the Americas
       TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
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CITY: New York
STATE: New York
COUNTRY: USA
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Best Local Similarity
     JS-08-672-345C-23
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     Best Loca
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                                                                                                                      April 22, 2003, 13:21:20 ; Search time 28 Seconds (without alignments) 7.356 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                    GenCore version 5.1.4 p5_4578 (c) 1993 - 2003 Compugen Ltd.
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US-08-672-345C-26

US-08-672-345C-29

US-09-214-095D-23

US-09-214-095D-26

US-09-214-095D-26

US-09-214-095D-20

US-08-672-345C-80

US-08-672-345C-80

US-08-214-095D-20

US-08-214-095D-20

US-08-214-095D-30

US-08-25-808-9

US-08-353-400-31

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US-08-450-776-38-20

US-09-017-628-20

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US-08-637-647-11
US-07-987-264-5
US-08-450-363-20
                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                       262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
                                                                                                                                                                                                                                 1 LMSTRAS
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Maximum DB
                                                                                       OM protein
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Result No.

us-09-674-716b-5.closed.rai

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7;
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Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DAIR: 1999-07-19
AUTHOR OF SEQ ID NOS: 121
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Patent No. 6280987
GENERAL INFORMATION:
APPLICANTION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION WHOBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 31; DB 2; I
100.0%; Pred. No. 1.9e+05;
tive 0; Mismatches 0;
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100.0%; Score 31; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0;
          NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
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Best Local Similarity 100.0
....has 7; Conservative
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ORGANISM: Murinae gen. sp.
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; ORGANISM: Murinae gen. sp.
US-09-214-095D-26
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MOLECULE TYPE: peptide

US-08-672-345C-29
                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
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US-09-214-095D-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 23
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US-08-672-345C-26

| Sequence 26, Application US/08672345C
| Patent No. 594865B
| GENERAL INFORMATION:
| APPLICANT: Landry Donald, W.
| TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
| NUMBER OF SEQUENCES: 108
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Cooper and Dunham Lip | STREET: 1185 Avenue of the Americas
| CITY: New York | STATE: New York | STA
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; Sequence 29 Application US/08672345C
; Patcht No. 5948658
; Patcht INCOMPTION:
   APPLICANT: Landry Donald, W.
   TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
   ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; STREET: New York
; STATE: New York
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                     CURITATION OF THE COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: The PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FLING DATE: 24-UN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELEPRATION NUMBER: 212-278-0400
TELEPRAX: 212-278-0400
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARATTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
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; Sequence 80, Application US/08672345C
; Pattent No. 5948658
; Pattent No. 5948658
; Pattent INFORMATION:
APPLICANT: Landry Donald, W.
TITILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
; STATE: New York
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/09214095D; Patent No. 6280987; GRNRRAL INFORMATION: JARLELANT: Landry Donald; TITLE OF INVENTION: APPLICANT: Landry Donald; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY; CURRENT FILING DATE: 1999-07-19
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
JENGTH: 7
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ZUNTRY: USAS

ZUNTRY: USAS

COMPUTER READABLE FORM:

MEDIUM TYEE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: 24-JUN-1996

FILING DATE: 24-JUN-1996

CLASSIFICATION WHERE: US/08/672,345C

FILING DATE: 24-JUN-1996

CLASSIFICATION NUMBER: US/08/675/51400

REGISTRATION NUMBER: 05.75/51400

TELEPROMINICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPRATION NUMBER: 02.75/51400

TELEPRATION NUMBER: 02.75/51400

TELEPRATION NUMBER: 02.75/51400

TELEPRATION NUMBER: 02.75/51400

TELERATION NUMBER: 02.76/51

TELERATION NUMBER: 02.78/51

TELERATION NUMBER: 02.78/51

TELERATION NUMBER: 03.0400

TELERATION NUMBER: 0
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Pred. No. 1.9e+05;
1; Mismatches 0
85.7%; Pred. No. 1.9e+05;
tive 1; Mismatches 0
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Best Local Similarity 85.7%;
Matches 6; Conservative
                                 6; Conservative
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   Best Local Similarity
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1 LMSTRSS 7
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                                     Matches
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                                                                                                                                US-09-214-095D-29

Sequence 29, Application US/09214095D

Patent No. 6280987

GENERAL INFORMATION:

APPLICANT: Landry, Donald

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

FILE REPERENCE: 51400-APCT-US

CURRENT APPLICATION NUMBER: US/09/214,095D

CURRENT FILING DATE: 1999-07-19

NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patentin version 3.0

SEQ ID NO 29

LENGTH: 7
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; Sequence 20, Application US/08672345C
; Sequence 20, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
    APPLICANT: Landry Donald, W.
    TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
    NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Cooper and Dunham LLP
    STREET: 1185 Avenue of the Americas
    CITY: New York
    STATE: New York
    COUNTRY: USA
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DUTA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATCARREY/AGENT INFORMATION:
NAME: White, John P. REFERENCES/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF ST8-0400
TELEBRAGE: 212-278-0400
TELEBRAGE: 212-278-0400
TELEBRAGE: 212-278-0400
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100.0%; Score 31; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0;
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LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Murinae gen. sp
US-09-214-095D-29
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MOLECULE TYPE: peptide

DB 2; Length 7;

90.3%; Score 28;

Query Match

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Gaps
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SEPARATION AND CONCENTRATION SYSTEMS BASED
ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.3%; Score 19; DB 3; Length 4; 100.0%; Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,860C FILING DATE: 24-JULY-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.3%; Score 19; DB 4; Le
ilarity 100.0%; Pred. No. 1.9e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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US-08-505-860C-9
Sequence 9, Application US/08505860C
Patent No. 6174700
GENERAL INFORMATION:
APPLICANT HAINES, CHARLES A., et al ATTLE OF INVENTION: SEPARATION AND CONCENTIONED OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESSE: RAB-VENTER LAW GROUP STREET: 260 Sheridan Ave., Ste. 440
CITY: Palo Alto
STRATE: California
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPACTIONED
COMPACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CBDT.017.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
REPERENCE/DOCKET NUMBER: CBDI
TELECOMMUNICATION INFORMATION:
TELEFANE: (650) 328-4400
TELEFANE: (650) 328-4477
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (650) 328-4477
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Local 4; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSTR
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Fatent No. 6048715
GENERAL INFORMATION:
APPLICANT ATMES, CHARLES A., et al
TITLE OF INVENTION: SEPARATION AND CONCENTRATION SYSTEMS BASED
TITLE OF INVENTION: ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: ADMINISTED: ADDRESSEE: RAE-VENTER LAW GROUP
STREET: 260 Sheridan Ave., Ste. 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
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NAME/KEY: CHAIN
LOCATION: (6)..(6)
COTHER INFORMATION: X at position 6 represents any amino acid
US-09-214-095D-80
                                                                                                                                                                1; Indels
                                                                                          Length 7;
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US-09-214-095D-80

15-09-214-095D-80

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,808
FLING DATE: 24-JULY-1996
CLASSIPICATION 1435
PRIOR APPLICATION NUMBER: 08/505,860
FILING DATE: 24-JULY-1995
ATTORNEY/AGENT INPORMATION:
NAME: REGISTRATION NUMBER: 32,750
                                                                                  87.1%; Score 27; DB 2; L
85.7%; Pred. No. 1.9e+05;
tive 0; Mismatches 1;
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Pred. No. 1.9e+05;
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85.7%; Pred. No. 1...
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                       Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Murinae gen.sp.
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1 LMSTRXS 7
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            US-08-672-345C-80
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US-08-685-808-9
                                                                                          Query Match
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(416) 868-1482
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Best Local Similarity
نامع 4; Conserva
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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              TELEPHONE:
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Sequence 25, Application US/08264093
Fatent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION:
TITLE OF INVENTION: AUTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Ridout & Maybee
STREET: 2300 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
COUNTRY: Canada
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FITHATOR DATA:
CURRENT APPLICATION DATA:
FITHATOR DATA:
CURRENT APPLICATION DATA:
FITHATOR DATA:

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                                                                                                                                    APPLICANT:
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CONTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/08/353,400
FILING DATE:
CASSIFICATION NUMBER: US/08/353,400
FILING DATE: 03-DEC-1993
PRIOR APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-UN-1994
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
munns. sminn acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.1%; Score 18; DB 1; Length 7; 80.0%; Pred. No. 1.9e+05; Live 0; Mismatches 1; Indels
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PRIOR APPLICATION DATA: No. 5639863 applicable ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
                        Sequence 31, Application US/08353400
Patent No. 5665357
GENERAL INFORMATION:
APPLICANT:
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Best Local Similarity 80.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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US-08-353-400-31
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APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gook, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: McMillan, Lynette J.
APPLICANT: McMillan, Ecombinant ILS Antagonists Useful in TITLE OF INVENTION: Recombinant of ILS Mediated Disorders NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
STRRET: P. O. Box 1539-UW2220
CITY: King of Prussia
STRRET: Pennisylvania
                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                              Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7;
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: BM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/467,420A

FILING DATE: 23-DEC-1994

ATTORNEY/AGENT INFORMATION:

MAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: P50282

TELECOMMUNICATION INFORMATION:

MAME: Sutton, Jeffrey A.

REFERENCE/DOCKET NUMBER: P50282

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610 270-5094
                                                                                                                                                                                                                              Score 17; DB 1; 1
Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17; DB 1; Dred. No. 1.9e+05;
                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 11, Application US/08467420A; Patent No. 5683892
                                                                                            TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
US-08-264-093-25
                                                                                                                                                                                                                    54.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.8%;
80.0%;
TELEPAX: (416) 362-0823
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
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                                                                                                                                                                                                                                                                          Conservative
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MOLECULE TYPE: protein
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Mat	срев	4 ;	Matches 4; Conservative 0; Mismatches	0;		1,	1, Indels	0;	0, Gaps	0 ;
ò	m	3 STRAS 7			ļ					
q	m	STRES	7							
Searc Job t	th con	mpleted : 29 se	Search completed: April 22, 2003, 13:25:06 Job time : 29 secs	, 13	:25:06					

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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 22, 2003, 13:28:56 ; Search time 14 Seconds (without alignments) 61.801 Million cell updates/sec Run on:

US-09-674-716B-7 48 Title: Perfect score:

1 QQLVEYPFT 9 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

789

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	-	Description	alpha-2-macroglobu	major protein anti	TRH-like tripeptid		Ig heavy chain CRD	angiotensin-conver	peptidyl-dipeptida	dermorphin - Rohde		dermorphin (Trp-4,	aggrecan - bovine	cardioacceleratory	locustamyotropin I	ATP-binding protei	subesophageal gang	halo-toxin - Pseud	bHLH transcription	Ig mu chain D regi	glucuronosyltransf	hypothetical L2 pr	hypothetical prote	vitamin D3 26-mono	bradykinin-like pe	Thr-6 bradykinin -	bradykinin-like pe	bradykinin - commo	7		cardioactive pepti
																															•
-		ΠD	866635	E60274	A43391	A32039	PT0240	PQ0009	JN0861	A61324	836662	821230	842620	<b>S66646</b>	A61620	B49712	JS0319	A61049	151317	E33932	PX0008	I56695	S16324	S15850	A61358	A61057	A26744	A61363	A60579	A26363	839766
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		Score	21	19	16	14	14	14	14	14	14	14	14	14	14	14	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13
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cardioactive pepti bradykinin - horn	<pre>buk ca binding pro</pre>	cardioactive pepti hydroxyproline-3-b pap fimbrial requl	phytosulfokine alp pilE protein - Esc amine oxidase (cop	capsid protein VP- neuropeptide calla neuropeptide calla serum albumin - do
S27233 S65433	PT0080 PT0285 S10784 146023	S39767 A43065 B37325	JT0870 S25266 A38081	PL0184 D47393 E47393 B45800
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27.1	27.1 27.1 27.1	27.1 27.1 25.0	25.0 25.0 25.0	25.0 25.0 25.0
13	13 13	13 21	1221	1222
30	3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	36 37 38	39 40 41	64 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6

### ALIGNMENTS

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CjAccession: S66635
R;Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottrn
R;Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottrn
R;ESS Lett. 372, 93-95, 1995
A;Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain o
A;Reference number: S66634; MUID:96032553; PMID:7556651
A;Accession: S66635
A;Accession: S66635
A;Accession: Special minary
A;Molecule type: protein
A;Residues: 1-9 <DOL>
alpha-2-macroglobulin isoform 1 - bovine (fragment)
C;Species: Bos primigenius indicus (zebu cattle)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
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Gaps ; 0 Query Match 43.8%; Score 21; DB 2; Length 9; Best Local Similarity 75.0%; Pred. No. 2.8e+05; Matches 3; Conservative 1; Mismatches 0; Indels

.. 0

5 EYPF 8 |:|| 3 EFPF 6 ờ. A

major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: E60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
A;Title: Immun. 59, 372-382, 1991
A;Reference number: A60274; MUID:91099989; PMID:1898899
A;Accession: E60274
A;Accession: E60274
A;Molecule type: protein
A;Residues: 1-5 <NAG>

Gaps ö 39.6%; Score 19; DB 2; Length 5; 75.0%; Pred. No. 2.8e+05; vative 0; Mismatches 1; Indels Query Match 39.6 Best Local Similarity 75.0 Matches 3; Conservative

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6 YPFT 9 2 YPIT ò g

RESULT 3

A43391 TRH-like tripeptide - alfalfa C;Species: Medicago sativa (alfalfa)

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peptidyl-dipeptidase A inhibitory peptide C111 - striped bonito
()Species: Sarda orientalis (striped bonito)
C)Accession: JN0861
R)Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. S7, 1743-1744, 1993
A)Title: Isolation and characterization of anglotensin I-converting enzyme inhibitory pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Experimental source: liver
C.Comment: The carboxyl end is essential for the protein's expression of angiòtensin I-c
C.Superfamily: bradykinin-potentiating peptide
C.Keywords: anglotensin-converting enzyme inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A61324

dermorphin - Rohde's leaf frog

C, Species: Phyllomedusa rohdei, Rohde's leaf frog)

C, Species: Phyllomedusa rohdei, Rohde's leaf frog)

C, Date: 17-Jul-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999

C, Accession: A61324 #sequence_revision 05-Aug-1994 #text_change 07-May-1999

R, Montecucchi, P.C.; De Castiglione, R.; Erspamer, V.

Int. J. Pept. Protein Res. 17, 316-321, 1981

A, Patitle: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Braz. A; Reference number: A61324; MUID:82029915; PMID:7287302

A, Rosiduse: 1-7 ** AWON

C, Supertamily: dermorphin precursor; dermorphin precursor amino-terminal homology

C; Reywords: anidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin F; Z/Modified site: D-alanine (Ala) #status experimental

F; Z/Modified site: anidated carboxyl end (Ser) #status experimental

F; Z/Modified site: anidated carboxyl end (Ser) #status experimental
                                                                                                               angiotensin-converting enzyme inhibitor (FLP-2) - common fig
N.Alternate names: ficus latex peptide 2
C.Species: Ficus carica (common fig)
C.Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C.Accession: P00009
R.Maruyama, S.; Miyoshi, S.; Tanaka, H.
A.Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A.ATitle: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A.Reference number: P00008
A.Reference number: D00008
A.Reference number: A.Residues: 1-5 AMR>
A.Residues: 1-5 AMR>
A.Residues: 1-5 AMR>
C.Resymords: angiotensin-converting enzyme inhibitor
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Les 2; Conserv
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3 YP 4
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C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A43391
R;Lackev.
D: Backev.
J: Balol. Chem. 267, 17508-17511, 1992
A;Title: Isolation and Structural determination of a novel TRH-like tripeptide, pyrodlu-A;Feference number: A43391, MUID:92388092; PMID:1517203
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
C;Keywords: amidated carboxyl end; pyroglutamic acid
C;Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:3/Modified site: amidated carboxyl end (Pro) #status experimental
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**Horvath, A.; Kastin, A.J.
J. Biol. Chem. 264, 2175-2179, 1989

A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor A;Reference number: A32039; MUD:89123285; PMID:2563371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Increase the CRD3 region (clone 2-100B) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: Pr0240
B; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
B; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
B; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
A; Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A; Reference number: Pr0222; MUID:91108337; PMID:1899102
A; Molecule type: DNA
A; Residues: 1.4 < YAM>A; Residues: 1.4 < YAM>A; Residues: Immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine C; Species: Bos primigenius taurus (cattle)
C; Date: 31-011-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
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C;Keywords: amidated carboxyl end
F;4/Modified site: amidated carboxyl end (Gly) #status experimental
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A, Experimental source: brain
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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Gaps

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ATP-binding protein p46 - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Date: 03.May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Accession: B49712
R;Nigam, S.K.; Goldberg, A.L.; Ho, S.; Rohde, M.F.; Bush, K.T.; Sherman, M.Y.
J. Biol. Chem. 269, 1744-1749, 1994
A;Title: A set of endoplasmic reticulum proteins possessing properties of molecular chap A;Reference number: A49712; MUID:94124514; PMID:8294423
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A. Insect Biochem. Mol. Biol. 22, 447-452, 1992
A;Title: Isolation, identification and synthesis of locustamyotropin III and IV, two add A;Reference number: A61620
A;Accession: A61620
                                                                                                                                                                                                                                                                                                                                                                   C,Accession: S66646
R;Huesmann, G.R.; Cheung, C.C.; Loi, P.K.; Lee, T.D.; Swiderek, K.M.; Tublitz, N.J.
FEBS Lett. 371, 311-314, 1995
A;Title: Amino acid sequence of CAP(2b), an insect cardioacceleratory peptide from the tA;Reference number: S66646; MUID:96013159; PMID:7556618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Locusta migratoria (migratory locust)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
C;Accession: A61620
                                                                                                                                                                                                                                                                                                    cardioacceleratory protein 2b - tobacco hornworm
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
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A;Molecule type: protein
A;Mesidues: 1.9 <26CH>
C;Keywords: amidated carboxyl end; neuropeptide
F;9/Modified site: amidated carboxyl end (Leu) #status experimental
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                                             Length 7;
                          29.2%; Score 14; DB 2; L4 conservative 0; Mismatch.
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Best Local Similarity 33.3.
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                   Query Match
Best Local Similarity
Local 2; Conserva
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-8 <HUE>
C, Keywords: cartilage
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R; Mignogna, G:, Severini, C:, Simmaco, M.; Negri, L.; Falconieri Erspamer, G:, Kreil, RBS Lett. 302, 151-154, 1992
A; Title: Identification and characterization of two dermorphins from skin extracts of A; Reference number: S21152; MUID:92339502; PMID:1633846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: 821230
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIG>
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
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CiDate: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
CiDate: 19-Mar-1997 #sequence_revision 24-Jul-1998
CiAccession: S42620
R;Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.
Matrix Biol. 14, 171-179, 1994
A;Title: Aggrecan in bovine tendon.
A;Reference number: S42620; MUID:94340214; PMID:7520336
A;Accession: S42620
                                                                                                                                                                                                                                                    dermorphin (Lys-7) [validated] - two-colored leaf frog
C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 10-Dec_1993 #sequence_revision 13-Mar-1997 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment) C;Species: Phyllomedusa bicolor (two-colored leaf frog) (C;Date: 19-Mar.1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000 C;Accession: S21230
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29.2%; Score 14; DB 1; Length 7; larity 100.0%; Pred. Mo. 2.8e+05; Conservative 0; Mismatches 0; Indels
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subsophageal ganglion pentapeptide - house cricket (Species Acheta domesticus (house cricket) (Species Acheta domesticus (house cricket) (Species Acheta domesticus (house cricket) (Spate: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000 (SACCESSION: JS0319 A.Wicker, C. (SP, 185-187, 1987) (Spate: C.; Wicker, C. (Spate: C.) Wicker, C. (Spate: Spate: Spa
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Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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A;Molecule type: protein
A;Residues: 1-9 <NIG>
C;Keywords: ATP; endoplasmic reticulum; molecular chaperone
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GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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OM protein - protein search, using sw model

April 22, 2003, 13:25:11 ; Search time 24 Seconds (without alignments) 15.554 Million cell updates/sec Run on:

US-09-674-716B-7 48 1 QQLVEYPFT 9 Perfect score:

Title:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

231 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ption	bothrops ja	homo sapien	treponema h	carcinus ma	carcinus ma	locus	homod	рошо	achet				periplaneta	carcinus ma	homo sapien	carcinus ma	daucus caro	lactobacill	carcinus ma	carcinus ma	carcinus ma	carcinus ma	cydia pomon	ascaris suu	carcinus ma	carcinus ma	carcinus ma	cydia pomon	_	-	-	-	carcinus ma
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SUMMARIES	ΙD	ANG2 BOTJA	UPAA HUMAN	FLA2 TREHY	AL17 CARMA	AL11_CARMA		UPA3_HUMAN	UPA7 HUMAN	SUGA ACHDO	FAR1 HELTI	CNO6_PINPS	PPK2 PERAM	PPK3_PERAM		UHA2 HUMAN	AL14_CARMA		ASP2 LACSN			ALL4 CARMA	ALL5_CARMA	ALL7_CYDPO	FAR2_ASCSU	AL12 CARMA	AL15_CARMA	AL18_CARMA	ALL3_CYDPO	ALL4_CALVO		ALLS_CALVO	ALLS_CYDB0	ALL7_CARMA
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P81811 carcinus ma	81812 carcinus ma	22396 locusta mig	81813 carcinus ma	80975 thunnus obe	04277 homo sapien	82072 litoria rub	01151 sus scrofa	82071 litoria rub	82073 litoria rub	25418 libellula a	14595 tabanus atr
P8	P8	P2	P8	PB	ЪС	P8	PC	28	9d	P2	E
ALL8_CARMA	CARMA	LOCMI	CARMA	THUOB	HUMAN	LITRU	PIG	LITRU	LITRU	IBAU	ABAT
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### ALIGNMENTS

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1; Indels Length 8;

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Malacostraca, Bumalacostraca, Bucarida, Decapoda, Pleocyemata,
Brachyura, Bubrachyura, Portunoidea, Portunidae, Carcinus.
NCBI_TaxID=6759;
                                                                Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
                                                                                                                                             8 AA; 858 MW; C82879D5AB46D865 CRC64;
                                                TISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
                                                                                                                                                                Score 14; DB 1; I
Pred. No. 1.1e+05;
                                                                                                                                                                                  1; Mismatches
                                                                                                                                                               29.2%;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Carejnustatin 17.
Careinus maenas (Common shore crab) (Green crab)
Eukaryota, Metazoa, Arthropoda, Mandibulata; Pancrustacea, Crustacea,
                                                                                                                    Gaps
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Flagellar filament outer layer protein flaA2 (35 kDa sheath protein)
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                                                                                                 Length 8;
                                                                                                                  2; Indels
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                                                                                                                                                                                                                                                         Treponema hyodysenteriae (Serpulina hyodysenteriae).
Bacteria; Spirochaetales; Brachyspiraceae; Brachyspira
NCBI_TaxID=159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA; 1129 MW; 855A19C68B4772D1 CRC64;
                                                                     8 8 8 8 8 8 8 8 8 8 8 8 9 0 9 MW; 86677BS9D1A72042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            FLAB3 (32 kDa).
-!- SUBCELLULAR LOCATION: Periplasmic flagellum. Plagella, Periplasmic.
                                                                                                31.2%; Score 15; DB 1; 1 60.0%; Pred. No. 1.1e+05;
                                                               /FTId=VAR_000004.
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                                                                                                                 0; Mismatches
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Best Local Similarity 42.9
Matches 3; Conservative
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Best Local Similarity
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Malacostraca; Eumalacostraca; Eucarida; Decapoda; Plecyemata;
Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
NCBI_TaxID=6759;
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Eur. J. Biochem. 250:777-734 (1997).
-1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
MOD RES 9 AMIDATION.
SEQUENCE 9 AA; 927 MW; 832D79CDCB46D861 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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                                                                                                                                                                                    Carcinus maenas (Common shore crab) (Green crab).
                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Cerebral ganglion, and Thoracic ganglion, MEDLINE=98121193; PubMed=9461295;
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                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Locustamyotropin 3 (LOM-MT-3).
Locusta migratoria (Migratory locust).
9 AA.
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NCBI_TaxID=9606;
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01-NOV-1995
01-NOV-1995
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                                                                                                                                                                             "Isolation, identification and synthesis of locustamyotropin III and IV, two additional neuropeptides of Locusta migratoria: members of the locustamyotropin peptide family.";
Insect Biochem. Mol. Biol. 22:447-452(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
-!- MISCELLANEGUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
SWISS-2DPAGE; P. 1099; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCF-2001 (Rel. 40, Last annotation update)
16-OCF-2001 (Rel. 40, Last annotation update)
Homo sapiens (Human).
Bukaryota, Merazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P., de Loof A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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MEDLINE=93082937; PubMed=1459097;
MEDLINE=93082937; Paquet N., Ravier F., Pasquali C., Sanchez G.J., Frutiger S., Paquet N., Ravier F., Pasquali C., Sanchez G.-C., James R., Tissot J.-D., Bjellqvist B., Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14; DB 1; Length 9;
Pred. No: 1.1e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          MOD RÈS 9 9 AMIDATION.
SEQÜENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;
                                                                                                                                                                                                                                                                                  (MYOTROPIC ACTIVITY).

-1- SIMILARITY: BELÖNGS TO THE PYROKININ FAMILY.

InterPro, IPRO01484; Pyrokinin.

PROSTITE; PS00539; PYROKININ; 1.

Neuropeptide; Amidation; Pyrokinin.
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01-APR-1993 (Rel. 25, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0%;
Matches 2; Conservative
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                                                                                                       SEQUENCE, AND SYNTHESIS.
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4 FPXT 7
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UPA7_HUMAN
ID UPA7_HUMAN
AC P30093;
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2 QOPF
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NON TER
SEQUENCE
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UPA3_HUMAN
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Insecta, Pterygota, Neoptera, Orthopteroldea, Orthoptera, Ensifera,
Gryllidae, Gryllinae, Acheta.
NCBI_TaxID=6997;
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                                                                                                                                                                                                                                                                                                                                                                                        "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714 (1992).
-!- MISCELLANBOUGS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.05, ITS MW IS: 37 kDa.
SWISS-2DPAGE; P30093; HUMAN.
                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
01-APR-1993 (Rel. 25, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 18) (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                 MEDLINE=93092937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochbtrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.1%; Score 13; DB 1; Length 5; larity 100.0%; Pred. No. 1.1e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.2%; Score 14; DB 1; Length 9; llarity 50.0%; Pred. No. 1.1e+05; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;
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GANGLIA.

PIR, JS0319, JS0319.

GROHENCE 5 AA; 476 MW; 69D76DDDDDDDDDC000 CRC64;
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(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
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Best Local Similarity
2, Conserva
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es 2; Conserv
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16-OCT-2001 (Rel. 40, Last annotation update)
Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
Periplaneta americana (American cockroach).
Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Perrygota, Neoptera, Orthopteroidea, Dictyoptera, Blattcidae,
NCBI_TaxID=6978,
                                                                                                                                                                                                                                                           TISSUE SPECIFICITY.
MEDLINE=20189894; PubMed=10723010;
Predel R., Eckert M.;
"Tagma-specific distribution of FXPRLamides in the nervous system of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY.
MEDLINE=20189894; PubMed=10723010;
Predel R., Eckert M.;
"Tagma-specific distribution of FXPRLamides in the nervous system of
                                                                                                                                                  TISSUB=Corpora cardiaca;
MEDLINB=97353923; PubMed=9210163;
Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
"Isolation and structural elucidation of two pyrokinins from the retrocerebral complex of the American cockroach.";
Peptides 18:473-478(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
TISSUB-Retrocerebral complex;
MEDILINE-99212469; PubMed=10196736;
Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede
"Differential distribution of pyrokinin-isoforms in cerebral and
abdominal neurohemal organs of the American cockroach.";
Insect Blochem. Mol. 18101. 29:139-144(1999).
                                                                                                                                                                                                                                                                                                                       the American cockroach.";
J. Comp. Neurol. 419:352-363(2000).
-i- FUNCTION: MEDITARES VISCERAL MUSCLE CONTRACTILE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the American cockroach.;
J. Comp. Neurol. 419:352-363(2000).
-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Periplaneta americana (American cockroach).
Bukaryota, Metazoa, Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera;
Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                 (WOUTROPIC ACTIVITY).

-1 TISSUE SPECIFICITY: CORPORA CARDIACA.

-1 MASS SPECTROMETRY: WHE883, WETHOD=WALDI.

-1 STULTARLY: BELONGS TO THE PYROKININ FAMILY.

InterPro, IPR001484; Pyrokinin.

PROSITE; PS00539; PYROKININ; FALSE NEG.

NOUROPEPIGE; Amidation; Pyrokinin.

NOD RES

SEQÜENCE 8 AA, 884 MW; C834176DD9D77775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.1%; Score 13; DB 1; Le larity 100.0%; Pred. No. 1.1e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
(Pea-PK-3) (FXPRL-amide).
                                                                                                                                      SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MYOTROPIC ACTIVITY).
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16-OCT-2001
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                                                                                                                TISSUE=Kidney;
MEDLINE=94286417; PubMed=7912428;
Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
"FMRFamide-related peptides from the kidney of the snail, Helisoma
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                 Helisoma trivolvis (Snail).

Bukaryota, Metazoa, Mollusca, Gastropoda, Pulmonata, Basommatophora, Planorbidae, Helisoma.

NCBL TaxID=27815;
                                                                                                                                                                                            Peptides 15:31-36(1994).
-!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL_1999 (Rel. 38, Created)
15-JUL_1999 (Rel. 38, Last sequence update)
15-JUL_1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of needles (N141) (Fragment).
Plub pinaeter (Maritime pine).
Bukaryota, Viridiplantee, Stroptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A., Frigerio J.-M., Plomion C., "Separation and characterization of needle and xylem maritime pin
                                                                                                                                                                                                                       THE KIDNEY, MANTLE AND SKIN.
-!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
-!- SIMILARITY: BELONGS TO THE FARP (FWRFAMIDE RELATED PEPTIDE)
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-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS
PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
                                                                                                                                                                                                                                                                                                                                                   27.1%; Score 13; DB 1; Length 7; 100.0%; Pred. No. 1.1e+05; ive 0; Mismatches 0; Indels
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larity 100.0%; Pred. No. 1.1e+05;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                         7 7 AMIDATION.
7 AA; 851 MW; 69D40729D76AA810 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 AA; 823 MW; 69D76724486B5740 CRC64;
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(Rel. 40, Last sequence update)
           PMRFamide-like neuropeptide GDPFLRF-amide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
TISSUB=Needle;
MEDLINE=99274088; PubMed=10344291;
                                                                                                                                                                                                                                                                                        Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                             trivolvis."
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UN06_PINPS
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Gape

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Length 8; Indels Gaede G.;

Hexapoda; Blattaria;

8 AA.

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RESULT 15
UHA2_HUMAN
ID UHA2_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
Tenebrio molitor (Yellow mealworm), and
Spodoptera eridania (Southern armyworm).
Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Crustacea,
Brachyraca, Bumalacostraca; Bucarida, Decapoda, Pleocyemata,
Brachyra; Eubrachynra, Portunoidea; Portunidae; Carcinus.
NCBI_TaxID=6759, 7130, 7067, 37547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation and identification of a cardioactive peptide from Tenebrio
                                                                                                                                                                                                                 Gaps
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Stangier J., Hilbich C., Beyreuther K., Keller R.;
"Unusual cardioactive peptide (CCAP) £rom pericardial organs of the
Shore crab Carciuus maenas.";
Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=M.sexta;
MEDLINE=99050243; PubMed=1426284;
Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
Trimary structure of a cardioactive neuropeptide from the tobacco hawkmoth, Manduca sexta.";
FEBS Lett. 313:165-168(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M., Schooley D.A.;
-1- MASS SPECTROMETRY: WW=996.5; METHOD=MALDI.
-1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
Neuropeptide; Amidation; Pyrokinin.
MADD RES
SRQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carcinus maenas (Common shore crab) (Green crab)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=T.molitor, and S.eridania; TISSUE=Head; MEDLINE=94176032; PubMed=8129851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-DEC-1998 (Rel. 37, Last annotation update)
Cardioactive peptide (CCAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA.
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tes 2; Conserv
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CCAP CARMA
ID CCAP CARMA
AC P38556;
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MEDLINE=95203287; PubMed=7895732;
Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
"The human myocardial two-dimensional gel protein database: update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Electrophoresis 15:1459-1465(1994).
-1- MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.0, ITS MW IS: 55.3 kDa.
NON TER.
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                    01-PEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Unknown protein from 2D-page of heart (Spot 5603) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.1%; Score 13; DB 1; Length 9; 50.0%; Pred. No. 1.1e+05; Live 1; Mismatches 1; Indels
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     9 AA.
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     PRT;
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STANDARD;
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3 VTEY 6
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099197 caloglossa
099593 caloglossa
099438 caloglossa
09138 caloglossa
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08196 caloglossa
08278 caloglossa
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09986 spinacia ol
0998725 saccharomyc
09003 homo sapien
09003 homo sapien
09073 streptomyce
090073 streptomyce
090073 bombina ori
083059 bombina ori
083059 bombina var
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STRAIN=V2785;
Wyvold C., Birkelund S., Christiansen G.;
The Mycoplasma hominis P120 membrane protein gene contains a 659 base pair hypervariable domain.";
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U22025; AAA67455.1; -.
caloglossa
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Last annotation update)
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(TrEMBLrel. 20, Last sequence update)
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  PRELIMINARY;
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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wes 3; Conserv
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 P120 (Fragment).
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09uc36 homo sapien
09uruz caloglossa
09ti85 caloglossa
09ti80 bostrychia
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P82858 puccinia re
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                                                                                      April 22, 2003, 13:27:31 percent time 28 Seconds (without alignments) 66.229 Million cell updates/sec
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               GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UND-2002 (TrEMBLrel. 21, Last annotation update)
GAP-3, GTPBAS-activating protein (Fragment).
Bos taurus (Bovine).
EMARYPOTAL Metasoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                "The purification of a Rapl GTPase-activating protein from bovine
                                                                                                                                                                                                                                                                                                                                                                                  Nice B.C., Fabri L., Hammacher A., Holden J., Simpson R.J., Burgess A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 33.3%; Score 16; DB 6; Length 9; Similarity 50.0%; Pred. No. 6.7e+05; 2; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AA; 1063 MW; 89EDA77B47604B5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      brain cytosol.";
J. Biol. Chem. 267:1546-1553(1992).
NON TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=PLACENTA;
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Q15898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21561594; PubMed=11703875;
Destions H.A., Garrido M.J., Kessing B.D.;
"Demographic history of Diadema antillarum, a keystone herbivore on
Caribbean reefs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chloroplast.

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids II; Asterales, Asteraceae, Cardueae, Jurinea.

NCBI_TaxiD=41594;
                                                                                          Mitochondrion.
Bukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa;
Echinoidea, Euechinoidea, Diadematacea, Diadematoida, Diadematidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
O'Hanlon P.C., Briese D.T.;
O'Hanlon P.C., Briese D.T.;
S'Evidence for hierarchical and non-hierarchical evolution in the Carduinae thistles.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF129846; AAF78138.1; -.
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                                                                                                                                                                                                                                              STRAIN=DCA3;
MEDLINE=21323357; PubMed=11430656;
Lessios H.A., Kessing B.D., Pearse J.S.;
Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema.";
Evolution 55:955-975(2001).
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Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.4%; Score 17; DB 8; Length 9; Best Local Similarity 57.1%; Pred. No. 6.7e+05; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
EMBL: AY012858; AAL33832.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER 1 1 SEQUENCE 9 AA; 1115 MW; BDF8DB1B173B46CA CRC64;
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Last sequence update)
Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Cytochrome oxidase subunit II (Fragment).
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8 AA; 788 MW; 457451B5A76DDB10 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                    Diadema antillarum.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                 NCBI_TaxID=105358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jurinea humilis.
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SEQUENCE
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                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                        Caskey C.T.H.;

"Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and Commid libraries.";

Hum. Nol. Genet. 0:0-0(1995).

EMBL: L32078; AAA73888.1; -.

ENDL: ER 1 1 1

NON_TER 9 8

SEQÜENCE 8 AA; 938 MW; 34A415B0477B45BB CRC64;
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                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
(clone XP6AllB) (Fragment).
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PRT;
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50.0%;
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Query Match
Best Local Similarity 50.00,
Best Local Similarity 50.00,
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PRELIMINARY;
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Q14277
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SEQUENCE FROM N.A.
STRAIN=G66; TRANSPOSON=TN5037;
Kalyaeva E.S., Kholodii G.Y., Bass I.A., Gorlenko A.M., Yurieva O.V.,
Nikiforov V.G.;
"Th5037, a Th21-like mercury resistance transposon from Thiobacillus
ferrooxidans.";
Russ. J. Genet. 37:972-975(2001).
                                                                                                                                                                                       Viruses; ssRNA posttive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Torovirus.
NCBI_TaxID=11156;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=90080137; PubMed=2293666;

Snijder E.J., Horzinek M.C., Spaan W.J.M.;

Snijder E.J., Horzinek M.C., Spaan W.J.M.;

A 3'-coterminal nested set of independently transcribed mRNAs is generated during Berne virus replication.";

J. Virol. 64:331-338[1990].

EMBL; M33502; AAA42817.1; -.

NON TER
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NCBL_TaxID=920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UTN-2001 (TrEMBLrel. 17, Last annotation update)
Uricase (EC 1.7.3.3) (Urate oxidase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 9 AA, 1234 MW, D8EE736B5451AB19 CRC64;
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Last annotation update)
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Last annotation update)
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larity 66.7%; Pred. No. 6.7e+05;
Conservative 1; Mismatches 0;
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                                         9 AA.
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TEMBLrel. 19, Last ann
                                                                                      Created)
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                                                                                   01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
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                                         PRELIMINARY;
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ses 2; Conserv
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                                                                                                                                                         ORF3 (Fragment)
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O934S4;
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Q65711;
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P82858
ID P82858
AC P82858
DT 01-MAD
DT 01-MAD
DT 01-TAD
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RESULT 8
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MEDLINE=94366755; PubMed=8084609; Ceccherini I., Hofstra R., Yin L., Stulp R., Barone V., Stelwagen T., Bocciardi R., Nijven H., Bolino A., Seri M., Ronchetto P., Pasini B., Bozzano M., Buys C., Romeo G., "DNA polymorphisms and conditions for SSCP analysis of the 20 exons of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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MEDLINE=21250995; PubMed=11352571;
Nakabayashi K., Scherer S.W.;
Nakabayashi K., Scherer S.W.;

Urhe human contactin-associated protein 2 (CNTNAP2) spans over 2 Mb
DNA at chromosome 7q35.";

Genomics 73:108-112 (2001).

EMBL; AF318295; AAK49906.1; -.

NON TER 9 9
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                  Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=94071887; PubMed=7902707;
Ceccherini I., Bocciardi R., Luo Y., Pasini B., Hofstra R.,
Takahashi M., Romeo G.;
"Exon structure and flanking intronic sequences of the human RET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RET protein short form (Fragment).
                                                                                                                                                                                                                                                                                                                                     proto-oncogene.";
Biochem. Biophys. Res. Commun. 196:1288-1295(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contactin-associated protein 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the ret proto-oncogene.";
Oncogene 9:3025-3029(1994).
EMBL; Ull532; AAC50102.1; -.
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                                                                                                                 Homo sapiens (Human).
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hes 3; Conserv
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                                                                                                                                                                            NCBI_TaxID=9606;
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2 ISHAFT 7
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RESULT 7 Q96T78

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STRAIN=991614;
Schmidt B., Walter H., Moschik G., Paatz C., Werwein M., Schwingel E.,
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Kato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.;
Kato K., Shinohara H., Goto S., Inaguma Y., Morishita B., Asano T.;
"Copurification of small mate shock protein with alpha B crystallin from human skeletal muscle.";
J. Biol. Chem. 267:7718-7725 (1992).
NON TER 1 1
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Chloroplast.
Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTM-2001 (TrEMBLrel. 17, Last annotation update)
Ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit
                                                                                                                                                                                                                                                                       "Recovery of HIV-1 pol gene sequences by direct sequencing of amplification products darived from plasma samples."; submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF347458; AAK32535.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.2%; Score 14; DB 15; Length 8; Best Local Similarity 75.0%; Pred. No. 6.7e+05; Matches 3; Conservative 0; Mismatches 1; Indels
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2002 (TrEMBLrel. 11, Last annotation update)
28 kDa heat shock protein homolog fragment 1 (Fragment).
Homo sapiens (Human).
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Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                           NON TER 1 1 1
SEQUENCE 8 AA; 845 MW; 72CDDB1DD736CAE8 CRC64;
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STRAIN=F-I/RGM;
Mage R.G., Chen H.-T., Alexander C.B., Chen F.F.;
Mabit DG52 and DH Gene Rearrangements in Early B-cell Development.";
MOI. Immunol. 0:0-0(1996).
EMBL; U62585; AAB18735.1; -.
EMBL; U62585; AAB18735.1; -.
NON_TER B 8
SEQUENCE 8 AA; 845 MW; SCA861B5ABS8677B CRC64;
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             Puccinia recondita f. sp. triseti.
Eukaryota, Fungi, Basidiomycota, Urediniomycetes, Urediniomycetidae,
Uredinales, Pucciniaceae, Puccinia.
                                                                                                                                                                             SEQUENCE, FUNCTION, AND DEVELOPMENTAL STAGE.
TISSUE-SPORE;
Aguilar M., Montalbini P., Fineda M.;
Submitted (NOV-2000) to the SWISS--ROT data bank.
-1- PUNCTION: INVOLVED IN HOST-PARASITE RELATIONSHIP BETWEEN PLANTS
                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: URATE + O(2) + H(2)O = 5-HYDROXXISOURATE + H(2)O(2) (5-HYDROXXISOURATE DECOMPOSE TO FORM ALLANTOIN).
-!- SUBCELLULAR LOCATION: PEROXISOMAL (BY SIMILARITY).
-!- DEVELOPMENTAL STAGE: GERMINATION.
-!- SIMILARITY: BELONGS TO THE URICASE FAMILY.
Interpre, IPROGOG42; Uricase.
PROSITE; PSO0366; URICASE; PARTIAL.
Oxidoreductase; Purine metabolism; Peroxisome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.2%; Score 14; DB 3; Length 8; 66.7%; Pred. No. 6.7e+05; tive 1; Mismatches 0; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Truncated pol protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Germline DH (Df) gene (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER 8 8 ST 77 MW; 98C1ADD735B9D76D CRC64;
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nes 2; Conservative
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DT 01-JU
DT 01-JU
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GN POL.
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EMBL; AB023384; BAA88918.1; -.
                                 Kamiya M., West J.A., Zucarello G.C., Kawai H.;
"Calogloss intermedia sp. nov. (Delesseriaceae, Rhodophyta),
morphologically intermediate between C. leprieurii and C. monosticha,
from the western Atlantic coast.",
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB030266, BAA90253.1;
EMBL, AB030264; BAA90251.1;
EMBL, AB030265; BAA90259.1;
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Chloroplast.
Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
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09TJ85;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit RAGU.
STRAIN=SOUTH CAROLINA USA, NEW JERSEY USA, AND GEORGIA USA;
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29.2%; Score 14; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 1; Indels
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Similarity 75.0%; Pred. No. 6.7e+05;
3; Conservative 0; Mismatches 1; Indels
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SEQUENCE 9 AA; 977 MW; CAIA4DC1B771AB02 CRC64;
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Best Local Similarity
Matches 3; Conserv
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NCBI_TaxID=88391;
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2 VETP 5

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16.428 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                             US-09-674-716B-7
48
                                                                                                                                                                                                                                                                                                                                                                                                                 1 QQLVEYPFT 9
                                Copyright
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17:
19:
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Perfect score:
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                                                                                                                                 OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
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                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Light chain CDR L3	Light chain CDR3 o	Light chain CDR3 o	Murine 13H10 light	C242:11 MAb kappa	Complementary dete	Humanised antibody	VEGF antagonist an	Anti-human CD154 a	Complementarity de
SUMMARIES	ID	AAY32256	AAW39823	AAW39817	AAY92171	AAR30450	AAY97234	AAE13142	AAB82708	AAB82896	AAG63993
	DB	21	19	19	21	14	21	22	22	22	22
	Query Match Length DB	6	6	σ	0	σ	σ	0	6	6	σ
æ	Query	100.0	91.7	, 75.0	70.8	68.8	64.6	64.6	64.6	64.6	64.6
	Score	4.8	44	36	34	33	31	31	31	31	31
;	Regult No.	Н	7	m	4	ស	9	7	60	O	10

Light chain comple Mouse PAF receptor Light chain CDR3 o Light chain CDR3 o Human immunoglobul CDR3 of light chain Light chain CDR3 b Light chain CDR3 b	Light chain variab Amino acid sequenc Peptide fragment f Humanised anti-CDI Mouse ganglioside Hepatitis C virus Hepatitis C virus	Hepatitis C virus CDR-3 of rWI2 ligh Light chain CDR3 o Anti-p53 monoclona Humanised antibody ErbB2-reactive VL Humanised Fab vers	Analgesic heptapep Blood triglyceride Peptide fragment o Haemorphin peptide Heptapeptide which Oligopeptide compo Anti-stress agent	Peptide inhibitor Peptide fragment o Haemorphin peptide Peptide fragment o Haemorphin peptide Human anti-tissue Ab2 variable light
	20001244	14 AAR35878 18 AAW33435 19 AAW39877 9 20 AAW89158 9 21 AAY95235 9 22 AAB60407	71117 700 700 700 700 700 700 700 700 70	
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11 12 13 14 15 16	7 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	, 222225 32225 33098		W 4 4 4 4 4 O O H G E 4 D

## ALIGNMENTS

CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; slogren's syndrome; allergy; asthma; rhinitis; eczema; insulitis; graff-vergus-host disease; COPD; bronchitis; diabetes; Light chain CDR L3 of mouse anti-CD23 MAb C11. AAY32256 standard; Peptide; 9 AA. 99WO-GB01434. 98GB-0009839. graft-versus-host disease; B-cell malignancy; therapy (first entry) (GLAX ) GLAXO GROUP LTD. Mus musculus, WO9958679-A1 07-MAY-1999; 09-MAY-1998; 15-FEB-2000 18-NOV-1999 AAY32256; 

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                                                                                                                                          This sequence represents complementarity determinating region 3

(CDR L3) of the light chain of murine anti-CD23 (FCERII) monoclonal

antibodis (1) (see also AAY32262). The invention provides altered
antibodies, such as chimeric or humanised antibodies, which comprise
sufficient of the amino acid sequences of C11 light and heavy chain

CDRs (see AAY32254-59) to render them capable of binding to the CD23

CDRs (see AAY32254-59) to render them capable of binding to the CD23

CDRs (see AAY32254-59) to render them capable of binding to the CD23

CDRs (see AAY32254-59) to render them capable of binding to the CD23

CDRs (see AAY32254-59) to render them capable of binding to the CD23

CDRs (see AAY32254-59) to render them capable of binding to the CD23

CDRs (see AAY32254-59) to render them capable of binding to the CD23

CDRs (see AAY32254-59) to render them capable of binding to the CD23

CDRs (see AAY32254-59) to render them capable of binding to the CD23

CDRs (see AAY32254-59) to render asthmatic exacerbation, rhinitis, capable of particularly chronic bromoditis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful convenience the controls between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzolc acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                        receptor specific antibodies useful for treating e.g. arthritis, etes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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 Shearin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 48; DB 21;
100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
 Rapson NT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Light chain CDR3 of catalytic antibody 2A10.
Ellis JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW39823 standard; peptide; 9 AA.
                                                                                                                     Claim 1; Page 40; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                the binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0672345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US10965
Bonnefoy JMP, Crowe SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                            WPI; 2000-053101/04.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QQLVEYPFT 9
                                           N-PSDB; AAZ34741
                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AA;
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                                                                                        diabetes,
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Matches
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determining regions (CDRs) of the catalytic antibody 2A10, which is able to degrade cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of release 3H-benzola and used to immunise mice for production of release 3H-benzola and used to all-phenyl cocaine. The 2A10 antibody was identified using TSA1, which is an immunogenic conjugate of a phosphate monester transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo
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                                                                                                    AAW39821-23 represent the sequences of the light chain complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variable domain, lambda light chain, catalytic antibody; degradation, cocaine, cocaine transition state analogue; TSA; benzoic acid, phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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smaller doses than antibodies that antagonise cocalne binding
                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 19; Length 5; Pred. No. 7.88+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Light chain CDR3 of catalytic antibody 3B9.
                                                                                                                                                                                                                                                                                                                                            concentration that can be achieved).
                                                              Claim 15; Page 82; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 81; 147pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                              91.7%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overdose; addiction.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      9 AA;
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9 AA;
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QRLEYPFT
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                                                                                                                                                                                                                                                                                                              03-JUL-1992;
                                                                                                                                                                                                                                                                                                                                        03-JUL-1991;
                                                                                                                                                                                                              endocytosis.
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                                                                                                                            06-MAY-1993
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                                                                                                                                                                                                                                       Synthetic.
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identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a pubject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
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                                                                                                                                                                                                                                                                                                                                               Light chain, variable region; complementarity determining region; CDR anti-Tie2 kinase receptor; monoclonal antibody; 15BB; angiogenetic; vascular-general; proliferative; antiischemic; cerebroprotective; cardiant; agonist; antibody inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tie2 receptor agonist antibodies useful for promoting angiogenesis in patients suffering from strokes and myocardial infarctions
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                                                                                                                                       Gaps
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                                                                                                            Score 36; DB 19; Length 9;
Pred. No. 7.8e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                           Murine 13H10 light chain variable region CDR 3.
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                                                                                                                                                                                                                                                 AAY92171 standard; Peptide; 9 AA
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                                                                                                            75.0%;
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                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                       Conservative
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                                                                                                                      Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
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                                                                                         Sequence
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                                                                                                               Query Match
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Gaps
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                                                                                                                                                                                                                         Kappa; chain; heavy; complementarity determining region; CDR; MAb; monoclonal antibody; C242:II; murine; IgG; hybridoma; cell line; spleen; human; colonic; adenocarcinoma; myeloma; Sp2/0; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementary determining region (CDRL3) of anti-SI(KDR) antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody reacting with CA-242 antigen - obtd. by culturing hybridoma cell line C242:11 or mutants, useful for diagnosis and therapy of pancreatic or colorectal cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin; antibody; complementary determing region;
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Pred. No. 7.8e+05;
1; Mismatches 1;
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AAR30450 standard; peptide; 9 AA.
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                                                                                                                                                                      C242:11 MAb kappa chain CDR3.
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ilarity 75.0%;
Conservative
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                                                                                                              (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; light chain hypervariable region; VL; myelocytic leukaemia; lymphCcytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; complementarity determining region-3; CDR-3; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel immunoglobulin molecules binding kinase insert domain-containing receptor with the same affinity as vascular endothelial growth factor, used to reduce tumour growth
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VEGF; vascular endothelial growth factor; KDR; kinase insert domain containing receptor; multivalent; monovalent; humanised antibody; chimeric antibody; tumour; diabody; triabody; glioblastoma multiforme; hemangioblastoma; ADS; central nervous system neoplasms; AIDS associated Karposi's sarcoma; acquired immune deficiency syndrome; AIDS; human.
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                                                                                                                                                                                                                                                                                                                   99US-0240736.
                                                                                                                                                                                                                                                           28-JAN-2000; 2000WO-US02180
                                                                                                                                                                                                                                                                                                                                                      (IMCL-) IMCLONE SYSTEMS INC.
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                                                                                                                                                                                                                                                                                                                                                                                          Zhu Z, Witte L;
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                                                                                                                                                                                    WO200044777-A1.
                                                                                                                                  Homo sapiens.
Synthetic.
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Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -

(IMCL-) IMCLONE SYSTEMS INC. (CORR ) CORNELL RES FOUND INC. 31-MAR-2000; 2000US-0540770. 30-MAR-2001; 2001WO-US10504.

WPI; 2001-662942/76. N-PSDB; AAD21668.

Witte L, Rafii S;

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The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised VEGFR monoclonal antibodies of antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to antibody murine light chain hypervariable region (VL) CDR-3 used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF; vascular endothelial growth factor; angiogenesis; antiangiogenic; antitumour; neoplasm; collagen-vascular disease; autoimmune disease; tumour; breast carcinoma; lung carcinoma; prostate carcinoma; colon carcinoma carcinoma; neuroblastoma; glioblastoma multiforme; melanoma; therapy; light chain; CDR; complementarity determining region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.6%; Score 31; DB 22; Length 9; 66.7%; Pred. No. 7.8e+05; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 15; 68pp; English.
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Chimeric - Homo sapiens.
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CD154 binding molecule, in particular antibody to human CD154 for use in treatment, prevention of autoimmune, inflammatory diseases, atherosclerosis, Alzheimer's disease and prevention of transplant

(NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

Schuler W;

Di Padova FE,

WPI; 2001-590062/66.

rejection

14-MAR-2001; 2001WO-EP02875. 16-MAR-2000; 2000GB-0006398

20-SEP-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD154; gp39; CD40-L; antibody; ABI793; transplant rejection; autoimmume disease; inflammation; atherosclerosis; Alzheimer's disease; antiinflammatory; antiarteriosclerotic; immunosuppressive; therapy; complementarity determining region;
                                                                                                                                                                                                                                                                                            Treating or controlling an angiogenic dependent condition (e.g. neoplasm, collagen-vascular or autoimmune disease) in mammal by administering a combination of an antiangiogenic molecule and a
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Pred. No. 7.8e+05;
0; Mismatches 3; Indels
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                                                                                                                                                      (SUNN-) SUNNYBROOK HEALTH SCI (IMCL-) IMCLONE SYSTEMS INC.
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Best Local Similarity 66.7%;
Matches 6; Conservative
                                                       29-JAN-2001; 2001WO-US02839.
                                                                                                2000US-0178791
                                                                                                                 31-MAR-2000; 2000US-0539692
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                                                                                                                                                                                                                                                                                                                                                         chemotherapeutic agent
                                                                                                                                                                                                                                                         WPI; 2001-514531/56.
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                02-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interactions is therefore the first interaction of interactions is therefore the first interactions is therefore the first interaction of macrophage associated inflammatory processes and in the treatment of diseases where suppression of antibody responses to antigens is prevention of call, The CD154 binding molecules are useful for prevention of call, tissue or organ graft rejection, in the prevention and treatment of autofimmune or inflammatory diseases, atheroselerosis or Alzheimer's disease, and also for inhibiting sell proliferation of B or B or all tolerance or inhibition of the growth of tumour calls expressing CD154 antigen. Such conditions include autoimmune and non-autoimmune disorders, in particular, Addison's disease, Celiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of complementarity determining region 3 (CDR3) of the light chain variable region (VL, see also AAB82890) of mouse anti-human CD154 monoclonal antibody ABI793. The invention provides a CD154 binding molecule, in particular an antibody to ABI793 VH and the VI region has the CDR1, CDR2 and CDR3 of ABI793 VH and the VL region has the CDR1, CDR2 and CDR3 of ABI793 VL. The CD154 binding molecule is especially a human antibody in which the VH and VL domains are essentially those of ABI793, with constant regions from human heavy and light chains. The antibodies are used to inhibit an immune response mediated by CD154-Positive cell interactions with CD40-positive cells, in the treatment and/or modulation and/or interference with or inhibition of the CD154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sprue, glomerulonephritis, Grave's disease, Hashimoto's thyroiditis, demonlytic disease of the newborn, Keratitis, multiple sclerosis, polymyositis, psoriasis, rheumatic fever, rheumatoid atrhritis, sarcoidosis, syphilis, tuberculosis, ulcerative colitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity determining region of light chain of antibody 2C4.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG63991-93 represent the complementarity determining regions (CDRs) of the light chain variable region of murine monoclonal antibody 2C4. This antibody binds to human sialoadhesin factor-2 (SAF-2). The antibody is useful for treating or preventing allergic rhinitis, allergies, asthma, anemia, eczema or diseases such as lymphoma, leukemia or systemic mastocytosis in a mammal. It is also useful for detecting the presence of a call, especially ecsinophil in a sample, by detecting binding of the antibody to SAF-2. The antibody can be coupled to toxins, antiproliferative drugs or radionuclides to kill cells in areas of excessive SAF-2 expression.
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allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
leukemia; eosinophil.
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Pred. No. 7.8e+05;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 34; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. (UYJO ) UNIV JOHNS HOPKINS.
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Abrahamson JA,
                                                                                                                                                    WO200166126-A1
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                                                                                                                                                                                                              13-SEP-2001
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                                                                                          Mus sp
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   NAMES OF STREET 
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The invention describes an antigen-binding protein (I) comprising a complex of two polypeptides (PI) and two second polypeptides (P2) which are stably associated in an immunoglobulin like complex. Pl has an antigen-binding site located to the N terminus of immunoglobulin (Ig) light chain constant domain (CL domain), and P2 has an antigen-binding site located to the N terminus of the CH1 domain. (I) is useful for:

CC site located to the N terminus of the CH1 domain. (I) is useful for:

CC reducing the activation of a vascular endothelial growth factor

CC (VEGF) receptor; reducing tumour growth; inhibiting angiogeneais;

CC reducing endothelial cell proliferation; inhibiting upgGF induced

CM migration of human leukaemia cells; blocking interaction of a protein and its ligand, promoting interactions between immune cells and target cells; and in vivo and in vitro for investigative, diagnostic or treatment companies. The design of (I) provides for efficient production so that substantially all of the antigen-binding proteins produced are assembled in the desired configuration. (I) is bivalent and bispecific, homogeneous compinement for provide other antibody functions can be present. There is no requirement for provessing in vitro to obtain the complete product. This peptide sequence represents the light chain variable domain companies or complementarity determining region 13 (CDRL3) incorporated into an extra antigen-binding protein described in the method of the invention.
                                                                                                                                                             New bispecific immunoglobulin-like antigen-binding protein for reducing tumour growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDR; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse PAF receptor antibody light chain hypervariable region CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin light chain; hypervariable region; PAF; CDR; antiplatelet activating factor receptor; murine; chimeric; anti-PAF; complementarity determining region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB 23; Length 9; Pred. No. 7.8e+05; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.6%; Scur-
66.7%; Pred
0; F
                                                                                                                                                                                                                                         Claim 55; Page 57; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW59175 standard; Protein; 9 AA.
 24-MAY-2000; 2000US-206749P.
                                      (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96JP-0317047.
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Best Local Similarity 66.7-
6; Conservative
                                                                                                           WPI; 2002-106189/14.
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                                                                                                                          N-PSDB, AAS20282
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AAW59175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          simply binding
                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                               WO9749800-A1
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                                                  Sequence
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                                                                                                This sequence represents the complementarity determining region (CDR) 3 of the light chain hypervariable region of an antibody recognising the platelet activating factor (PAF) receptor. The variable region of mouse anti-PAF receptor monoclonal antibody is useful for the preparation of chimeric antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                   Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid; phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
                                            Polypeptide comprising variable region of antibody recognising PAF receptor - useful for the preparation of chimeric antibody
                                                                                                                                                                                                                   ó
                                                                                                                                                                                             Length 9;
                                                                                                                                                                                         Score 30; DB 19; Length 9;
Pred. No. 7.8e+05;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                Light chain CDR3 of catalytic antibody 6A12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 82; 147pp; English.
                                                                             Claim 2; Page 10; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                AAW39820 standard; peptide; 9 AA.
(SUME ) SUMITOMO ELECTRIC IND CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COLUMBIA NEW YORK.
                                                                                                                                                                                         62.5%;
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                                                                                                                                                                            Cuery Match
Best Local Similarity 66.79,
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                        WPI; 1998-355043/31
                                                                                                                                                                                                                                                                                                                                                                                                                                        overdose; addiction
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                                                                                                                                                                                                                                                          1 QOYNTYPFT 9
                                                                                                                                                                    9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           simply binding
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subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variable domain, lambda light chain, catalytic antibody, degradation, cocaine, cocaine transition state analogue, TSA, benzoic acid, phenyl cocaine, immunogenic conjugate, reduction, cocaine, treatment;
                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by
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                                                                                                                                                                     ; Score 30; DB 1
; Pred. No. 7.8e+
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Light chain CDR3 of catalytic antibody 12H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; Page 83; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW39826 standard; peptide; 9 AA.
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                                                                                                                                                                        62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0672345.
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                                                                                                                                       Query Match
Best Local Similarity 55.00,
100 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           overdose; addiction.
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1 QHFEDYPFT 9

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A novel composition has been developed which comprises an immunoglobulin (Ig) having an affinity constant (Ka) of at least 2 multiply (100000000 M-1 for binding to a predetermined human antigen. The present sequence represents a human light chain CDR3 region peptide which forms part of an immunoglobulin comprising a VkL15 segment, and the present light chain CDR3 region. The articD4 antibodies may be used in therapeutic and diagnostic applications, especially for the treatment of human diseases. These antibodies reduce activity of CD4 cells and reduce undesirable autoimmune reactions, inflammatory response and transplant rejection. Transgenic animals are capable of producing heterologous antibodies of multiple isotypes by undergoing isotype switching. These animals of multiple isotypes by undergoing isotype switching. These animals conduce a first Ig type that is necessary for antigen-stimulated B-cell maturation and can switch to encode app produce one or more subsequent conducts.
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                                                                                                                                                                         Ig; affinity constant; human; antigen, hybridoma; B cell; transgene; transgenic; mouse; CD4; antibody; autoimmune; inflammatory; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel anti-CD4 antibody produced by transgenic mice - used in the treatment of auto-immune disease etc.
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                                                                                                                                       Human immunoglobulin light chain CDR3 region peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 60; Page 287; 396pp; English.
                                 AAW24776 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                          96WO-US16433
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                                                                                                    03-DEC-1997 (first entry)
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Matches 5; Conservative
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                                                                                                                                                                                                                                                  Homo sapiens
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                                                                    AAW24776;
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RESULT 15
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Search completed: April 22, 2003, 13:30:30 Job time : 74 secs

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Sequence 6, Appli
Sequence 6, Appli
Sequence 51, Appl
Sequence 16, Appl
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Sequence 6, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 16, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
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Sequence 15, Appl
Sequence 16, Appl
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Sequence 5, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                         April 22, 2003, 13:31:41 ; Search time 41 Seconds (without alignments) 17.589 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT NEW FUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USOB PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USOB PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USOB PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-865-198-6

US-09-288-708-51

US-10-091-236-16

US-10-091-313-6

US-09-155-106-6

US-09-155-106-6

US-09-293-854-7

US-09-996-288-16

US-09-996-288-16

US-09-9977-797A-62

US-09-977-797A-62

US-09-808-037-17

US-09-808-037-17

US-09-808-037-19

US-09-808-037-19

US-09-808-037-19

US-09-808-037-19

US-09-808-037-19

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US-09-808-037-19

US-09-808-037-19

US-09-771-415-15

US-09-771-415-15
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Maximum Match 100%
Listing first 45 summaries
                                                               sw model
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Gapop 10.0 , Gapext 0.5
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                                                               OM protein - protein search, using
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Match Length
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88:
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111:
13:
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No.
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Sequence 6, Appli	Seguence 61, Appl	Sequence 47, Appl		Sequence 7, Appli	23	Sequence 53, Appl		Sequence 28, Appl	Sequence 20, Appl	Sequence 18, Appl	Sequence 4, Appli	Sequence 50, Appl	Sequence 61, Appl		Sequence 4, Appli	~	Sequence 61, Appl	Sequence 19, Appl	Sequence 13, Appl	Sequence 6, Appli	Sequence 1, Appli	Sequence 13, Appl	Sequence 32, Appl		Sequence 26, Appl	
US-09-996-288-6	US-09-996-288-61	US-10-144-644-47	US-10-144-644-48	0 US-09-796-848A-7	0 US-09-796-848A-23	US-09-782-672-53	US-10-144-644-12	0 US-09-910-059-28	₽	0 US-09-808-037-18	0 US-09-809-739-4	0 US-09-974-449-50	US-09-423-800-61	US-09-875-221A-6	US-10-015-535-4	US-09-269-921-5	US-10-182-018-61	0 US-09-286-240-19	_	0 US-09-949-559-6	0 US-09-434-965-1	0 US-09-870-472-13	US-10-046-801-32	US-09-900-590-88	US-09-782-672-26	
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2.1	2.1	52.1	7.7	7.	52.1	0.	0.0	50.0	6.7	47.9	6.7	7.9	5.8	5.8	8.	5.8	8	8.	ω. 8	8.	5.8	3.8	3.8	43.8	3.8	
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25	25	25	25	25	25	24	24	24	23	23	23	23	22	22	22	22	22	22	22	22	22	21	21	21	21	
20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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Sequence 6, Application US/09865198

Sequence 10. US20020103345A1

Setent No. US20020103345A1

SETENT INFORMATION:

TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methory TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102

CURRENT APPLICATION NUMBER: US/09/865,198
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              Sequence 6, Application US/09976787

Sequence 6, Application US/09976787

Patent No. US20020064528A1

GENERAL INFORMATION:

APPLICANT: Witte, Larry

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REFERENCE: 11245/46505

CURRENT FILING DATE: 2001-10-12

PRIOR PILITED OF INVENTION NUMBER: US 09/493,539

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARRE: WordPerfect 8:0 for Windows

SETURNO 6

SETURNO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Mus musculus
US-09-976-787-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
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9-181-916-00-SD
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Sequence 6, Application US/10091313

Sequence 6, Application US/10091313

Publication No. US2003004406A1

GENERAL INFORMATION:

HAPLICANT: DINGTVAN, CHRISTINE

TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING INFLAMMATORY OR AUTOIMMUNE

TITLE OF INVENTION: PROPHYLACTIC OR THERAPEUTIC AGENTS

TITLE OF INVENTION: PROPHYLACTIC OR THERAPEUTIC AGENTS

CURRENT APPLICATION NUMBER: US/10/091,313

CURRENT APPLICATION NUMBER: US 60/273,098

PRIOR FILING DATE: 2001-03-02

PRIOR FILING DATE: 2001-03-02

PRIOR FILING DATE: 2001-03-03

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.1

SEQ ID NO 6
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                    Query Match 56.2%; Score 27; DB 9; Length 9; Best Local Similarity 50.0%; Pred. No. 2.7e+05; Matches 4; Conservative 1; Mismatches 3; Indels
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Matches 5, Conservative
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Sequence 16, Application US/10091236

Patent No. US20020168360A1

Sequence 16, Application US/10091236

Fatent No. US20020168360A1

SEQUENCE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION: DISORDERS BY ADMINISTERING INFLAMMATORY OR AUTOIMMUNE

TITLE OF INVENTION: DISORDERS BY ADMINISTERING INTEGRIN ALPHA-V-BETA-3 ANTAGONISTS

TITLE OF INVENTION: COMBINATION WITH OTHER PROPHYLACTIC OR THERAPEUTIC AGENTS

TITLE OF INVENTION: COMBINATION WITH OTHER PROPHYLACTIC OR THERAPEUTIC AGENTS

FURRENT PRILING DATE: 2002-03-04

PRIOR FILING DATE: 2001-03-04

PRIOR FILING DATE: 2001-03-01

PRIOR FILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 51, Application US/09828708

Patent No. US20020146753A1

GENERAL INFORMATION:

APPLICANT: Ditcal, H..

APPLICANT: Burton, D.

APPLICANT: Burton, D.

APPLICANT: Schaller, M.

TITLE OF INVENTION: autoimmune disease

FILE REFERENCE: 1361.005US1

CURRENT APPLICATION NUMBER: US/09/828,708

CURRENT PAILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                    Score 31; DB 10; Length 9; Pred. No. 2.7e+05; 0; Mismatches 3; Indels
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION WINDER: US 60/206,749
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-6
                                                                                                                                                                                                                      64.6%;
                                                                                                                                                                                                                                         Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Homo sapiens
US-09-828-708-51
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; ORGANISM: Mus sp.
US-10-091-236-16
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US-10-091-236-16
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US-09-828-708-51
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Jiao, Jin-an
Esperanza, Nieves
Lawrence, Luepschen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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CITY: Boston
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54.2%; Score 26; DB 9; Length 9;
Best Local Similarity 55.6%; Pred. No. 2.7e+05;
Matches 5; Conservative 1; Mismatches 3; Indels
                            Score 27; DB 9; Length 9; Pred. No. 2.7e+05; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,854
FILING DATE: 16-Apr-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/814,806
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: COTIESB, PEEER F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFRAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: N-terminal ONIGINAL SOURCE: SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-09-293-854-7
                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09293854
Patent No. US20020168357A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDENESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                            h 56.2%;
Similarity 50.0%;
4; Conservative 1
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MA
COUNTRY: USA
                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QOVYSSPFT 9
                                                                                                                       2 QLVEYPFT 9
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US-09-996-288-16
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US-09-293-854-7
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Publication No. US20030068320A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS OF ADMINISTERING/DOSING CD2 ANTAGONISTS FOR THE PREVENTIC

TITLE OF INVENTION: AND TREATMENT OF AUTOIMMUNE DISORDERS OR INFLAMMATORY DISORDERS
TITLE OF INVENTION: AND TREATMENT OF AUTOIMMUNE DISORDERS OR INFLAMMATORY DISORDERS
TITLE OF INVENTION: AND TREATMENT OF AUTOIMMUNE DISORDERS
TITLE OF TRICK TO TOWNER: US/10/091,268
CURRENT APPLICATION NUMBER: US 60/273,098

PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02

PRIOR FILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PALENTIN VETSION 3.1

SOFTWARE: PALENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                     HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS
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                       56.2%; Score 27; DB 9; Length 9; 50.0%; Pred. No. 2.7e+05; Live 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOE
TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
NUMBER OF SEQUENCES: 45
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,106
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-WAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-WAR-1996
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                      US-09-155-106-6
; Sequence 6, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
Query Match
Best Local Similarity
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US-10-091-268-6
                                                                                                                2 OLVEYPFT 9
                                                                                                                                                                2 QFTHYPYT 9
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5 EYPYT 9
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US-10-091-268-6
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Sequence 17, Application US/09808037

Facence 17, Application US/09808037

Facence 17, Application US/09808037

GENERAL INFORMATION:

APPLICANT: SOLOMON, Beka

APPLICANT: SOLOMON, BERA

TITLE OF INVENTION: NETHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF

TITLE OF INVENTION: NETHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF

TITLE OF INVENTION: NETHODS AND COMPOSITIONS FOR THE REPERRICE SOLOMON=2D

CURRENT APPLICATION NUMBER: US/09/608,037

CURRENT APPLICATION NUMBER: US 09/473,653

PRIOR FILING DATE: 1999-12-29

PRIOR FILING DATE: 1999-12-29

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Version 3.0

TEMPLICATION OF THE PATENCE 
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Sequence 19, Application US/09808037
Patent No. US30020052311A1
GENERAL INFORMATION:
APPLICANT: SOLOMON, Beka
TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
TITLE OF LINGATION NUMBER: US/09/808,037
CURRENT FILING DATE: 2001-03-15
CURRENT FILING DATE: 2000-07-31
PRIOR PPLICATION NUMBER: US/05/971
PRIOR FILING DATE: 2000-07-31
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Pred. No. 2.7e+05;
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Pred. No. 2.7e+05;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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           PRIOR APPLICATION NUMBER: 09/129,026
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 08/905,825
PRIOR FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 136
SOFTWARE: Patentin version 3.1
SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                 54.2%;
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62.5%;
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Matches 5; Conservative
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Matches 5; Conservative
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ORGANISM: Homo sapiens
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US-09-808-037-19
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Sequence 16, Application US/0996288

Patent No. US20020177126A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Young, James
APPLICANT: Lealie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTMARE: Patentin version 3.1
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US-09-977-797A-62
; Sequence 62, Application US/09977797A
; Publication No. US20030044772A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Wu, Herren
; TILE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
; TILE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
; FILE OF INVENTION: METHOD STE: 2002-06-25
; CURRENT APPLICATION NUMBER: US/09/977,797A
; CURRENT FILING DATE: 1998-08-04
; PRIOR FILING DATE: 1998-08-04
; PRIOR FILING DATE: 1998-08-04
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 62
LENGTH: 9
: LENGTH: 9
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US-09-977-797A-66
US-09-977-797A-66

Sequence 66, Application US/09977797A

Sequence 66, Application US/09977797A

SERNERAL INFORMATION:

APPLICANT: Watkins, Jeffrey D.

APPLICANT: Wu, Herren

TITLE REPRENCE: AME-06805

CURRENT APPLICATION NUMBER: US/09/977,797A

CURRENT FILING DATE: 2002-06-25
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Pred. No. 2.7e+05;
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62.5%;
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Best Local Similarity 62.5
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Best Local Similarity 55...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-996-288-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-797A-62
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LENGTH: 9
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; Sequence 2, Application US/0994078
; Publication No. US20030032774A1
; GENERAL INFORMATION:
; APPLICANT: BROWN, WILLIAM
; APPLICANT: BROWN, WILLIAM
; APPLICANT: MARTEL, PETER
; APPLICANT: MARTEL, PERRE
; APPLICANT: MARTEL, PIERRE
; APPLICANT: MARTEL, DIANE
; APPLICANT: MARTER, DIANE
; TILE REFERENCE: MS/81823/282437
; CURRENT APPLICATION NUMBER: 09/159,518
; PRIOR FILING DATE: 1998-09-11-26
; PRIOR FILING DATE: 1998-09-13
; PRIOR FILING DATE: 1996-10-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PATENT IN VET: 2.1
; SEQ ID NO 2
; LENGTH: 4
; TVPE: DET
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ORGANISM: Artificial Sequence
FATURE:
CHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-994-078-2
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PRIOR FILING DATE: 1999-12-29
PRIOR PELICATION NUMBER: US 60/152,417
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
LENGTH: 9
                                                                                                                                                                                                                                     ; OTHER INFORMATION: synthetic peptide US-09-808-037-19
                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-994-078-2
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Search completed: April 22, 2003, 13:39:11 Job time : 42 secs

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/ Match 91.7%;
Local Similarity 88.9%;
nes 8; Conservative (
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: New York
RY: USA
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CITY: New
STATE: Ne
Query Match
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RESULT
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26, Appl
26, Appl
26, Appl
24, Appl
30, Appl
31, Appl
31,
                                                                                              April 22, 2003, 13:29:16 ; Search time 14 Seconds (without alignments) 18.915 Million cell updates/sec
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Sequence 1,
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': /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

'cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

'cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

': /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

': /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

': /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

': /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
       GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-214-095D-27

US-09-214-095D-21

US-09-214-095D-21

US-09-406-532-20

US-08-46-033-26

US-08-464-033-26

US-08-672-345C-34

US-08-672-345C-34

US-08-672-345C-34

US-08-672-345C-30

US-08-672-345C-30

US-08-114-095D-24

US-08-114-095D-30

US-08-144-095D-30

US-08-974-899-15

US-08-974-899-15

US-08-974-818-362

US-08-974-818-362

US-08-444-818-363

US-08-444-818-363

US-08-444-818-363

US-08-444-818-363

US-08-444-818-363

US-08-444-818-363

US-08-444-818-363

US-08-170-769A-24

US-08-170-769A-24

US-08-170-769A-24

US-08-515-882A-7

US-08-515-882A-7

US-08-515-882A-7
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                                                                                                                                                                                                                                                                                                                                262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                             US-09-674-716B-7
48
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Match Length
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Pred. No. 1.9e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATION
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, Ubn P
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0525
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHRARACTERISTICS:
LENGTH: 9 amino acids
TWO TELEPHONE: AND ACTUAL SECOND ACTUAL SECON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION
GENERAL INVENTION
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
             US-09-052-546-6
US-08-55-827-17-5
US-08-114-806-7
US-08-114-806-7
US-08-114-806-7
US-08-114-806-7
US-08-150-260A-521
US-08-350-260A-521
US-08-467-420A-49
US-08-467-420A-49
US-08-470-110A-48
US-08-470-110A-48
US-08-470-110A-48
US-08-470-110A-48
US-08-470-110A-48
US-08-470-110A-48
US-08-677-763A-47
US-08-677-763A-47
US-08-677-763A-47
US-08-677-763A-47
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US-09-214-095D-27

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Gaps
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Pred. No. 1.9e+05;
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                 RESULT 4
US-09-214-095D-21
Sequence 21, Application US/09214095D
Sequence 21, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
TITLE OF INFORMATION:
TITLE OF INFORMATION:
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-438-123-3
; Sequence 3, Application US/08438123
; Sequence 3, ES52293
; Patent No. 5552293
; PAPLICANT: Lindholm et al APPLICANT: Lindholm et al TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
70.8%; Score 34; DB 4; I
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 1; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-406-532-20

| Sequence 20, Application US/09406532A
| Patent No. 6365154
| GENERAL INFORMATION:
| APPLICANT: Connie L. Erickson-Miller
| APPLICANT: Stephen D. Holmes
| APPLICANT: James D. Winkler
| TITLE OF INVENTION: TIE2 Agonist Antibodies
| FILE REFREENCE: P50843
| CURRENT APPLICATION NUMBER: US/09/406,532A
| CURRENT APPLICATION NUMBER: 60/102,098
| PRIOR RPLING DATE: 1998-09-28
| NUMBER OF SEQ ID NOS: 21
| SOFTWARE: FeatSEQ for Windows Version 3.0
| SEQ ID NO 20
| LENGTH: 9
                                                                                                                                                                                                                                                                                                                                        75.0%; Scc...
v 66.7%; Pred. No. 1...
... 1; Mismatches
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COTHER INFORMATION: light chain CDR 3
US-09-406-532-20
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Murinae gen.sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QQLVEYPFT 9
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2 QRLEYPFT 9
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                                                                                                                                                                                                                                            SEQ ID NO 21
LENGTH: 9
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                                                                                                                                                                                                                                                                                                 Score 44; DB 4; Length 9; Pred. No. 1.9e+05; 0; Mismatches 1; Indels
Sequence 27, Application US/09214095D
Sequence 27, Application US/09214095D
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILICATION NUMBER: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Flogby disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 0575/51400
TELECOMMUNICATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.7%;
88.9%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: 81
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              🖈 1 QOLVEYPFT 9
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1 QHFVDYPFT 9
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Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                      66.7%; Score 32; DB 1; Length 9; 62.5%; Pred. No. 1.9e+05; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
COMPUTER: EN PC Compatible
CORRENT MAPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFRERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/08672345C
Patent No. 5948658
GENERAL INFORTION:
APPLICANT: Landary Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
          NOVOP/106A/7551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: L185 Avenue of the Americas CITY: New York COUNTRY: USA ZIP: USA ZIP: USA ZIP: USA ZIP: USA
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                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
  REFERENCE/DOCKET NUMBER: NOV TELECOMNUNICATION: TELEPHONE: (416) 868-1482 TELEPHONE: (416) 362-0823 INPORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.5%;
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Best Local Similarity 62.5%;
....hes 5; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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US-08-672-345C-30
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US-08-672-345C-24
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GENERAL INFORMATION:
APPLICANT: Michael D. Dan
ITITE OF INVENTION: HUMAN MONOCICONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Adelaide Centre
CITY: Toronto
STREET: 101 Richmond Street West
CITY: Toronto
STREET: Diskette - 3.5 inch, 1.4 Mb storage
COUNTRY: Canada
ZIP: MSH 221 FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
APPLICATION NUMBER: US/08/264,093
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0
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PRIOR APPLICATION DATA: No. 5639863 applicable ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
'ADDRESSEE: Lowe, Price, LeBlanc & Becker STREET: Suite 300, 99 Canal Center Plaza CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                FILLING MALE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/906,350
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: J.G. Mulline
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 149-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
                                                                                                                   ZIP: 22314
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,123
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/08264093
Patent No. 5639863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: Polypeptide US-08-438-123-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                       STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QHLEYPFT 9
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Gaps . 0

us-09-674-716b-7.closed.rai

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Score 30; DB 4; Length 9; Pred. No. 1.9e+05; 1; Mismatches 3; Indels
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Pred. No. 1.9e+05;
                             RESULT 11
US-09-214-095D-30
Sequence 30, Application US/09214095D
Sequence 30, Application US/09214095D
Sequence 30, Application US/09214095D
Sequence 30, Application
Three of the sequence 30, Application
TITLE OF INFORMATION:
TITLE OF INFORMATION:
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT APPLICATION NUMBER: US/09/214,095D
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ALLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
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Sequence No. 5830470

GENERAL INFORMATION:

APPLICANT: NATAMURA, KAZUYASU

APPLICANT: SHITARA, KENYA

APPLICANT: SHITARA, KENYA

APPLICANT: HABAI, NOBUO

APPLICANT: HABAI, NOBUO

TITLE OF INVENTION: HUMANIZED ANTIBODIES

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON A. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32,955
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SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
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55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 55.6
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QQLVEYPFT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 30
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10

US-09-214-095D-24

; Sequence 24, Application US/09214095D

; Patent No. 6280967

; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TILL OF THE OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                             CUDNICAT: USAN

ZIP: 10036

COMPUTER READABLE FORM:
MEDILUM TYPE: Floppy disk
COMPUTER: END FO Compatible
COMPUTER: END FO Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLESSIFICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLESSIFICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLESSIFICATION NUMBER: US/08/672,345C
FILING DATE: 21-JUN-1996
CLESSIFICATION NUMBER: US/075/51400
FEGISTRATION NUMBER: US/075/51400
FELEFRATION UND US/075/51400
FELEFRATION UND US/075/51400
FELEFRATION US/075/51400
FELEFRA
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CHFEDYPFT 9
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LENGTH: 9
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Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/08974899;
Patent No. 6037454
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
HUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                  APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SECURCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
CONTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSENT APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION NUMBER: 0386
TELEFERM: (703)816-4000
THELEFMX: (703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winfratin (Genericch)
CURRENT APPLICATION NUMBER: US/08/974,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 91014R1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 99: SEQUENCE CHARACTERISTICS: LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.0
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide US-08-483-528B-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rypE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QOLVEYPFT 9
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        APPLICANT:
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Pred. No. 1.9e+05;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIREET: ILON NORTH GLEBE KOAD
CITY: ARLINGTON
STATE: VIRGINIA
COMPUTER TRADABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: QS-93
CLASSIFICATION: QS-93
CLASSIFICATION: WARY J.
REGISTRATION: WARY J.
REGISTRATION: WARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELERDHONE: (703)816-4000
TELERDHONE: (703)816-4000
                                                                                                                                                                          Sequence 11, Application US/08438562
Patent No. 5874255
GENERAL INFORMATION:
APPLICANT: NAKAWURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HANBAA, VOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-481-528B-99
US-08-481-528B-99
Sequence 99, Application US/08483528B
Patent No. 5939532
APPLICANT: NARAWURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
                                                                                                                                                                                                                                                                                                                                                                                                                           3: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 55.6
Matches 5; Conservative
  5; Conservative
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MOLECULE TYPE: peptide

US-08-438-562-11
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3Y: linear
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                                         1 QQLVEYPFT 9
                                                                            1 QORSSYPYT 9
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Matches
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                                                                                                                                                                                                                                                                                           Search completed: April 22, 2003, 13:32:17
Job time : 15 secs
TELEPHONE: 650/225-1994

TELEPAX: 650/952-9881

INPORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
ILENGTH: 9 amino acids
TYPE: Amino Acid
US-08-974-899-15
                                                                                                                                                                                                               1 QQLVEYPFT 9
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April 22, 2003, 13:38:27 ; Search time 43 Seconds (without alignments) 11.178 Million cell updates/sec
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                      Run on:
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US-09-674-716B-9 33 1 GYWMS S Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

206 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: * PIR Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description sult Query No. Score Match Length DB

***************************************	dut nentanentide	cholecystokinin-5	globulin IV alpha	Ig heavy chain CRD	bradykinin-potenti	RPCH-related neuro	. T-cell receptor be	T-cell receptor be	Φ	ote	Iq heavy chain CRD	T-cell receptor be		gene p20K protein	in-I	eir	imbrial re	X-like or	hypoxanthine phosp	Leu-enkephalin - b	Met-enkephalin - b	cocoonase (EC 3.4.	dulati	carbon-monoxide de	COI intron 16 prot	heavy chain	- 6	a)	TRH-like tripeptid
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	JH0253	A32516	S09478	PT0308	F37196	A34626	B53284	PT0661	A60803	G37196	PT0281	PT0729	PT0580	150412	A32480	870154	B37325	140469	A37114	B61445	A61445	B61168	GKHU	PL0140	I38888	PT0278	869237	A22565	A43391
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	9.09	48.5	39.4	39.4	33.3	33.3	33.3	33.3	33.3	33.3	33.3	33.3	33.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	٠	•	4.	24.2	٠	21.2	٠
	20	16	13	13	:	11	11	11	11	11	11	;	11	σ	თ	σ	σ	o	თ	σ	o ·	σ	ω	œ	ω	æ	ထ	7	7
	н	7	e	4	ហ	9	7	ω .	σ		11	12	13	14	15	16	17		19									28	29

blood cell protein tyrosine-melanocyt	phenol 2-monooxyge protamine P1 - ora Ig heavy chain CRD	ly ma chain v regiptoremine Pl - Cer protamine Pl - Ger protamine Pl - Bav protecolin - Americ ribosomal protein	ribosomal protein ribosomal protein major protein	<pre>x-pnycoerythin ga angiotensin-conver photosystem I 10.4</pre>
3 3 S68328 4 2 A32039	4 2 A37832 4 2 I61883 4 2 PT0240 4 2 S43959	4 2 137013 4 2 137013 5 1 HOROHA 5 2 139964	5 2 139966 5 2 139965 5 2 E60274	5 2 PQ0009 5 2 PQ0689
7 21.2	7 211.2 7 211.2 7 21.2		7 21.2	7 21.2 7 21.2
30	2 6 6 6 2 6 4 6	9 3 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 4 4 0 4 6 4	4 4 5 4 0

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Guraches Anguilla japonica (Japanese eel)
C.Species: Anguilla japonica (Japanese eel)
C.Species: Anguilla japonica (Japanese eel)
C.Species: Anguilla japonica (Japanese eel)
C.Accession: Ji-Mar. 1992 #sequence_revision 31-Mar. 1992 #text_change 11-Apr. 1995
C.Accession: JH0253
R.Juseaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A.Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A.Accession: JH0253
A.Accession: J
RESULT 1
```

Score 20; DB 2; Length 5; Pred. No. 2.8e+05; 1; Mismatches 0; Indels

Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative 1 1 GFW 3 1 GYW 3 ઠ g

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Gaps

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RESULT 2

cholecystokinin-5 - dog N;Alternate names: CCK-5

Nightermace names: C.C.-3 C;Species: Canis lupus familiaris (dog) C;Species: Canis lupus familiaris (dog) C;Species: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000 C;Accession: A32516 Ashively, J; Reeve Jr., J.R; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H A.Pitle: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intest A;Reference number: A32516; MUID:87153871; PMID:3826354 A;Mocession: A32516 A;Molecule type: protein A;Molecule type: protein A;Molecule type: protein A;Residues: 1-5 <ABIL> C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecyston C;Superfamily: qastrin C;Superfamily: qastrin C;Keywords: amidated carboxyl end; neuropeptide F;S/Modified site: amidated carboxyl end (Phe) #status experimental

Gaps ö Query Match 48.5%; Score 16; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels

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2 WM 3 g

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RPCH-related neuropeptide - ferruginous spindle
C;Species: Fusinus ferrugineus (ferruginous spindle)
C;Species: Fusinus ferrugineus (ferruginous spindle)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C;Accession: A34626
R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
Biochem. Biophys. Res. Commun. 167, 273-279, 1990
A;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A;Reference number: A34626; MUID:90179762; PMID:2310394
A;Accession: A34626
A;Accession: A34626
A;Accession: A34626
C;Keywords: neuropeptide
C;Keywords: neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C.Accession: B53284
R.Harindranath, N.; Alexander, C.B.; Mage, R.G.
A.O. Immunol. 28, 881-888, 1991
A.Title: Evolutionarily conserved organization and sequences of germline diversity and j
A.Reference number: A53284; MUID:91342695; PMID:1678859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Decession: P70661
R;Feeney, A.J.
C;Accession: P70661
R;Feeney, A.J.
C;Accession: P70661
R;Feeney, A.J.
R;Feeney, A.
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A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C;Keywords: T-cell receptor
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33.3%; Score 11; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 1; Conservat
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-4 < HAR.>
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                    셤
                                                                                                                                                Globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)
NyAlternate names: 11S globulin alpha subunit gamma chain
C;Species: Cucurbita sp. (cucurbit)
C;Species: Cucurbita sp. (cucurbit)
C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
C;Accession: S09478
A;Chmiya, M.; Hara, I.; Matsubara, H.
Plant Cell Physiol. 21, 157-167, 1980
A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and A;Reference number: S09066
A;Reference number: S09066
A;Reference procession: S09478
A;Residues: 1-4 <OHM>
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(Species: Bothrops insularis (island jararaca)
(Species: Bothrops insularis (island jararaca)
(Species: Bothrops insularis (island jararaca)
(Spacession: F37136
(Spacession: 
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Accession: P70308
R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A; Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A; Reference number: P70308
A; Reference number: P70308
A; Reference number: P70308
A; Residues: 1-5 x/AM>
A; Residues: 1-5 x/AM>
A; Residues: 1-5 x/AM>
A; Residues: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.4%; Score 13; DB 2; Length 4; 100.0%; Pred. No. 2.8e+05; tive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 2; Conservative
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Length 5;

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riofli receptor beta chain V-D-J region (120-1J) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: Pr0640; Pr0685; Pr0729
R; Feeney, A.J.
J; Exp. Med. 174, 115-124, 1991
A; Title: Juncilonal sequences of fetal T cell receptor beta chains have few N regions.
A; Recession: Pr0640
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-5 <FES>
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-5 <FES>
A; Experimental source: newborn thymus, strain BALB/c, clone 120-1J
A; Residues: 1-5 <FES>
A; Residues: 1-5 <FES
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: P10580
B;Feeney, A.J.
C;Accession: P10580
B;Feeney, A.J.
C;Accession: P10580
B;Feeney, A.J.
A;Fitle: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: P10580
A;Reference number: P10580
A;Retaus: translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Restimental source: day 19 fetal thymus, strain BALB/C
C;Keywords: T-cell receptor
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A;Experimental source: newborn thymus, strain BALB/c, clone 135-1AG
C;Keywords: T-cell receptor
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                                                                                                                                                  Query Match 33.3%; Score 11; DB 2; Le Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 1; Conservative 0; Mismatches 0;
   A,Residues: 1-5 < YAM>
A,Experimental source: B lymphocyte
C,Keywords: heterotetramer; immunoglobulin
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Best Local Similarity
Matches 1; Conserva
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G37196

Bradykinin-potentiating peptide 7 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C;Accession: G37196
C;Accession: G37196
A;Cintra, A.C.O.; Vieira, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: G37196
A;Accession: G37196
A;Residues: preliminary
A;Molecule type: profein
A;Residues: 1-5 c(IN)
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
C;Speciaes: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0281
R;Yamada, M; Masserman, R; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyaccesion: AG0803

Right D.; Grimmellkhuijzen, C.J.P.

Right D.; Grimmellkhuijzen, C.J.P.

Right D.; Grimmellkhuijzen, C.J.P.

Right Es. 442, 354-358, 1988

A;Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2, a novel neuropeptide from sea anemones.

A;Reference number: A60803; MUID:88222764; PMID:2897223

A;Accession: A60803

A;Molecule type: protein

A;Residues: 1-5 <GRA>

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F;J,Modified site: pyrrolidone carboxylic acid (Gin) #status experimental

F;5/Modified site: amidated carboxyl end (Trp) #status experimental
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Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
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A; Note: stereochemistry of the active form confirmed by chemical synthesis
B; Ishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto
FEBS Lett. 307, 253-256, 1992
A; Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro
(H-Gly-Phe-Ala-Asp-OH).
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N;Contains: achatin-II
C;Species: Achatina fulica (giant African snail)
C;Species: Achatina fulica (giant African snail)
C;Accession: A32480
B;Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sun Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989
A;Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica feru A;Reference number: A32480; MUID:89273551; PMID:2597281
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C.Reywords: D-amino acid
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GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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RB32 LITRU
ACHI ACHFU
GRWM HITMAN
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RE32_LITRU
ID _RE32_LITRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACH1_ACHFU
P35904;
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1 GFF 3
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                                                                                                                                                                                                                                                                        1 GYW 3
                                                                                                              Toxin.
NON TER
SEQUENCE
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2 GFF
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Matches
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sea moses sole (Pardachirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Venom;

MEDLINES-90351557; PubMed=2386615;

Cintra A.C.O., Vieira C.A., Giglio J.R.;

Cintra A.C.O., Vieira C.A., Giglio J.R.;

"Primary structure and biological activity of bradykinin potentiating peptides from Bochrops insularis snake venom.";

J. Protein Chem. 9:221-227(1990)

J. PROTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.

IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.

PIR, G37196, G37196.
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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30-MX-2000 (Rel. 39, Last sequence update)
16-OCT-2000 (Rel. 40, Last annotation update)
16-OCT-2000 (Rel. 40, Last annotation update)
Pardachi II (PXII) (Fragment).
Pardachirus marmoratus (Red sea moses sole).
Pardachirus marmoratus (Red sea moses sole).
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Nooteleostei, Acanthomorpha, Acanthomorpha, Acanthopterygii, Percomorpha, Pleuronectiformes, Soleidei, Soleidae, Pardachirus.
                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
                                                                                                                                                                                                                                                                                                                                                                  Bothrops insularis (Island jararaca) (Queimada jararaca).
Eukaryota, Metazoa, Chordata, Craniata, Verrebrata, Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
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د
                  Score 15; DB 1; Length 5; Pred. No. 1.1e+05; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 11; DB 1; Le
Pred. No. 1.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87057369; PubMed=3782138; Lazarovici P., Primor N., Loew L.M.; Purification and pore-forming activity of polypeptides from the secretion of the Red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ļ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 261:16704-16713(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                     PRT;
                    45.5%;
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                                                           Conservative
                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=31087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8723;
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                                                                                                  1 GYW 3
                                                                                                                                                                                                                                     BOTIN
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                                                                                                                                       GRW
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Best Local S
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P81864;
                                                                                                                                                                                                                                     BPP7 BO'
P30425;
                                                                                                                                                                                              RESULT 3
BPP7_BOTIN
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                                                           Matches
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Achatinacea, Achatinidae, Achatina.
NCBI_TaxID=6530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                      PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
-!- SUBUNIT: MONOMER. IN AQUEDUS SOLUTION EXISTS AS A TETRAMER.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: SCOTE OF THE PARDAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog Lilori electrica. Comparison with the skin peptides from Litoria rubella.",
Aust. J. Chem. 52:639-645(1999).
-I- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
STRAIN=Ferussac; TISSUE=Ganglion;
MEDLINE=89273551; PubMed=2597281;
Kamateni Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
Pelodryadinae, Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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-!- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                      5 AA; 614 MW; 7769C9C9C8100000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.3%; Score 10; DB 1; I
llarity 33.3%; Pred. No. 1.1e+05;
Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                           30.3%; Score 10; DB 1; I
33.3%; Pred. No. 1.1e+05;
iive 2; Mismatches 0;
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Litoria rubella (Desert tree frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 AA.
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                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Local Similarity
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                                                                                                                                                                                                                        NCBI_TaxID=9606;
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P19916;
                                                                                                      GRWM HUMAN
P01157;
                              1 GF 2
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SEQUENCE
                1 GY 2
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                                                                            KESULT 8
GRWM_HUMAN
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PSECH
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Matches
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                                                                                                                                                                                                                                            (H-G1y-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid residue.";

Int. J. Pept. Protein Res. 39:258-264(1992)

Int. J. Pept. Protein Res. 39:258-264(1992)

Int. J. Pept. Protein Res. 39:258-264(1992)

INCREASES THE IMPULSE FREQUENCY AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.

PIR; A32480; A32480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20336815; PubMed=10876044;
Iwakoshi E., Hisada M., Minakata H.;
"Cardioactive peptides isolated from the brain of a Japanese octopus,
                                                                        STRAIN=Ferussac; TISSUE=Heart atrium; MEDLINE=91264856; PubMed=1675568; Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K., Yoshida M., Harada A., Muneoka Y., Kobayashi M.; Fuzification of achatin-I from the atria of the African giant snail, Achatina fulica, and its possible function."; Biochem. Biophys. Res. Commun. 177:847-853(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
"Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
fulica Perusasa containing a D-amino acid residue.";
Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
                                                                                                                                                                                           MEDLINE-93014529; PubMed-1399265;
Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
Ilwashita T., Nomoto K.;
"Crystal structure and molecular conformation of achatin-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS648:

15-UNA-2002 (Rel. 41, Created)

15-UNA-2002 (Rel. 41, Last sequence update)

15-UNA-2002 (Rel. 41, Last sequence update)

15-UNA-2002 (Rel. 41, Last annotation update)

Cardioactive peptides Ocp-1/Ocp-2.

Octopus minor (Octopus).

Bukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;

Incirrata; Octopodidae; Octopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Score 9; DB 1; Length 4; Pred. No. 1.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.3%; Score 9; DB 1; Length 4; 50.0%; Pred. No. 1.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 D-PHENYLALANINE.
4 AA; 394 MW; 6AA879C810000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            4 AA; 408 MW; 6AADD9C81000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
-!- MASS SPECTROMETRY: WW=395.2; METHOD=MALDI.
Hormone; D-amino acid.
                                                                                                                                                                                                                                                                                                                                                                 D-PHENYLALANINE
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R
                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          active than Ocp-1.
                                                                                                                                                                                                                                                                                                                                                                                                       27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Octopus minor.";
Peptides 21:623-630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 27.3
Best Local Similarity 50.0
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                    Hormone; D-amino acid.
                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY
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Matches 1; Conserv
                                                                CHARACTERIZATION
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--- COFACTOR: Molybdenum (molybdopterin).
--- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kraut M., Hugendieck I., Hervig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in
carboxydotrophic bacteria.";
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                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
Growth-modulating peptide.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                     MEDLINE=77162369; PubMed=858356;
Schlesinger D.H., Pickart L., Thaler M.M.;
Schlesinger D.H., Pickart L., Thaler M.M.;
Experientia 33:324-325(1977)

-!- MISCELLANGOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULA GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas carboxydohydrogena.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group.
NCBI_TaxID=290;
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase large chain (BC 1.2.99.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.2%; Score 8; DB 1; Length 3; 50.0%; Pred. No. 1.1e+05;
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Pred. No. 1.1e+05;
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3 AA.
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PRT;
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Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

Identification of RPamide neuropeptides in the medicinal leech.";

Peptides 12:897-908(1991).

-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
MEDLINE=92195954; PubMed=1686933;
Bvans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
Evans B.D., rohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of Remaide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
-!- SIMILARITY: BELONGS TO THE PARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFamide-like neuropeptide YLRF-amide.
Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformees; Hirudinidae; Hirudo.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFamide-like neuropeptide YMRF-amide.
Hirudo medicinalis (Medicinal lecch).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
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4 AA; 598 MW; 69D4073B30600000 CRC64;
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100.0%; Pred. No.
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Conservative
                                                                                       STANDARD:
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Best Local Similarity
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ID FAR4_HIRME
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P42562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIME=93391436; PubMed=8397415;
MCFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.
"The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-Kamide and Antho-Riamide.";
Proc. R. Soc. Lond., B. Biol. Sci. 253:183-188 (1993)
-!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding
                                    15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Antho-Rlamide I (Contains: Antho-Rlamide II)
Enkaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria; Nymancheae; Actiniidae; Anthopleura.
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Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
NCBI_TaxID=6759;
                                                                                                                                                                                                                                                                                           Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D., Grimmelikhuijzen C.J.P.;
Grimmelikhuijzen C.J.P.;
"Isolation of two novel neuropeptides from sea anemones: the biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its Ges-phenyllactyl fragment Tyr-Arg-Ile-NH2.";
Peptides 12:1165-1173(1991).
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ANTHO-RIAMIDE II.
L-3-PHENYLLACTYL.
AMIDATION.
60441B59A000000 CRC64;
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Pred. No. 1.1e+05;
0; Mismatches 0;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
  4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dehaviour in sea anemones.
-!- SUBCELLUAR LOCATION: Secreted.
-!- TRSUB SPECIFICITY: Neuron-specific.
InterPro; IPR001023; Hsp70.
Neuropeptide; Amidation.
  PRT;
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STANDARD;
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Search completed: April 22, 2003, 13:40:08 Job time : 11 secs
  MEDLINE=81225865; PubMed=6113690;
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Terricola; Geoplanidae; Arthurdendyus.
NCBI_TaxID=132421;
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MEDLINE=76074708; PubMed=576;
Starratt A.N., Brown B.E.;
"Structure of the pentapeptide proctolin, a proposed neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Periplaneta americana (American cockroach),
Limulus polyphemus (Atlantic horseshoe crab), and
Carcinus maenas (Common shore crab) (Green crab).
Bukaryota; Matazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
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SEQUENCE, AND SYNTHESIS.
MEDLINE=94211927; PubMed=7909164;
Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
Maule A.G., Shaw C. Halton D.W., Curry W.J., Thim L.;
May a turbellarian PMRPamide-related peptide (Farp).";
Regul. Pept. 50.37-43(1994).
-! SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
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                                                                                                                 21.2%; Score 7; DB 1; Length 5; ilarity 100.0%; Pred. No. 1.1e+05; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.2%; Score 7; DB 1; Length 5; 100.0%; Pred. No. 1.18+05; tive 0; Mismatches 0; Indelu
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
NAD RES 5 5 AMIDATION (POPERS SEQÜENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

        MOD RES
        5
        AMIDATION

        SEQUENCE
        5 AA; 754 MW; 69D4004B44600000 CRC64;

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(Rel. 01, Last sequence update)
(Rel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FWRFamide-like neuropeptide RYIRF-amide.
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MOD_RES 5 5
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Best Local Similarity
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SPECIES=P.americana;
                                                                                                Query Match
Best Local Similarity
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21-JUL-1986 (
01-FEB-1995 (
Proctolin.
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P01373;
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Gaps
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MEDLINE=66232789; PubMed=2872661;
Stangier J., Dirckenn H., Keller R.;
Stangier J., Dirckenn H., Keller R.;
Identification and immunocytochemical localization of proctolin in pericardial organs of the shore crab, Carcinus maenas.";
Pericardial organs of the shore crab, Carcinus maenas.";
-1- FUNCTION: STIMILATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
-1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN THE CRAB PERICARDIAL ORGANS.
PIR; A01644; HOROHA.
PIR; A60411; A60411.
                                                                                                                                                                                                                                                                                                        "Identification of proctolin in the central nervous system of the horseshoe crab, timulus polyphemus."; Peptides 11:205-211(1990).
O'Shea M., Adams M.E.; "Pentapeptide (proctolin) associated with an identified neuron."; Science 213:567-569(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                              SPECIES=L.polyphemus;
MEDLINE=90287800; PubMed=2356151;
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
Shabanowitz J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.2%; Score 7; DB 1; Length 5; 100.0%; Pred. No. 1.1e+05; ive 0; Mismatches 0; Indels
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Best Local Similarity
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SEQUENCE 5
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Hordeum vulgare (Barley).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, Pooideae,
Triticeae, Hordeum.
                                                                                                                                                                                                                                                                                                                           EMBL; X54643; CAA38455.1; -.
Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination; Calcium; Multigene family.
NON TER
SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;
                                                                                                                                    STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER; MEDLINE=91329704; PubMed=1831055; Jacobsen Jv., Close T.J.; Close T.J.; Close T.J.; acobsen of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley
                                                                                                                                                                                                              aleurone layers.";
Plant Mol. Biol. 16:713-721(1991).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES POLYASACCHARIDES.
-!- COPACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
-!- MISCELLANBOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1196;
                                                                                                                                                                                                                                                                                                                                                                                                                     18.2%; Score 6; DB 10; Length 5; 50.0%; Pred. No. 6.7e+05; tive 1; Mismatches 0; Indels
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01-0CT-2001 (TYEMBLrel. 18, Last sequence update)
01-0CT-2001 (TYEMBLrel. 18, Last annotation update)
88 kDa protein (Fragment).
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Last annotation update)
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STRAIN=NCIMB 11796;
Browne N., Dowds B.C.A.;
Submitted (JUL-2001) to the SWISS-PROT data bank.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence
01-JUN-2002 (TrEMBLrel. 21, Last annotati
PMRFamide-like neuropeptide (LPLRP-amide)
Alpha-amylase (EC 3.2.1.1) (Fragment)
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P83073 bacillus ce
P83308 gallus gall
Q08433 rattus norv
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                                                                                                    April 22, 2003, 13:37:57; Search time 82 Seconds (without alignments) 12.564 Million cell updates/sec
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              GenCore version 5.1.4 p5 4578 (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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sp_rodent:*
sp_vins:*
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sp_vortebrate:*
sp_unclassified:*
sp_vins:*
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sp_archeap:*
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sp_phage:*
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sp_bacteria:*
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
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sp_human:*
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
10P-Glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPGT)
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                       TISSUB-BRAIN;
PubMed=6137771;
PubMed=6137771;
PubMed=6137771;
"A novel active pentapeptide from chicken brain identified by antibodies to FMRFamide.";
Nature 305:328-330(1983).
-I- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
-I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato H., Aono S., Kashiwamata S., Koiwai O.,
"Genetic defect of bilirubin UDP-glucuronosyltransferase in the
hyperbilirubinemic Gunn rat.",
Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
-I- FUNCTION: UDPCT IS OF MAJONE IMPORTANCE IN THE CONJUGATION AND
SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
ENDOGENOUS COMPOUNDS.
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9.1%; Score 3; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 6.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels
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-!- SUBCELLULAR LOCATION: MICROSOME.
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                                                                                                                                                                                                  SEQUENCE, AND SYNTHESIS.
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April 22, 2003, 13:32:01; Search time 33 Seconds (without alignments) 20.189 Million cell updates/sec
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

24944

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 5

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Humanised monoclon Tumour antigen ant Anti-TANGO 268 scF Human FAPAlpha spe Anti (MCP)-1 antib MAD 55.1 heavy cha Murine MC-1 antibo ScFv (FWP51) CDRIH. Light chain CDR H1 Murine anti-human Description SUMMARIES AAY32257
AAR62882
AAR97316
AAY05038
AAB61293
AAO17609
AAR76739
AAR76779
AAR85499 H 22 23 23 23 23 23 23 23 23 Query Match Length DB 100.0 87.9 81.8 81.8 81.8 81.8 75.8 Score 222777777 Result

f rWI2 h 8 hyperv F-1 anti M heavy	H-CDR-1 of anti-id H-CDR-1 of anti-id CDR #1 of r101-2 h Anti-Fas MAD HFE7A MOUSE anti-HM1_24 Chimeric H chain V	onal anticial CDR (antigen humanised	Mouse anti-Fas ant Human CDRI for IL- Murine anti-Fas an Murine 15B8 heavy Chimeric anti-CD25 Antibody L chain V	A P B B B B B B B B B B B B B B B B B B	Ant.TANGO 268 scF Human joint diseas Humanised anti-Fas Mumanised anti-Fas Mouse antibody Act Synthetic pentapep Tissue factor pept
18 AAW2342 20 AAW9347 22 AAB6286 23 ABB0735		1000015	21 AAB14/7 21 AAB1217 21 AAW9089 21 AAY9215 21 AAY97751	5 22 AAOG7116 5 22 AAG67116 5 22 AAG63398 5 22 AAG64780 5 22 AAB76913 5 22 AAB76913	
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## ALIGNMENTS

CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; psoriasis; urflammatory bowel disease; ulcerative collitis; crohn's disease; Sjogren's syndrome; altergy, asthma; rhintis; eczema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes; Light chain CDR H1 of mouse anti-CD23 MAb C11. AAY32257 standard; Peptide; 5 AA. B-cell malignancy; therapy. (first entry) WO9958679-A1. Mus musculus 15-FEB-2000 18-NOV-1999 AAY32257; RESULT 1 AAY32257 

99WO-GB01434. 07-MAY-1999; 98GB-0009839. 09-MAY-1998;

(GLAX ) GLAXO GROUP LTD.

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Armour KL, Hansen HJ;
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N-PSDB; AAQ78734
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                                                                                                                           (CDR HI) of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11 (see also ANY32263). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the antho acid sequences of C11 light and heavy chain CDRs (see ANY3254-59) to render them capable of binding to the CD23 C type II molecule expressed on haemacopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, clabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic gindbetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, colitis, Crohn's disease, COPD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Atherosclerosis, atherosclerotic plaque; anti-hydroxysteroid antibody, murine monoclonal antibody; heavy chain variable region: CDR1; complementarity determining region; imaging; plaque ablation.
                                                       Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
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                                                                                                                   sequence represents complementarity determinating region 1
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Shearin J;
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
Rapson NT,
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Crowe SJ, Ellis JH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR62882 standard; peptide; 5 AA.
                                                                                            Claim 1; Page 40; 81pp; English.
                                                                                                                                                                                                                                                                                                                         determining the binding agents
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                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
                      WPI; 2000-053101/04.
N-PSDB; AAZ34742.
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Bonnefoy JMP,
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Matches
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AAR62882
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New humanised anti-CEA monoclonal antibody - having engrafted murine CDRs, used for diagnosis, imaging and therapy of CEA-producing
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                                                                                                                                                                                                                                                                                                   Mice were immunised with an extract of human atherosclerotic plaque, then spleen cells were fused with SP2/01-Ag-14 myeloma cells. Hybridomas were screened by ELISA for reactivity with the immunogen and clone 22D3 was isolated. The Z2D3 antibody reacts specifically with atherosclerotic tissue; it recognises a non-protein antigen containing cholesterol (or similar steroid that is a substrate for phosphatidylcholine or related compound that is a substrate for phosphalipase C). The CDR sequences for the heavy and light chains of Z2D3 were determined; peptides comprising the CDRs are claimed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapa
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New antigen comprising hydroxy:steroid and quat. ammonium salt and related antibodies, useful e.g. for imaging, ablating or treating atherosclerotic plaque, and detecting plaque specific antibodies
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Pred. No. 7.8e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             including chimeric (CDR-grafted) murine-human antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanised monoclonal antibody heavy chain CDR.
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                                                                                                                                                                                                                                        Claim 199; Page 147; 288pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR97316 standard; peptide; 5 AA.
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Best Local Similarity 80.0
Matches 4; Conservative
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This sequence represents a heavy chain complementarity determining region (CDR) from a tumour antigen specific antibody. The invention relates to a method for identifying a binding molecule having selective affinity for a ligand comprising: (a) selectively immobilising a diverse population of binding molecules to a solid support, (b) simultaneously contacting the diverse population immobilised on the solid support with 2 or more ligands; and (c) determining at least one binding molecule which selectively binds to one or more of the ligands. The method allows for the rapid and efficient methods for the identification of binding molecules which exhibit selective affinity for one or more ligands of interest. They are used particularly for identifying tumour-specific binding polypeptides which can be used as targeting agents for cancer therapy that minimises impact on non-tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour antigen; antibody; CDR; complementarity determining region;
binding molecule identification; tumour-specific binding polypeptide;
cancer therapy; heavy chain.
of the parental murine MAb but are less immunogenic in a human subject than the parental MAb. The humanised antibodies can be used in diagnosis, imaging and therapy of CRA-producing cancers and patients receiving the humanised antibodies and conjugates show improved therapeutic results, decreased immune responses and decreased immune-mediated adverse effects compared to the parent antibody. This sequence is a murine derived CDR region which corresponds to CDR 1 in the heavy chain of the humanised MAb. See
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying binding molecules for ligands, particularly tumour antigens - by selectively immobilising a population of binding molecules to a solid support and screening for binding to two more ligands
                                                                                                                                                                                                                 81.8%; Score 27; DB 17; Length 5; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour antigen antibody heavy chain CDR1 clone F15.
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                                                                                                                                                                                                                                   Local Similarity
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The present sequence is given in a specification relating to an isolated nucleic acid molecule encoding a platelet membrane glycoprotein receptor glycoprotein V (GPVI), also called TANGO 26s. The GPVI polymucleorides and polypeptides and their modulators, e.g. antisense nucleic acids, ribozymes and antibodies, are useful for preventing, treating and disorders associated with aberrant expression or activity of GPVI. These disorders include bleeding disorders
(e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g. thrombocic occlusion of the coronary arteries), haemorrhagic disorders, coronary artery and cerebral artery diseases (e.g. stroke and isorders, coronary artery and cerebral artery diseases (e.g. stroke and isorders), immunological diseases (e.g. therosclerosis and myocardial infartion), immunological diseases (e.g. platelet disorder) and cardiac isohaemia following angioplasty and metastatic cancers, especially of the colon and liver.
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                                                                                                                                                                                                                                                                                                                                                                       Human; antibody; scFv; CDR; complementarity determining region; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant; thrombolytic; antiatreriosclerotic; haemostatic; glycoprotein VI; GPVI; platelet membrane glycoprotein receptor; bleeding disorder; blood vessel injury; thrombotic disorder; haemorrhagic disorder; ischaemia; cardiovascular disease; immunological disease; liver disorder;
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                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, treating and diagnosing hemorrhagic disorders, thrombotic diseases and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vainchencker W,
                                               Score 27; DB 20; Lengtn 5, Pred. No. 7,88+05; Indels
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                                                                                                                                                                                                                                                                                                                                          Anti-TANGO 268 BCFv CDR, SEQ ID NO: 61.
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                                                  81.8%; Scc.
100.0%; Prev
                                                                                                                                                                                                                                           AAB61293 standard, Peptide, 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-1999; 99US-0345468.
06-DEC-1999; 99US-0454824.
14-FEB-2000; 2000US-0503387.
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                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                Conservative
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                                                         Query Match
Best Local Similarity
                                5 AA;
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Human, antibody; MCP; monocyte chemoattractant; antiasthmatic;
antiallergic; antiinflammatory; idiopathic thrombocytopaenia;
minaulosuppressive; cytostatic; vasotropic; antiatratiossclerchic;
minaunosuppressive; cytostatic; vasotropic; antidartatiossclerchic;
minaunoglobulin heavy chain; monocyte migration; T cell migration;
CC-type chemokine; ectaxin; allergy; allergic rhinitis; cancer;
M hypersensitivity response; allergic contact dermatitis;
inflammatory disease; asthma; psoriasis; COPD; osteoporosis;
inflammatory bowel disease; multiple sclerosis; autoimmune disease;
M rheumatory bowel disease; multiple sclerosis; autoimmune disease;
M non disease; osteoporosis; osteoarthritis; periodoncal disease;
M neucocyte infiltration; restenosis; arteriosclerosis; CDRI.
                                                                                       Anti-(MCP)-1 antibody heavy chain protein hypervariable region CDR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
        AAU75739 standard; Peptide; 5 AA.
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                                                              08-MAY-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                             WO200202640-A2
                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                       10-JAN-2002.
                                    AAU75739;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a human or humanised antibody (Ab) which specifically binds to fibroblast activating protein alpha (FAPalpha). The antibodies are useful for preparing a composition for the treatment of cancer, and for imaging tumours associated with activated stromal fibroblasts, such as colorectal cancer, non-small-cell lung cancer, breast cancer, head and neck cancer, non-small-cell lung cancer, cancer, pancreatic cancer and metastatic or brain cancer, and diseases associated with the same, such as inflammation and wound healing. The present sequence is a peptide described in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human humanized antibody that specifically binds to fibroblasts activating protein alpha, useful for treating cancer or tumor, and for imaging tumors associated with activated stromal fibroblasts, e.g. lung or breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                    Gaps
                                                                                                                                                                                                                                                                                      Human, FAPalpha, fibroblast activating protein alpha, antibody, Ab, gene therapy, cancer, wound healing, inflammation, cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mersmann M;
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                        Length 5;
                                                                                                                                                                                                                                                             Human FAPalpha specific VL region from VH50 CDR1 peptide.
                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garin-Chesa P, Pfizenmaier K, Moosmayer D,
                        DB 22; L
               81.8%; Scc.
100.0%; Pred. No.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BOEH ) BOEHRINGER INGELHEIM PHARMA KG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 6C; 109pp; English.
                                                                                                                                                                              AAO17609 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAR-2000; 2000DE-1013286.
11-SEP-2000; 2000GB-0022216.
                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2001; 2001WO-EP04716
                                                                                                                                                                                                                                  08-AUG-2002 (first entry)
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-041180/05.
                       Query Match
Best Local Similarity
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5 AA;
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                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                              2 YWMS 5
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Schmidt A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
                                                                                               2 YWWS
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                                                                                                                                                                                                      AA017609;
 Sequence
                                                     Matches
                                                                                                                                                  RESULT 6
AAO17609
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Di Padova FE;

Urfer R,

Payne TG,

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This invention relates to a molecule that binds MCP-1 (human monocyte chemoattractant protein-1). The molecule has at least one antigen binding site comprising at least one immunosolbobinin (Ig) heavy and/or light chain variable domain (Wh. VI). The antibody of the invention inhibite binding of MCP-1 (and also eotaxin) to specific receptors, so preventing migration of monocytes and T cells. These are human tribodies with very high affinity for MCP-1, but no significant reaction with other human CC-type chemokines or MCP-1 from other species. The MCP-1 binding molecules, specifically antibodies that cross react with eotaxin, are used to prevent or treat MCP-1 or eotaxin-mediated disorders, particularly those that involve migration or mediated disorders, particularly those that involve migration or activation of monocytes and T cells, e.g. allergies (allergic rhimitis, Miseases (asthma, psoriasis, allergic contact dermatitis), inflammatory diseases (asthma, psoriasis, diseases of bone and cartilage (osteoporosis) autoimmune disease (rheumatoid arthritis disease) (costeoporosis, osteoarthritis, periodontal disease) heematological disorders (haemolytic anaemia, idiopathic thrombocytopaenia) graft rejection, cancers that include leucocyte inflaration, (rejection, cancers that include leucocyte inflaration, (reletiosic) osteoporosis and many other diseases listed in the specification. The present sequence represents the human anti-(MCP) increases of cancers the human anti-(MCP) increases of cancers the human anti-(MCP) increases of cancers the increase the include leucocyte increases of bone and cancers and cancers and many other diseases between the human anti-(MCP) increases of cancers and many other diseases between the human anti-(MCP) increases of cancers and cancers the human anti-(MCP) increases and
New compound that binds human monocyte chemoattractant protein-1, useful e.g. for treating inflammation, comprises immunoglobulin chains with specific hypervariable regions
                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 35; 42pp; English.
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DB 23; Length 5;

81.8%; Score 27;

5 AA;

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YWMS 5

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7 RESULT

Query Match

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Murine MC-1 antibody heavy chain variable domain (VH) CDR1 peptide.
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                                                                                                        WO200220615-A2
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                                                                                                                                                                                                                                                            disorders
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                                                                                          Mus sp.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                           An antigen binding structure is based on the CDRs (given in AAR76078-84) of the heavy and light chains of MAD 55.1 (ECACC 93081901), which recognises the colorectal tumor-associated antigen CAS55.1. It is optionally humanized and in the form F(ab/2, F(ab)', Fab, Fv, scFv or V-min, and is produced in transgenic animals or plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
               Gaps
                                                                                                                                                                                                                                                                                                                                                            Antigen binding structures containing CDRs recognising the CA55.1 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
                                                                                                                                                       Antigen binding structure; complementarity determining region; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monoclonal antibody; Mab; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering; humanized antibody; immunotoxin.
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               Indels
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      7.8e+05;
hes 0;
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Pred. No. 7.8e+05;
1; Mismatches 0
      Pred. No. 7.8
Mismatches
                                                                                                                                                                                                                                                                                                                    Copley CG, Hall SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE22200 standard; peptide; 4 AA.
100.0%; Pic
                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 96; 121pp; English.
                                                                                         AAR76079 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.8%;
75.0%;
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                                                                                                                                        MAb 55.1 heavy chain CDR1.
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                                                                                                                         (first entry)
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               Conservative
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Wright AF;
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Best Local Similarity
Matches 3; Conserv
      Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AA;
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03-DEC-1993;
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1 GYWI 4
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                               2 YWMS 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of an antibody and/or chemokine construct that binds to a chemokine receptor, for eliminating cells latently infected with primate immunodeficiency virus, or treating, preventing and alleviating immune
                             skin disease; immunological disorder; autoimmune disease; psoriasis; multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease; diabetes; skin inflammation; atopic dermatitis; inflammatory disease; inflammatory renal disease; HIV-1; transplant rejection; murine; CDR1, heavy, chain variable domain; VH; complementarity determining region 1;
Chemokine construct; human immunodeficiency virus 1; allergic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the use of an antibody and/or chemokine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4;
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Pred. No. 7.8e+05;
1; Mismatches 0; Indels
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larity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-2001; 2001WO-EP10433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-SEP-2000; 2000EP-0119694
05-SEP-2001; 2001US-0948004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mack M, Schloendorff D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MICR-) MICROMET AG.
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es 3; Conserv
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This sequence represents the complementarity determining region-1 (CDR-1) of the rWI2 heavy Chain. This sequence is used in an antibody of the invention. The antibody of the invention is a chimeric or humanised anti-idiotype antibody of the invention is a chimeric or humanised anti-idiotype antibodies (cAb and hAb, respectively) or a fragment which specifically binds to the idiotype region of an anti-carcinoembryonic antigen (CBA), where: (i) cAb comprises the rWI2 light (L) and heavy (H) chain variable regions, or silent mutations, and (ii) hAb comprises rWI2 complementarity determining regions (CDR) and humanised framework (FR) regions. The hAb is used as a vaccine to stimulate an immune response in a patient against cancers expressing CBA. The hAb, can be used to clear non-targeted antibody in a method of diagnosis or treatment of a patient where a CBA antibody is used as a (pre-)targeting or therapy agent. The cAb is used to detect the presence of an antibody that specifically binds to CBA in a sample.
                                           Chimeric and humanised anti-carcinoembryonic antigen anti-idiotype antibodies - useful in detection of anti-CEA antibodies and as vaccine to stimulate immune response against cancer
                                                                                                                                                                                                                                                                                                                                                          72.7%; Score 24; DB 18; L. 75.0%; Pred. No. 7.8e+05; ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW93474 standard; Protein; 5 AA.
                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 75.0 es 3, Conservative
                                                                                                   Claim 3; Page 30; 46pp;
                   WPI; 1997-479997/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-182094/16.
N-PSDB; AAX23235.
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                                                                                                                                                                                                                                                                                                                                     Complementarity determining regions (CDRs) CDR1H, CDR2H and CDR3H (AAR85496-98) and CDR1L, CDR2L and CDR3L (AAR85502-04) are components of the heavy chain variable region and light chain variable region, respectively, of single chain antibody scrv(FWP51) (AAR85495). The CDRs are derived from mouse monoclonal antibody FWP51 (BCACC 90112118) directed to the human growth factor receptor HERS. The scrv is used as the tumour antigen binding domain of a bifunctional protein that is expressed in cytotoxic T-lymphocytes (CTLs), allowing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; complementarity determining region; CDR; heavy chain; rat; CEA; rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                            - contg.
                                                                                                                                                                                                                                                       New bifunctional proteins for use in killing tumour cells - cortumour antigen binding domain, a hinge region and a zeta chain derived from a T-cell antigen receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24; DB 16; Length 5;
Pred. No. 7.8e+05;
1; Mismatches 0; Indels
monoclonal antibody; cancer; adoptive immunotherapy; complementarity determining region; CDR.
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                                                                                                                                                                                                                                                                                                             Disclosure, Page 6, 46pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW23429 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  adoptive immunotherapy of cancer
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75.0%;
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                                                                                                                                                                           CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                      Moritz D;
                                                                                                                                                                                                                              WPI; 1995-393085/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                 WO9530014-A1
                                                                                                                     20-APR-1995;
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                                                                                                                                                                                                      Groner B,
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                                         Synthetic
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Gaps

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Length 5;

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Monoclonal antibody, hypervariable domain; heavy chain; CDR1; neutralise; Cobstridium difficile; epitope; ligand domain; immunotherapy; disease; translocation domain; catalytic domain; humanised antibody; enterotoxin; toxin A; toxin B; pseudomembranous colitis.
                                                                          mAk TTC8 hypervariable domain heavy chain CDR1 protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibodies specific for Clostridium difficile toxins especially humanised antibodies for treating pseudomembranous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Von Eichel-Streiber C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VBIC/) VON EICHEL-STREIBER C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97DE-1039685
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11-JUN-1999 (first entry)
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Gaps

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This invention relates to sialoadhesin factor-1 (SAF-1) monoclonal antibodies 13G3 and 11G4. A neutrophil-priming dose of SAF-1 agonist antibodies 13G3 and 11G4. A neutrophil-priming dose of SAF-1 agonist useful for treating or preventing an infectious disease state such as bacterial infection, viral infections, sepsis, antibiotic resistant bacterial infection, viral infections and those involving intracellular pathogens and parasites such as Listeria monocytogenes, Salmonella and lesibmania in a mammal. Nucleic acid sequences encoding the variable light chain and heavy chain peptide sequences are useful for mutagenic introduction of specific changes within the nucleic acid sequences encoding the (complementarity determining regions) CDRs or framework and for incorporation of the resulting modified or fusion nucleic acid sequence into a plasmid for expression. The CDR-encoding regions comprising silent mutations are used in construction of humanized
This invention describes a novel monoclonal antibody that is directed against a Clostridium difficile toxin and recognises and neutralises an epitope in the ligand domain, translocation domain or catalytic domain of the toxin. Humanised antibodies are desribed which are expressed in plants and can be used for immunotherapy of diseases caused by Clostridium difficile enterctoxin (toxin A) or cytotoxin (toxin B), especially pseudomembranous colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New sialoadhesin factor-1 agonist antibody having the characteristic of monoclonal antibody 13G3 or 11G4 for treating osteomyelitis, deep seated wound infections and antibiotic resistant bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sialoadhesin factor-1; SAF-1; anti-SAF-1 monoclonal antibody; 13G3; 11G4; osteomyelitis; wound infection; sepsis; Listeria monocytogene; Salmonella; Leishmania; heavy chain variable region; mouse; complementarity determing region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-SAF-1 antibody 13G3 H chain V region CDR peptide SEQ ID 3.
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                                                                                                                                                                                                    Score 24; DB 20; Length 5;
Pred. No. 7.8e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              King AG,
                                                                                                                                                                                                                                                                                                                                                                                                                             AAB62861 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erickson-Miller CL, Holmes SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 22; Fig 1; 43pp; English.
                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-AUG-2000; 2000WO-US22663,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0149753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                               5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating or preventing immunoglobulin-mediated reperfusion or ischemic injury resulting from e.g. angioplasty or bypass surgery, by administering an inhibitor of pathogenic immunoglobulin and ischemic antigen interaction
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                                                                                                                                  Gaps
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   present sequence
heavy chain variable
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antibodies or other engineered antibodies. The present segu
represents anti-SAF-1 monoclonal antibody 13G3 heavy chain
region complementarity determining region peptide sequence.
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Pred. No. 7.8e+05;
1; Mismatches 0; Indels
                                                                                                 Score 24; DB 22; Length 5;
Pred. No. 7.8e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   22A5 IgM heavy chain variable region CDR1 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moore FD, Hechtman HB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 54; Page 72; 77pp; English.
                                                                                                                                                                                                                                                                                 ABB07357 standard; peptide; 5 AA
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 75.07
Best Local 3; Conservative
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                                                                                                               Local Similarity
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                        H-CDR-1 of anti-idiotype antibody against human anticancer antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel anti-idiotype antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.
                                                                                                                                                                                                                    Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; complementarity determining region.
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                                                                                                      AAR74929 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 2; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                      93JP-0272950
                                                                                                                                                                                                                                                                                                                                                        93JP-0272950
                                                                                                                                                              19-JAN-1996 (first entry)
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2 YWMN 5
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Search completed: April 22, 2003, 13:39:53 Job time : 35 secs

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US-09-977-797A-76
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Sequence 1, Appl
Sequence 1, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 62, Appl
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Sequence 31, Appl
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Sequence 15, Appli
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Sequence 1, Appli
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Sequence 23, Appl
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                                                                                                                          April 22, 2003, 13:41:42 ; Search time 15 Seconds (without alignments) 26.710 Million cell updates/sec
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-09-253-794-23

US-09-968-561A-265

US-09-155-106-11

US-09-192-854-151

US-09-423-800-62

US-09-2921-6

US-09-977-797A-90

US-10-182-018-62
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US-09-832-312-49
US-09-770-002-1
US-09-291-417-40
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US-10-156-820-31
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US-09-750-754-15
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Maximum Match 100%
Listing first 45 summaries
                                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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20 18 54.5 5 12 US-10-156-820-34 Sequence 34, Appl 22 16 48.5 4 8 US-09-977-797A-88 Sequence 36, Appl 23 16 48.5 4 9 US-09-987-791-15 Sequence 19, Appl 24 16 48.5 4 10 US-09-982-172-194 Sequence 19, Appl 26 16 48.5 4 10 US-09-982-172-194 Sequence 19, Appl 26 16 48.5 5 9 US-09-982-172-194 Sequence 19, Appl 27 16 48.5 5 9 US-09-982-172-19 Sequence 11, Appl 27 16 48.5 5 9 US-09-982-172-19 Sequence 11, Appl 28 15 45.5 4 10 US-09-981-19 Sequence 11, Appl 30 15 45.5 4 10 US-09-981-19 Sequence 11, Appl 31 15 45.5 5 9 US-10-165-015-10 Sequence 11, Appl 31 15 45.5 5 9 US-10-105-910-67 Sequence 11, Appl 32 15 45.5 5 9 US-10-105-910-67 Sequence 11, Appl 32 15 45.5 5 9 US-09-788-006-95 Sequence 97, Appl 36 15 45.5 5 9 US-09-788-006-97 Sequence 97, Appl 36 15 45.5 5 10 US-09-788-006-97 Sequence 97, Appl 37 15 45.5 5 10 US-09-788-006-97 Sequence 97, Appl 37 15 45.5 5 10 US-09-972-788-78 Sequence 97, Appl 37 15 45.5 5 10 US-09-972-84-89 Sequence 97, Appl 40 14 42.4 4 9 US-09-788-426-58 Sequence 59, Appl 42.4 4 9 US-09-788-78 Sequence 59, Appl 42.4 4 9 US-09-788-78-88 Sequence 58, Appl 42.4 4 9 US-09-788-198-58 Sequence 58, Appl 42.4 4 9 US-09-185-908-24 Sequence
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## ALIGNMEN

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US-09-777-977-76

US-09-777-977-76

US-09-777-977-76

US-09-777-977-76

US-09-777-977-76

Publication No. US20030044772A1

GENERAL INFORMATION: Jeffrey D.

APPLICANT: Watkins, Jefres

TILE REPERBNCE: Jame-06805

CURRENT FILE REPERBNCE: J002-06-28

FILE REPERBNCE: J002-06-28

FRIOR FILING DATE: 1998-08-04

FRIOR FILING DATE: 1998-08-04

FRIOR FILING DATE: 1997-08-04

FRIOR FILING DATE: 1997-08-04

FRIOR FILING DATE: 1997-08-04

SOFTWARE: Patentin version 3.1

SOFTWARE: Paten
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US-09-968-561A-265

i Sequence 265, Application US/09968561A

i Patent No. US2002016442A1

j Retent No. US2002016442A1

j Retent No. US2002016442A1

j APPLICANT: Tomlinson, lan M

APPLICANT: Winter, Gregory

i TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands

i CURRENT APPLICATION NUMBER: US/09/968,561A

j FILE REFERENCE: 8039/1073B

j CURRENT PILING DATE: 1997-10-01

j PRIOR APPLICATION NUMBER: US 60/065,248

j PRIOR APPLICATION NUMBER: US 60/066,729

j PRIOR FILING DATE: 1997-11-13

j PRIOR FILING DATE: 1997-11-21

j PRIOR FILING DATE: 1997-11-21

j PRIOR FILING DATE: 1997-11-24

j RIOR APPLICATION NUMBER: US 09/511,939

j PRIOR FILING DATE: 1997-11-24

j RIOR APPLICATION NUMBER: US 09/511,939

j RIOR FILING DATE: 1998-10-20

j PRIOR FILING DATE: 2000-02-24

j NUMBER OF SEQ ID NOS: 350

j SOFTWARE: PatentIn Version 3.1
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Sequence 1, Application US/09155106

Publication No. US20030054003A1

GERERAL INFORMATION:

TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE

TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE

TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACENTIA Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/155,106

FILING DATE: 19-MAR-1997

FILING DATE: 19-MAR-1997

FILING DATE: 20-MAR-1996

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids
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                   Length 5;
                                                             Indels
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                   Score 27; DB 10; 1
Pred. No. 2.7e+05;
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Pred. No. 2.7e+05;
  81.8%; Scc...
100.0%; Pred. No. 4...
... 0; Mismatches
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80.08;
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Best Local Similarity 80.0.
                                                             Conservative
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; ORGANISM: Homo sapiens
US-09-968-561A-265
         Query Match
Best Local Similarity
Matches 4; Conserval
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1 GYYMS 5
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US-09-155-106-1
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APPLICANT: HANSEN, Kathryn L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
MOUSE MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/253,794

FILING DATE: 22-Feb-1999

CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 27; DB 10; Length 5; 100.0%; Pred. No. 2.7e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,157
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, BESTIANCH D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEPHONE: (202)672-5399
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-06-30
PRIOR PILING DATE: 1999-06-30
PRIOR PILING DATE: 1999-06-30
PRIOR PILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1899-06-30
PRIOR FILING DATE: 1899-06-30
PRIOR FILING DATE: 1899-06-30
PRIOR PILING PARE: PAST PENT
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 23:
U8-09-253-794-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23, Application US/09253794
Patent No. US20020018750Al
GENERAL INFORMATION:
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-832-312-61
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US-09-253-794-23
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GENERAL INFORMATION:

APPLICANT: Watkins, Jeffrey D.

APPLICANT: Watkins, Jeffrey D.

APPLICANT: Huse, William D.

APPLICANT: Whilliam D.

TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules

FILE REFRENCE: AME-06805

CURRENT APPLICATION NUMBER: U9/09/977,797A

CURRENT FILING DATE: 1998-004

PRIOR FILING DATE: 1997-08-04

PRIOR FILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 136

SOFTWARE: PALENTIN NUMBER: 08/05.825

BRIOR FILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 136

SOFTWARE: PALENTIN VERSION 3.1

LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                • OTHER INFORMATION: Amino acid sequence of CDR(1) of H chain V region of OTHER INFORMATION: mouse anti-HM 1.24 antibody
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                                                                                                                                                                                              Sequence 6, Application US/09269921
; Bequence 6, Application US/09269921
; Publication No. U320030045691A1
; GENERAL INFORMATION:
   APPLICANT: Onto, Koichiro
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimara, Yasushi
; APPLICANT: Koishimara, Yasushi
; APPLICANT: MUNGHER: US/09/269,921
CURRENT APPLICATION NUMBER: US/09/269,921
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: UP 8-264756
; EARLIER FILING DATE: 1996-10-04
; SEQ ID NOS: 137
; SEQ ID NOS: 137
; SEQ ID NOS: 137
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           Indels
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         Mismatches
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Best Local Similarity 75.03
Matches 3; Conservative
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         Conservative
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CORGANISM: Homo sapiens
US-09-977-797A-90
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Best Local Similarity
Matches 3; Conserv
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ORGANISM: murine
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US-09-269-921-6
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Fatent No. US20020068276A1

GENERAL INFORMATION:

APPLICANT: Winter, Greg

APPLICANT: Tomlinson, Ian

TITLE OF INVENTION: Methods for Selecting Functional Peptides

FILE REFERENCE: 3789/72916

CURRENT APPLICATION NUMBER: US/09/192,854

CURRENT FILING DATE: 1998-11-17

FARLIER APPLICATION NUMBER: 60/066,729

FARLIER APPLICATION NUMBER: 60/066,729

SAFLIER FILING DATE: 1998-11-21

NUMBER OF SEQ IN NOS: 212

SOFTWARE: PATENTIN VET. 2.0

SERVING DATE: 100 151
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                                                                                                                                            Score 24; DB 9; Length 5;
Pred. No. 2.7e+05;
1; Mismatches 0; Indels
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APPLICANT: SATO, KOH
APPLICANT: SATO, KOH
APPLICANT: ISHII, KIMIE
ITILB OF INVENTION: CACHEXIA REMEDY
FILE REFERENCE: 04853 0036
CURRENT APPLICATION NUMBER: US/09/423,800
CURRENT PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-01-13
PRIOR PILING DATE: 1999-05-13
PRIOR PILING DATE: 1997-05-15
PRIOR PILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PATON NUMBER: JP 194445/1997
PRIOR PILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PATON NUMBER: JP 18445/1997
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                                                                                                                                            72.7%;
75.0%;
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Best Local Similarity 75.0
Matches 3; Conservative
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Matches 4; Conservative
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-192-854-151
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1 GYYMS 5
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US-09-423-800-62
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US-09-155-106-1
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Sequence 1, Application US/09770002

Sequence 1, Application US/09770002

Patent No. US20020110558A1

GENERAL INFORMATION:

APPLICANT: Peter Lloyd Amlot

APPLICANT: Max H. Schreier

TITLE OF INVENTION: Use of CD25 binding molecules in the

TITLE OF INVENTION: Use of CD25 binding molecules in the

TITLE OF INVENTION: Use and US/09/770,002

CURRENT APPLICATION NUMBER: US/09/770,002

CURRENT PELING DATE: 2001-09-17

PRIOR APPLICATION NUMBER: PCT/EP99/05316

MANDER OF US APPLICATION DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.7%; Score 23; DB 10; Length 5; 100.0%; Pred. No. 2.7e+05; ive 0; Mismatches 0; Indels
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Pred. No. 2.7e+05;
1; Mismatches 0; Indels
                 GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-02-14
PRIOR PILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-09-291-417-40
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LENGTH: 5
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Sequence 62, Application US/10182018

Sequence 62, Application US/10182018

Bublication No. US2030049211A1

GENERAL INFORMATION:
APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA

ITITLE OF INTENTION:
CURRENT APPLICATION NUMBER: US/10/182,018

CURRENT APPLICATION NUMBER: US/10/182,018

PRIOR APPLICATION NUMBER: JP 2000-83034

PRIOR FILING DATE: 2000-01-25

NUMBER OF SEQ ID NOS: 75
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CCATION: (1)...(5)

OTHER INFORMATION: CDR1 of the heavy chain of antibodies Act-1 and
CTHER INFORMATION: LDP-02
US-09-748-960-12
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US-09-748-960-12

| Sequence 12. Application US/09748960
| Patent No. US20010046496A1
| GENERAL INFORMATION:
| APPLICANT: Brettman. Lee R. APPLICANT: Brettman. Lee R. APPLICANT: Allison, David Edward
| TITLE OF INVENTION: Method of Administering an Antibody CURRENT APPLICATION NUMBER: US/09/748,960
| CURRENT APPLICATION NUMBER: US/09/748,960
| PRIOR PILING DATE: 2000-12-27
| NUMBER OF SEQ ID NOS: 14
| SOFTWARE: FLANTES 2000-04-14
| SEQ ID NOI 12
| LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69.7%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 2.7 Matches 3; Conservative 0; Mismatches
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US-09-832-312-49
; Sequence 49, Application US/09832312
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-018-62
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Best Local Similarity
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SEQ ID NO 62
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US-10-029-301-4

i Sequence 4, Application US/10029301

publication No US20020188107A1

i GENERAL INFORMATION:

i APPLICANT: Brownerd, Christian

i APPLICANT: Eeek, Keith

TITLE OF INVENTION: Component of Stem Bromelain (as amended)

TITLE OF INVENTION: Component of Stem Bromelain (as amended)

TITLE OF INVENTION: Component of Stem Bromelain (as amended)

CURRENT APPLICATION UNMBER: US/10/029,301

CURRENT FILING DATE: 1099-08-25

PRIOR PTLING DATE: 1999-08-25

PRIOR APPLICATION NUMBER: GB 9704252.7

PRIOR APPLICATION NUMBER: GB 9704252.7

PRIOR APPLICATION NUMBER: GB 9704252.7

PRIOR APPLICATION NUMBER: GB 9703850.9

PRIOR APPLICATION NUMBER: GB 970382.7

PRIOR APPLICATION NUMBER: GB 970382.7

PRIOR APPLICATION NUMBER: GB 9703827.7

PRIOR PILING DATE: 1997-02-25

PRIOR PILING DATE: 1997-02-25

I BRIOR APPLICATION NUMBER: GB 9703827.7

PRIOR PILING DATE: 1997-02-25

I BRIOR PILING DATE: 1997-02-25

I BRIOR APPLICATION NUMBER: GB 9703827.7

PRIOR PILING DATE: 1997-02-25

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                                                                                                                                                                                                                                                                                                                                                                                                                                60.6%; Score 20; DB 9; Length 5; 100.0%; Pred. No. 2.7e+05; tive 0; Mismatches 0; Indels
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
                            FILE REFERENCE: 240/300
CURRENT APPLICATION NUMBER: US/09/291,417A
CURRENT FILING DATE: 1999-04-13
FEARLIER APPLICATION NUMBER: US 60/081,784
FARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 5
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Best Local Similarity 66.7
Matches 2; Conservative
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; ORGANISM: Ananas comosus
US-10-029-301-4
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Best Local Similarity
Matches 3; Conserve
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; ORGANISM: CCK4b
US-09-291-417-40
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Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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RESULT 1
US-08-480-434-22
US-08-480-434-22
Sequence 22, Application US/08480434
Fatent No. 5811248
Fatent No. 5811248
FATENCENT: Charles C. Ditlow, et al.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
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US-08-321-625-14

US-08-422-685-19

US-08-440-504A-2

US-08-440-504A-2

US-08-440-504A-2

US-08-413-613-2

US-08-611-179B-2

US-08-611-179B-2

US-09-411-083-14

US-09-155-613A-31

US-09-155-613A-31

US-09-155-613A-31

US-09-312-613A-31

US-08-312-071B-1

US-08-312-613A-31

US-08-312-613A-31

US-08-312-613A-31

US-08-312-613A-31

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Pred. No. 2e+05;
1; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-UNN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REPERENCE/DOCKET NUMBER: 7606-053
TELECHONE: (415) 854-3660
TELECHAX: (415) 854-3660
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
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Best Local Similarity 80.0%;
Matches 4; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Sequence 12, Appl
Sequence 23, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 20, Appl
Sequence 50, Appl
Sequence 50, Appl
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Sequence 50, Appl
Sequence 60, Appl
Sequence 60, Appl
Sequence 61, Appl
Sequence 64, Appl
Sequence 64, Appl
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                                                                                                                                                                                                                                                                                                                April 22, 2003, 13:39:17; Search time 28 Seconds (without alignments) 5.254 Million cell updates/sec
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Sequence 1,
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Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-08-480-434-31
US-08-6053-451B-32
US-08-053-451B-32
US-08-244-626-12
US-08-138-151B-32
US-08-318-151B-32
US-08-318-151B-32
US-08-318-970B-1
US-08-318-970B-1
US-08-318-970B-1
US-08-318-970B-1
US-08-318-970B-3
US-08-318-970B-3
US-08-318-970B-3
US-08-318-970B-3
US-08-318-970B-3
US-08-470-685-25
US-08-470-685-25
US-08-127-721A-50
US-08-127-721A-50
US-08-465-246A-50
US-08-469-141A-64
US-08-469-141A-64
US-08-469-13794-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -08-440-504A-1
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US-08-433-613-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262574 seqs, 29422922 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GYWMS 5
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seq length: 5
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Score

Result

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Sequence 31, Application US/08053451B
Fatent No. 595584
GENERAL INPORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ANTIEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIEROS. ANTIBODIES THERETO, AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STRATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.9%; Score 29; DB 2; Length 5;
80.0%; Pred. No. 2e+05;
iive 1; Mismatches 0; Indels
                                     MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC Compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTONNEY/AGENT INPORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REGISTRATION NUMBER: 25,227
REGISTRATION NUMBER: 25,227
REGISTRATION NUMBER: 25,227
RELEPHONE: 415-84-360
TELEFRAK: 415-84-364
TELERY: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acids
TYPE: ATRAUDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REGISTRATION NUMBER: 25,227
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFOKE 415-854-3660
TELEFAX: 415-854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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MOLECULE TYPE: I
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE: N
US-08-053-451B-22
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APPLICANT: Chen, Francis W.
APPLICANT: Ditlow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF NUMBER OF SEQUENCE: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREFT: 1155 Avenue of the Americas
CETY: New York
STATE: New York
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                                                                                                        Sequence 31, Application US/08480434
Patent No. 5811248
GENERAL INFORMATION:
APPLICANT: Charles C. Ditlow, et al.
TITLE OF INVENTION: ATTEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 88
CORRESPONDENCES. 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 2; Length 5;
Pred. No. 2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 87.9%; Score 29; DB Best Local Similarity 80.0%; Pred. No. 2e+C Matches 4; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-UNN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 7606-053
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 66141 PENNIE
INFORMATION FOR SEGO ID NO: 31:
SEQUENCE CHARACTERISTICS:
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US-08-053-451B-22
; Sequence 22, Application US/08053451B
; Patent No. 5955584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: D
HYPOTHETICAL: N
ANTI-SENSE: N
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1 GFWMS 5
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Sequence 23, Application US/08318157B

Patent No. 5874540

GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                         Sequence 32, Application US/08480434
Patent No. 5811248
GENERAL INFORMATION:
APPLICANT: Charles C. Ditlow, et al.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.8%; Score 27; DB 2; Length 5; 100.0%; Pred. No. 2e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Release #1.24
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/480,434
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 25,227
TELECOMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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US-08-318-1578-23
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                                                                               RESULT 6
US-08-480-434-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Waldmann, Herman
APPLICANT: Waldmann, Herman
APPLICANT: Walsh, Louise
APPLICANT: Crowe, James Scott
APPLICANT: Lewis, Alan Peter
TITLE OF INVENTION: CDR GRAFTED HUMANISED CHIMERIC T-CELL
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.
STREET: S55 Thirteenth Street, N. W.
CITY: Washington
STATE: D. C.
CCUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

81.8%; Score 27; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                         DB 2; Length 5;
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ZIP: Z0004

ZIP: 20004

COUNTEX READABLE FORM:

MEDIUW TYER: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATCHIL Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/244,626

FILING DATE: July 15, 1994

FILING DATE: July 15, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB92/0251

FILING DATE: December 4, 1992

CLASSIFICATION: 424

ATTORNEY/AGENT INVORMATION:

NAME: Ernet, Barbara G.

REGISTRATION NUMBER: 1808-153A

TELEPHONE: (202) 783-6040

TELEPHONE: (202) 783-6040

TELEPAN: (202) 783-6041

INFORMATION FOR SEQ ID NO: 12:

SEQUIRACE CHARACTERICIES:
                                                                                                                                                                                                                                                                    87.9%; Score 29; DB
80.0%; Pred. No. 2e+0
ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08244626
Patent No. 5502167
GENERAL INFORMATION:
; INFORMATION FOR SEQ ID NO: 3; SEQUENCE CHARACTERISTICS: LENGTH: 5 amino acids TYPE: amino acid STRANDENDESS: unknown TOPOLOGY: unknown MOLECULE TYPE: DNA HYPOTHETICAL: N ANTI-SENSE: N US-08-053-451B-31
                                                                                                                                                                                                                                                                    Query Match 87.9
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / MOLECULE TYPE: protein
US-08-244-626-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
GY: linear
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Gaps

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Gaps
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PACENT NO. 5185431

APPLICANT: YOSHIMATSU, KENTARO; SHIKATA, YASUSHI, TANAKA, ISAO;

HASBGAWA, YOSHIKAZU, SETO, TOSHIO; OSAWA, TOSHIO

TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR

NUMBER OF SEQUENCE: 31

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/392,841

FILING DATE: 11-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE:
                                                                                                                                                                                             81.8%; Score 27; DB 2; Length 5; 100.0%; Pred. No. 2e+05; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 75.8%; Score 25; DB 1; Length 5; Best Local Similarity 75.0%; Pred. No. 2e+05; Matches 3; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-UN-1994
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/08353400 Patent No. 5665357 GENERAL INFORMATION:
                                                                                                                                                                           Query Match
Best Local Similarity 100.
                                            STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-400-27
                            amino acid
                                                                                    MOLECULE TYPE: IT HYPOTHETICAL: N ANTI-SENSE: N US-08-053-451B-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GYWM 4
                                                                                                                                                                                                                                                                                   2 YWWS 5
                                                                                                                                                                                                                                                                                                                                                                                                                US-08-353-400-27
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Patent No. 555584
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Chenn, Francis W.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLERCTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ATHEROSCLERCTIC PLAQUE SPECIFIC
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 2; Le...
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,157B
FILING DATE: 05-OCT-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5300
TELEPHONE: SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TELEGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIIOM TYPE: Riopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE: 26-APR.1993
FILING DATE: 26-APR.1993
CLASSIFICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR.1993
CLASSIFICATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELEPATION INFORMATION:
TELEPATION INFORMATION:
TELEPATION INFORMATION:
TELEPAT: 415-854-3660
TELERAX: 415-884-3694
TELERAX: 415-884-3694
TELERAX: 6141 PENNIE
INFORMATION POR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
81.8%; Score 27; DB
Best Local Similarity 100.0%; Pred. No. 2e+
Matches 4; Conservative 0; Mismatches
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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US-08-053-451B-32
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Gaps
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                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: Diskette, 5.25 inch, 360 kb storage
COMPUTER: Diskette, 210; Intel 80 285 Microprocessor
COMPUTER: Diskette, 210; Intel 80 285 Microprocessor
COMPUTER: Diskette, Wession 5.1
SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/318,970B
FILING DATE: October 6, 1994
CLASSIPICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD A. Steinberg
REGISTRATION NUMBER: 6-2371
TELEPHONE: (703) 549-2282
TELEPHONE: (703) 549-2282
TELEPAX: (703) 636-6106
TELEPAX: (703) 636-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.7%; Score 23; DB 1; Length 5; 100.0%; Pred. No. 2e+05; trive 0; Mismatches 0; Indels
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; Patent No. 636154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
APPLICANT: Stephen D. Holmes
; APPLICANT: Stephen D. Holmes
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; CURRENT APPLICATION NUMBER: 00/102,098
; PRIOR FILING DATE: 1998-09-28
; VINMER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
CORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: H-CDR1-3
CTHER INFORMATION: hypervariable region
US-08-318-970B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRATURE:
NAME/KEY: SITE
LOCATION: (1)...(5)
CYTHER INFORMATION: 15B8 heavy chain CDR 1
US-09-406-532-5
CITY: 413 N. Washington Street CITY: Alexandria STATE: Virginia CONTRY: Her
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.(
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 YWM 4
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US-08-198-70B-1
IS-Gequence 1, Application US/08318970B
Sequence 1, Application US/08318970B
Sequence 1, Application US/08318970B
Sequence 1, Application US/08318970B
Sequence 1, Application US/08318970B
SEGUENCE 1 INCOMMATION:
MANIBODISE SEQUENCES OF ANTI-IDIOTYPIC
STATE OF INVENTION: ANTIBODISE AGAINET ANTI-CANGER HUMAN MONOCLONAL ANTIBODY
STREET 443 N Washington Street
COMPRESSORDER ADDRESSE:
ADDRESSEE LAW Office of Sherman and Shalloway
STREET: 443 N Washington Street
CONTRES: USA
CONTRES
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Barent No. 5589573

GENERAL INFORMATION:
APPLICANT: Hideaki HAGIWARA, et al.
TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Office of Sherman and Shalloway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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2e+05;
thes 0; Indels
                                                                                        Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2e+
Matches 3; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: H-CDR1-1
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US-08-318-970B-3
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Search completed: April 22, 2003, 13:43:03 Job time : 29 secs
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Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-869-933-21
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Fatent No. 5770396
GENERAL INFORMATION
TITLE OF INVENTION: 1SOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH APPINITY RECEPTOR FOR
TITLE OF INVENTION: 1MMUNOGLOBULIN
HUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/479,089A

FILING DATE:
                                                                                             Sequence 7, Application US/08479089A
Patent No. 6383487
GENERAL INFORMATION:
APPLICANT: Amlot, Peter L.
APPLICANT: Akbar, Arne N.
APPLICANT: Heinrich, Gunther
APPLICANT: Cammisuli, Salvatore
ITLE OF INVENTION: CD25 Binding Molecules
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6383487artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Prec. ... 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/669,545
FILING DATE:
FRICK APPLICATION NUMBER: 07/669,545
FRICK APPLICATION NUMBER: 08-58P-1990
ATTORNEY/AGENT INFORMATION:
NAME: FULMEN, Diame E.
REGISTRATION NUMBER: 100-7617
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: (908) 522-6924
TELEFAN: (908) 522-6955
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Conservative
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Matches 3; Conserv
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US-07-869-933-21
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                                                                                      US-08-479-089A-7
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2 YWM
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  CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: USA
ZIP: 22313-298
COUNTRY: USA
ZIP: 22313-2999
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLEASIFICATION STEPHON:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHD
TELECOMMUNICATION INFORMATION:
TELEFRAN: (703)836-9300
TELEFRAN: (703)836-9300
TELEFRAN: (703)83-4109
TELEFRAN: (703)83-4109
TELEFRAN: (703)83-4109
TELEFRAN: (703)83-4109
TELEFRAN: 4 amino acids
TUDNENT: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.6%; Score 20; DB 1; ilarity 66.7%; Pred. No. 2e+05; Conservative 1; Mismatches
usSEE: Foley & Lardner
T: 1800 Diagonal Road, Suite 500
Alexandria
'VA
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GenCore version 5.1.4 p5_4578 (c) 1993 - 2003 Compugen Ltd.
                 Copyright
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OM protein - protein search, using sw model

April 22, 2003, 13:46:48; Search time 14 Seconds Run on:

(without alignments)
130.468 Million cell updates/sec

US-09-674-716B-11 98

1 EIRLKSDNYATHYAESVKG 19 Perfect score: Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

3433 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 19

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:*
1: Pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

cat gene leader pe chloramphenicol O-Ig H chain V-D-J r T-cell receptor be Ig H chain V-D-J r leukotriene B-4 12 neuropeptide pep -flt3 ligand isofor amino-acid racemas trypsin (EC 3.4.21 T-cell receptor be T-cell receptor be aminotransferase c protein kinase GSK Ig H chain V-D-J r 24K antigen - Myco formaldehyde dehyd formate dehydrogen protein QA100044 urease (EC 3.5.1.5 T-cell receptor be hypothetical prote CD33 antigen homol lacz/IS1 mutant fu Ig heavy chain CRD cytochrome-c oxida Ig heavy chain CRD protein-disulfide Description SUMMARIES F49215 PQ0072 A41077 430330 [78838 S30494 B24362 PH1587 PH1471 A61334 PH0768 I56393 PT0238 S65388 559495 539387 T0301 Query Match Length DB Score Result No.

ribulose-bisphosph hypothetical proce IG H Chain V-D-J r	Ig H chain V-D-J r hypothetical prote Ig H chain V-D-J r	Tha p 1 - Thaumeto 26K kidney and gal leucosulfakinin-II	ranatachykinin B - leucosulfakinin II hypothetical prote	hypothetical prote proteinase E - bla Ig gamma-2b chain serine proteinase
			•	
\$17217 \$51610 PH1622	PH1589 C85956 PH1621	A59396 D58501 GMROL2	B61033 B60656 G64003	D28551 A34858 C30503 PN0125
0 0 0	0 0 0	224	000	0000
16 16 16	16 17 18	18 10 10	222	12 12 13
20.4 20.4 20.4	20.4 20.4 20.4	20.4 19.9	4. 6. 6. 4. 4. 4.	19 19 19 19 19 19 19
0 0 0 0 0 0 0 0	200	20 19.5 19	110 100 100	9 9 9 9 9 9 9 9
30 31 32	33 34 35	36 38 38	39 40 41	4 4 4 4 5 4 3 3

A39109

hypothetical protein 1 - hepatitis C virus C;Species: hepatitis C virus C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 18-Jun-1993

CiAccession: A33109
RiHan, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-RiHan, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-Rititle: Characterization U.S.A. 88, 1711-1715, 1991
A; Title: Characterization of the terminal regions of hepatitis C viral RNA: identification A; Reference number: A39109; MUID:91156678; PMID:1705704
A; A; Accession: A39109
A; Status: preliminary
A; Residues: 1-16 <- HAN>

A; Cross-references: GB: M58406

Gaps ä 27.0%; Score 26.5; DB 2; Length 16; 70.0%; Pred. No. 5.4e+02; Live 0; Mismatches 2; Indels 7; Conservative Local Similarity Query Match Best Loca Matches

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NYCLH-AESV 16 œ

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cytochrome-c oxidase (EC 1.9.3.1) chain VIIc - bigeye tuna (fragment)
C;Species: Thunnus obesus (bigeye tuna)
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
C;Accession: S77990

C;Accession: \$77990 R;Arnold, S.; Lee, J.; Klm, M.; Song, B.; Linder, D.; Lottspeich, F.; Kadenbach, submitted to the Protein Sequence Database, June 1997

m.

A; Reference number: S77980 A; Accession: S77990

A; Molecule type: protein
A; Residues: 1-10 <ARN>
A; Experimental source: heart; liver
C; Genetics:

A; Genome: nuclear C; Function:

A; Pathway: oxidative phosphorylation; respiratory chain C; Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Gaps . 0 h Similarity 80.0%; Pred. No. 5.6e+02; Asservative 1; Mismatches 0; Indels Query Match Best Local Similarity Matches 4; Conserv

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formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) class III low activity form - Atlau C,Species Gadus morhua (Atlantic cod)
C,Species (Gadus morhua (Atlantic cod)
C,Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1996
C,Accession: D46285
K;Danielsson, O,; Jornvall, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 9247-9251, 1992
A;Title: "Bnzymogenesis": classical liver alcohol dehydrogenase origin from the glutathic A;Reference number: A46285, MUID:93028441; PMID:1409630
A;Accession: D46285
A;Accession: D46285
A;Accession: D46285
A;Residues: preliminary
A;Molecule type: procein
A;Residues: 1-10 cDAN.
A;Residues: 1-10 cDAN.
A;Note: sequence extracted from NCBI backbone (NCBIP:116272)
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C; Species: Alcaligenes eutrophus
C; Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C; Accession: S59495
R; Friedebold, J; Mayer, F; Bill, E; Trautwein, A.X.; Bowien, B.
Bil. Chem. Hoppe-Seyler 376, 561-568, 1995
A; Title: Structural and immunological studies on the Goluble formate dehydrogenase from ;
A; Reference number: S59492; MUID:96145736; PMID:8561915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein QA100044 - Arabidopsis thaliana (fragment)
(Species Arabidopsis thaliana (mouse-ear cress)
(Species Arabidopsis thaliana (mouse-ear cress)
(Species 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
(Spacession: PA0046; PA0042
(Spacession: PA0046; PA0042
(Spacession: PA0046; PA0042
(Spacession: PA0046; PA0042
(Spacession: Ally 1994)
(Spacession: Separation and characterization of Arabidopsis proteins by two-dimensiona
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Pred, No. 1.7e+03;
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44.4%; Pred. No. 2.5e+03;
tive 2; Mismatches 3; Indels
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Similarity 83.3%; Pred. No. 2.7e+03;
5; Conservative 0; Mismatches 1;
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Matches 3; Conservative
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A; Accession: PA0046
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A; Status: preliminary
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1 MKIDNIITY
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Matches 4;
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PHIG31
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Modecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PHIS80; MUID:93301609; PMID:8315387
                                                       Cibere: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 07-May-1999 C;Accession: 539387 #sequence_revision 26-Jul-1996 #text_change 07-May-1999 C;Accession: 539387 #sequence_revision P. Biochem: J. 296, 15-19, 1993 A;Title: Inactivation of glycogen synthase kinase-3-beta by phosphorylation: new kinase A;Title: Inactivation of glycogen synthase kinase-3-beta by phosphorylation: new kinase A;Title: Inactivation of glycogen synthase kinase-3-beta by phosphorylation: new kinase A;Teference number: 539387; MUID:94071817; PMID:8250835 A;Reference number: 539387 A;Residues: 1-19 <SUT>
A;Residues: 1-19 <SUT>
C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: phosphotransferase; protein kinase
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CiSpecies: Mycobacterium bovis
Rifitis, T.; Costopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R.
Infect. Immun. 59, 800-807, 1991
A;Fitis: Purification and characterization of major antigens from a Mycobacterium bovis
A;Reference number: A60278; MUID:91147217; PMID:190061
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........ Kinase GSK-3-beta (EC 2.7.1.-) - rabbit (fragment)
;Species: Oryctolagus cuniculus (domestic rabbit)
;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 07-May-1999
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Pred. No. 1.8e+03;
1; Mismatches 3; Indels
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A;Residues: 1-15 cLEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin
              protein kinase GSK-3-beta (EC 2.7.1.-)
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Matches 4; Conservative
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A;Molecule type: protein
A;Residues: 1-16 <FIF>
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Matches 5: Conserv
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protein-disulfide reductase (glutathione) (BC 1.8.4.2) Q-5 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: L2-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 23-Jun-1993
C;Accession: A41077
B;Srivastava, S.P.; Chen, N.; Liu, Y.; Holtzman, J.L.
J. Biol. Chem. 266, 20337-20344, 1991
J. Biol. Chem. 266, 20337-20344, 1991
A;Aritle: Purification and characterization of a new isozyme of thiol:protein-disulfide or fic phospholipase C form 1A.
A;Reference number: A41077; MUID:92041865; PMID:1657921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       car game leader peptide - Streptococcus agalactiae plasmid pIP501
C;Species: Streptococcus agalactiae
C;Species: Streptococcus agalactiae
C;Species: Streptococcus agalactiae
C;Accession: 830494
R;Trieu-Cuot, P.; de Cespedes, G.; Horaud, T.
R;Trieu-Cuot, P.; de Cespedes, G.; Horaud, T.
A;Title: Nucleotide sequence of the chloramphenicol resistance determinant of the Strepting A;Reference number: JQ1950; MUID:93096867; PMID:1461942
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EMBO J. 4, 2295-2300, 1985
A;Title: Regulation of the inducible chloramphenicol acetyltransferase gene of the Staph;
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C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 11-May-2000
                                                                                                                                                        Gaps
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A,Residues: 1-9 <TRI>
A,Cross-references: EMBL:X65462; NID:g49071; PIDN:CAA46454.1; PID:g581554
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                                                                                      Length 18;
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Pred. No. 3.4e+03;
1; Mismatches 2; Indels
                                                                                                                                                 4; Indels
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                                                                            22.4%; Score 22; DB 2; I
38.5%; Pred. No. 3.2e+03;
tive 2; Mismatches 4
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                                                                                                                                                 Conservative
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A,Molecule type: protein
A,Residues: 1-19 <SRI>
C,Keywords: oxidoreductase
                                                                                                                                                                                                                   6 SDNYATHYAESVK 18
                                                                                                                                                                                                                                                                                  4 SDDY--HFGPGTK 14
                                         Query Match
Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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12 LKKSNFA 18
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             C;Keywords: receptor
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C;Species: Helicobacter mustelae
C;Species: Helicobacter mustelae
C;Species: Helicobacter mustelae
C;Accession: F49215
R;Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.
R;Turbett, G.R.; Horne, R.; Mee, B.J.
R;Turbett, G.R.; Hoj, P.B.; Hoj, P.B.; Horne, R.; Mee, B.J.
R;Turbett, G.R.; Horne, R.; M
                                                                                                                      167525

CD33 antigen homolog - mouse (fragment)

CD33 antigen homolog - mouse (fragment)

Cjspecies : Mus sp. (mouse)

A. Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is I

A. Reference number: I53392; MUID:94298870; PMID:8026526

A. Reference number: I53392; MUID:9429870; PMID:8026526

A. Residues: I-15 sk sk sk

A. Residues: I-15 sk sk sk

A. Residues: I-15 sk sk sk

A. Cross-references: GB:S71349; NID:9550037

Cjenetics:
A. Genetics:
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: P60072
R;Tanaka, A.; Ishiguro, N.; Shinagawa, M.
Submitted to JIPLD, May 1990
A;Reference number: JQ0472
A;Reference number: JQ0472
A;Reference number: JQ0472
A;Restell type: mRNA
A;Residues: 1-18 < TAN>
A;Resperimental source: T cell
A;Genetics:
A;Genetics:
A;Genetics:
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hes 3; Conserv
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4 RRDHYGSSY 12
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   1 AESKKG
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19.4 Chain V-D-J region (wild-type clone 11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Accession: PH1587
C;Accession: PH1587
C;Accession: PH1587
J; Exp. Med. 178, 317-329, 1993
J; Exp. Med. 178, 317-329, 1993
J; Rievinson, D.A.; Campos-Torres, J.; Leder, P.
J; Exp. Med. 178, 317-329, 1993
J; Reference number: PH1580; MUID: 93301609; PMID: 8315387
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-12 < LEV>
A;Residues: 1-12 < LEV>
A;Reperimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin
A;Reference number: A24362; MUID:86081739; PMID:3865770
A;Accession: B24362
A;Accession: B24362
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-9 < BNU->
A;Cross-references: GB:X02872; NID:g46536; PIDN:CAA26630.1; PID:g581555
C;Comment: Ribosome stalling in the translation of this leader peptide, caused by the eff malation of the chloramphenicol 0-acetyltransferase from a ribosome binding site located C;Genetics:
A;Genome: plasmid
C;Superfamily: unassigned leader peptides
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21.4%; Score 21; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 4; Mismatches 0; Indels
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us-09-674-716b-11.closed.rsp

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TISSUE-Heart, and Liver;
MISSUE-Heart, and Liver;
MISDLINES-9454291; PubMed-9310366;
Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
Kadenbach B.;
The subunit structure of cytochrome-c oxidase from tuna heart and
liver. J. Biochem. 248:99-103(1997).
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P80982 thunnus obe
P47733 locusta mig
P36884 staphylococ
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                                                                                                    April 22, 2003, 13:43:07; Search time 25 Seconds (without alignments) 31.522 Million cell updates/sec
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P83323
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GenCore version 5.1.4 p5_4578 (c) 1993 - 2003 Compugen Ltd.
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B_RANCA
7_CLOPA
1_ANAVA
1_THEAQ
0_RAT
RABBE
1_LITRA
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1_LITRA
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Maximum Match 100%
Listing first 45 summaries
                                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Staphylococcus aureus.";
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KSEDYSS 9
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Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
-i- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus, and Streptococcus agalactise.

Streptococcus agalactise.

Plasmid pSCS6, Plasmid pSCS7, Plasmid pUB112, and Plasmid pIP501.

Bacteria; Firmicutes; Bacillales; Staphylococcus.

NCBI TaxID=1280, 1311;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
Schoofs L., Holman G.L., Hayes T.K., Nachman R.J., de Loof A.;
Schoofs L., Holman G.L., Hayes T.K., Nachman R.J., de Loof A.;
(In) McCaffery A., Wilson I. (eds.); ...
Chromatography and ison I. (eds.); ...
PORCHION Bress, New York (1990).
-!- FUNCTION: MYOTROPIC PEPTIDE.
-!- FUNCTION: MYOTROPIC PEPTIDE.
-!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
PROSITE; PS00259; GASTRIN; I.
HORMONE; Amidation; Sulfation.
                                                                                                                                                                                          Score 25; DB 1; Length 10;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                    10 AA; 1059 MW; 126DE767687B1DCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SULFATION (POTENTIAL).
AMIDATION.
9B5B5DA9BD6B5AAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22; DB 1; I
Pred. No. 6.7e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sulfakinin (LOM-SK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Chloramphenicol resistance leader peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                       12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA.
                                                                                                                                                                                                           25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.4%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 AA; 1440 MW;
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                           Local Similarity
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RLKSDNY 9
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1 QLASDDY 7
                                                                                                                                                                                                                                                                                     THYAE 15
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1 SHYAE 5
                                                                                                                                                                                                                                                                                                                                                                                                                     LOSK LOCMI
P47733;
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SEQUENCE
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                                                                                                                                                                                                         Query Match
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LPCA STAAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=S.agalactiae, PLASMID=pIP501;
MEDLINE=93096867; PubMed=1461942;
Tribut-Cuot P., de Cespedes G., Horaud T.;
"Nucleotide sequence of the chloramphenicol resistance determinant of the streptococcal plasmid pIP501.";
Plasmid 28:272-276(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=S.aureus; PLASMID=pUB112; MEDLINE=86081739; PubMed=3865770; BEDLINE=86081739; PubMed=3865770; BEDLINE=86081739; PubMed=3865770; Bucekner R., Matzura H.; Regulation of the inducible chloramphenicol acetyltransferase gene of the Staphylococcus aureus plasmid pUB112."; EMBO J. 4:2295-2300(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence and structural relationships of a chloramphenicol acetyltransferase encoded by the plasmid pSCS6 from
                                                                                                  Schwarz S., Cardoso M.;
"Nucleotide sequence and phylogeny of a chloramphenicol
acetyltransferase encoded by the plasmid pSCS7 from Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Broad-specificity amino acid racemase (EC 5.1.1.-) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21; DB 1; Length 9; Pred. No. 1.1e+05; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Embu, Acc., 124362.
PRF, B24962; Antibiotic resistance; Plasmid.
Leader peptide; Antibiotic resistance; Plasmid.
                                                                                                                                                                                                                                                      Antimicrob. Agents Chemother. 35:1551-1556(1991)
SEQUENCE FROM N.A.
SPECIES=S.aureus; STRAIN=436; PLASMID=pSCS7;
MEDLINE=92027652; PubMed=1929326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Appl. Bacteriol. 72:289-293(1992)
                                                                                                                                                                                                                                                                                                                                                             SPECIES=S.aureus; PLASMID=pSCS6;
MEDLINE=92388047; PubMed=1517170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.4%;
42.9%;
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NCBI_TaxID=10116;
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                                                                            (Fragment).
Zea mays (Maize)
                              MAIZE
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SEQUENCE
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                              UC21 M
P80627
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            15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ribosome-inactivating protein momorgrosvin (rRNA N-glycosidase) (EC 3.2.2.2) (Fragment).
Siraita grosvenorii (Monk's fruit) (Luo han guo).
Siraita grosvenorii (Monk's fruit) (Luo han guo).
Suraryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Siraitia.
                                                                                                         CATALYTIC BASE SPECIFIC TO D-ALANINE (BY
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                         "Isolation and characterization of a new ribosome inactivating protein, momorgrosvin, from seeds of the monk's fruit Momordica
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Pred. No. 1.5e+03;
1; Mismatches 1; Indels
                                                                                                                                              Score 21; DB 1; Length 10; Pred. No. 1.46+03;
                                                                                                                                        8C6C2DA154362E07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 AA; 2032 MW; 476E15CE683E2446 CRC64;
                                                                                                                       PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                          18 AA
                                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                                                                                                           FUNCTION, AND GLYCOSYLATION.
                                                                                                                                                                                                                                          PRT;
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"Isolation and characterization
                                                                                         Isomerase, Pyridoxal phosphate.
NON TER 1 1 ACT_SITE 6 CA
                                                                                                                                                      21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.4%;
ilarity 66.7%;
Conservative
                                                                                                                                        1572 MW;
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 4; Conserv
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16
16 AA;
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       STRAIN=AKU 0813;
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5 LKADAY 10
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P83323;
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NON TER
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8 NYATHY 13

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TISSUB-Coleoptile;

Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,

Perrollet J.-C., Zivy M., de Vienne D.;

"The maize two dimensional gel protein database: towards an integrated
                                                                                                                               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                               genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-!- MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
-!- PROTEIN IS: 5.9, ITS MW IS: 26.5 kDa.
-!- SIMILARITY: TO L.A-SCORBATE PEROXIDASES.
Maize-2DPAGE; P80627; COLEOPTILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UNM-2002 (Rel. 41, Last annotation update)
Cytochrome c oxidase polypeptide VIIc, mitochondrial (EC 1.9.3.1)
(VIIIA) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY
                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 443)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
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Pred. No. 1.5e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 AA; 1938 MW; F32F6FEF038BAB8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 AA.
18 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
STANDARD;
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Matches 5, Conserv
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Electrophoresis 18:2795-2802(1997)
                                                                                                                                                                                                                                                  Local Similarity
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NON TER
SEQUENCE
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MEDLINE=20408845; PubMed=10951191;

Rozek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,

Rozek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,

Wallace J.C., Tyler M.J.;

The antibiotic and anticancer active aurein peptides from the australian bell frogs Litoria aurea and Litoria raniformis the solution structure of aurein 1.2.";

Eur. J. Blochem 267.5330-5341(2000)

- PUNCTION: ANTIMICROBIAL ACTIVITY AGAINST L.LACTIS, L.INNOCUA,

M.LUTEUS, S.AUREUS, S.EPIDERMIDIS AND S.UBERIS. PROBABLY ACTS BY DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.

C. SHOWS ANTICANCER ACTIVITY.

C. IS SUBCELLULAR LOCATION: SECRETED.

M. Amidation; Antibiotic.

M. Amidation; Antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                              ΒY
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE=88163340; PubMed=9504812;
Dunn M.J., Corbett J.M., Wheeler C.H.;
"HSC-APPAGE and the two-dimensional gel electrophoresis database of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
Canis.
                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae, Pelodryadinee, Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JULN-2002 (Rel. 41, Last annotation update)
ATP synthase beta chain, mitochondrial (EC 3.6.3.14) (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 1; Length 17; Pred. No. 2.1e+03;
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                       Score 20; DB 1; Length 10;
Pred. No. 1.2e+03;
1; Mismafches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMIDATION.
P6AC0A580428EAFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae;
NCBI_TaxID=9615;
    126DE767687B1B0B CRC64;
                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aurein 3.2.
                                                                                                                                                                                                             and
                                                                                                                                              17 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                           Litoria raniformis (Southern bell frog),
Litoria aurea (Green and golden bell fro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 17 AA; 1769 MW;
      1117 MW;
                        20.4%;
ilarity 60.0%;
Conservative
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Best Local Similarity
Matches 4; Conserv
                           Query Match
Best Local Similarity
      10 AA;
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TISSUE=Heart;
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      SEQUENCE
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AU32 LITRA
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SUBUNIT.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate + H(+) (Out).
-!- SUBUNIT: P-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
-!- SUBCELLULAR LOCATION: Mitcochondrial.
-!- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
HSC-2DPAGE; P99504; DOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peripjaneta americana (American cockroach).
Bukaryota; Metazoa, Arthropoda; Madibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                                                                        InterPro; IPR000194; ATPase a/bcentre.
PROSITE; PS00152; ATPASE ALPHA BETA; PARTIAL.
ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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SULFATION (IN L.MADERAE, BUT NOT IN
P.AMERICANA).
-i- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=L.maderae;
MEDLINE=87048769; PubMed=3778455;
Nachman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.;
"Leucosulfakinin-II, a blocked sulfated insect neuropeptide with homology to cholecystokinin and gastrin.";
Biochem. Biophys. Res. Commun. 140:357-364(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20; DB 1; I
Pred. No. 2.4e+03;
1; Mismatches 4;
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MEDLINE=90137190, PubMed=2615921,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1995 (Rel. 22, Last amnotation update)
Leucosulfakinin-II (LSK-II).
Leucophaea maderae (Madeira cockroach), and
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PIR; B60565; B60565.
InterPro; IPRO1651; Gastrin.
PROSITE; PS00259; GASTRIN; 1.
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Gaps

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RESULT 12 TKNB RANCA

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Comp. Biochem. Physiol. 117B:445-452(1997).
-1- FUNCTION: CYSTEINE PROTEINASE THAT HYDROLYSES BASIC PROTEINS.
HYDROLYZE BASIC PROTEINS SUCH AS HISTONE, SALMINE AND CLUPAINE BUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOT MILK CASEIN.
-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE WITH BASIC RESIDUES AT
                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NISI ANAVA STANDARD; PRT; 15 AA.
044507;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
Cysteine desulfurase 1 (BC 4.4.1.-) (Nitrogenase metalloclusters biosynthesis protein nifs1) (Fragment).
Anabaena variabilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Miltpain, new cysteine proteinase from the milt of chum salmon, Oncorhynchus keta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena
                                                                                                                                                                                                                      / Match 19.4%; Score 19; DB 1; Length 14; Local Similarity 41.7%; Pred. No. 2.5e+03; les 5; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.4%; Score 19; DB 1; Length 15; 80.0%; Pred. No. 2.7e+03; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
116-OCT-2001 (Rel. 40, Last annotation update)
Mitpain (EC 3.4.22.-) (Fragment).
Oncorbynchus keta (Chum salmon).
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Kawabata C., Ichishima E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 80.0 tes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                        3 NNXTIEDQGVKG 14
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P81037;
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SEQÜENCE
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SEQUENCE.
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MILT ONCKE
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NIS1 ANAVA
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                                                                   Gaps
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Regul. Pept. 46:81-88(1993).
-!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                              01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ranatachykinin B (RTK B).
Rana catesbelana (Bull frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Annva; Neobatrachia; Ranoidea; RanaillaxillaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=91254337; PubMed=2043143;
Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
"Isolation of four novel tachykinins from frog (Rana catesbelana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Unknown protein CP 37 from 2D-page (Fragment).
Clostridium pasteurianum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1501;
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MEDLINE=94023216; PubMed=8210506;
Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
"Four novel tachykinins in frog (Rana catesbeiana) brain and
                                    Length 10;
                                                                   0; Indels
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PR051TE; PS00267; TACHYKININ; 1.
Tachykinin; Neuropeptide; Amidation.
MOD RES 10 10 AMIDATION.
SEQÜENCE 10 AA; 1210 MW; 917E556B59D5BAB5 CRC64;
10 AA; 1255 MW; 9B4F5391E86B5AAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  brain and intestine.";
Biochem. Biophys. Res. Commun. 177:588-595(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
                                19.4%; Score 19; DB 1; I larity 60.0%; Pred. No. 1.7e+03; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 1; I
Pred. No. 1.7e+03;
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                                                                                                                                                                                                                  STANDARD;
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PIR; JE0427; JE0427.
PIR; B61033; B61033.
             5 KSDNY 9
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UN37 CLOPA
ID UN37 CLOPA
AC P81358;
DT 15-JUL-1998
DT 15-JUL-1998
DT 15-JUL-1998
DC 15-JUL-1998
DC Clostridium;
CC Clostridium;
CC Clostridium;
CC NACEL TAXID=1.
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Gaps

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-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- MISCELLANEOUS: BELONGS TO THE NIFT (GENE CLUSTER WHICH IS EXPRESSED IN HETEROCYST'S UNDER ANABROBIC CONDITIONS.
-!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES. NIFS/ISCS SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYANDDACTERIUM.",
Proc. Natl. Acad. Sci. U.S.A. 92:9358-9362(1995).
-!- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL STLFUR ATOMS FROM CYSTEINE TO PRODUCE ALANINE. SEBAS TO PARTICIPATE IN THE BIOSYNTHESIS OF THE WITROGENASE METALLOCIUSTERS BY PROVIDING THE INORGANIC SULFUR REQUIRED FOR THE FE-S CORE FORMATION (BY
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                                                                                                                                                                                                                                                                             EXPRESSION PATTERN.
STRAIN-PCC 7937 / ATCC 29413;
MEDLINE-96016168; PubMed=7568132;
Thiel T., Lyons E.M., Erker J.C., Ernst A.;
"A second nitrogenase in vegetative cells of a heterocyst-forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 2.7e+03;
0; Mismarches 1; Indels
                                                                          SEQUENCE FROM N.A.
STRAIN=PCC 7937 / ATCC 29413;
Monnerjahn U. Boehme H.;
Submitted (DEC-1992) to the EMBL/GenBánk/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00192; Aminotransfv.
PROSITE; PS00595; AA TRANSFER CLASS 5; PARTIAL.
Nitrogen fixation; Lyase; PyrIdoxal phosphate.
15 15
SEQÜENCE 15 AA; 1684 MW; 08B8F106DE65547D CRC64;
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80.0%;
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Best Local Similarity
Matches 4; Conserv
NCBI_TaxID=1172;
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Search completed: April 22, 2003, 13:48:59 Job time : 27 secs

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April 22, 2003, 13:45:28.; Search time 28 Seconds (without alignments) 139.818 Million cell updates/sec
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_bacteriap:*
sp_archeap:*
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Perfect score:
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                                                                                                                                                                                                                                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q73129 human immun	P83219 homo sapien	Q9ibm5 human immun	Q9uc27 homo sapien	Q91434 salmonella	Q9khj4 caulobacter	Q9uwh6 thermococcu	Q9trt6 sus scrofa	Q9trt4 sus scrofa	Q84863 unidentifie	Q9v2x3 methanobact	Q9twr4 tityus serr	Q93057 homo sapien	P70319 mus musculu	Q93le4 heliobacill	P96423 pseudomonas
er Er	073129	P83219	O9 IBMS	Q9UC27	Q9L434	Q9KHJ4	ЭНМП6О	Q9TRT6	Q9TRT4	084863	Q9V2X3	Q9TWR4	093057	·P70319	Q93LE4	P96423
DB	15	4	15	4	N	N	7	9	9	12	-	S	4	11	7	7
* Query Match Length DB	19	15	15	13	19	13	15	15	15	19	17	13	14	14	о	10
% Query Match	32.7	30.6	29.6	28.6	27.6	26.5	26.5	26.5	26.5	26.5	25.5	24.5	24.5	24.5	23.5	23.5
Score	32	30	29	28	27	26	26	56	26	26	25	24	24	24	23	23
Regult No.	-	7	m	4	S	9	7	80	6	10	11	12	13	14	15	. 16

P96347 helicobacte QBupi2 human immun Q97449 bordetella Q91441 archaeoglob Q9px1 struthio ca Q97444 peeudomonas Q97454 pleudomonas Q97456 helicobacte Q9756 helicobacte Q9756 helicobacte Q9756 helicobacte Q9757 ptrainia pe C60842 homo sapien Q9144 pyrococcus. P82346 asaphis dic Q9143 exprecolagus Q9248 asaphis dic Q9143 exprecolagus Q951399 bacillus th Q91418 oryctolagus Q95210 staphylococ Q4737 sechericola Q96121 craphylococ Q4737 sechericola Q96121 oryctolagus Q95234 shigella so Q96127 oryctolagus Q96133 eshigella so Q96136 alteromonas Q54349 streptomyce	pdate) update) update) tivirus. tivirus. Daniels M., Kunstman K.J., Koup R.A.; cy Virus Type 1 During the BJ databases. BJ databases.	CRC64; Length 19; ; Indels 0; Gaps 0;
2 P96347 2 Q9WH92 2 Q9WH93 2 Q9WH74 2 Q9R474 2 Q9R474 2 Q9R474 2 Q9R474 2 Q9R474 4 Q9WH71 1 Q9WH71 5 Q9V973 6 Q9TR18 6 Q9TR18 6 Q9TR18 6 Q9TR18 7 Q9TR18 6 Q9TR18 6 Q9TR18 6 Q9TR18 6 Q9TR18 7 Q9TR18 10 Q9CTR2 2 Q57337 2 Q57337 2 Q57337 2 Q57337 3 Q9TR18 10 Q9CTR2 2 Q57337 10 Q9CTR3 2 Q57337 3 Q9TR18 10 Q9CTR2 2 Q57337 3 Q9TR18 10 Q9CTR2 2 Q57337 3 Q9TR18 10 Q9CTR2 2 Q57337 3 Q9TR18 10 Q9CTR2 2 Q57337 3 Q9TR18 3 Q9TR18 4 Q9TR7 3 Q9TR18 4 Q9TR7 3 Q9TR18 4 Q9TR7 4 Q9TR7 5 Q9TR18 6 Q9TR7 6 Q9TR7 6 Q9TR7 7 Q9TR18 6 Q9TR7 7 Q9TR18 7 Q9TR1	ALIGNMENTS  PRT; 19 AA.  Created)  Last sequence upda  Last annotation up  gment).  Ne type 1.  Retroviridae; Lentiv  B.D., Safrit J.T., R  an Immunodeficiency  nn.;  te EMBL/GenBank/DDBJ  The EMBL/GenBank/DDBJ  The EMBL/GenBank/DDBJ  The EMBL/GenBank/DDBJ  The EMBL/GenBank/DDBJ	# E117102D52800EF4  # Score 32, DB 15;  # Pred. No. 1.5e+02;  # Mismatches
2233.55 2233.55 2233.55 2233.55 2233.55 2233.55 2233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 233.55 23	TIT 1  (23) (273129) (273129) (201129) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80) (201-80)	ER 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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Gapa
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                                                                                                                                                                                                                                                                                                                        Boue F., Duquenne C., Lassalle B., Lefevre A., Finaz C.;
"FLB1, a human protein of epididymal origin that is involved in the sperm-cocyte recognition process.";
Biol. Reprod. 52:267-278(1995).
SEQUENCE 13 AA; 1610 MW; 000A683B81B7A45B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robbe-Saule V., Coynault C., Ibanez-Ruiz M., Hermant D., Norel F., "Identification of a non-haem catalase in Salmonella and its regulation by Ross (sigma 8).", Mol. Microbiol. 39:153-1545(2001).

EMBL, AJ251362, CAB71038.1, -.
                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNAY-2000 (TrEMBLrel. 14, Last annotation update)
94 kDa epididymal cytokeratin-like protein (Fragment).
Homo sapiens (Human).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
NON TER 19 19 SEQUENCE 19 AA; 2448 MW; 05D3DB83C7CBE7E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9L434;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 2.4 kDa protein (Fragment).
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Proteolysis tag (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 2;
Pred. No. 1e+03;
13 AA.
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MEDLINE=21160188; PubMed=11260470;
                                                                                                                                                                                                                                                                                                           MEDLINE=95226590; PubMed=7536047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.6%;
Local Similarity 66.7%;
les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 66.7
Matches 4; Conservative
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PRELIMINARY;
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1 NYSTYY 6
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Q9KHJ4;
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                          Q9UC27;
Q9UC27
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Q9L434
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TISSUE-NASAL MUCUS;

X MEDILINE-2113725; Pubmed=1152286;

X COLE A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;

COLE A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;

XT COLE A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;

XT COLE A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;

XT COLE A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;

XT COLE A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;

XT COLE A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;

XT CALCANTON: POSSESSES ANTIFUNGAL ACTIVITY AGAINST C.ALBICANS AND IS

XALNEW.

XI ALSO ACTIVE AGAINST E.COLI AND P.AERUGINOSA BUT NOT

L., MONOCYTOGENER AND S. AUREUS.

XI ALSO ACTIVE AGAINST B. SAUREUS.

XI ALSO ACTIVE AGAINST C. THE C. TENTING P. HONGALDI.

XI AND ANTIMICROBIAL ACTIVITY IS ENHANCED BY ZNCL2.

XM ANTIMICROBIAL ACTIVITY IS E
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MEDLINE=95115054; PubMed=7815476;
Ahmad N., Baroudy B.M., Baker R.C., Chappey C.;
"Genetic analysis of human immunodeficiency virus type 1 envelope V3 region isolates from mothers and infafits after perinatal transmission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                         Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 4; Length 15;
Pred. No. 2.4e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 AA; 1794 MW; 747C6A62800EF4A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0cr-2000 (TrEMBLrel. 15, Last annotation update)
Envelope glycoprotein, V3 region (Fragment).
                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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EMBL; U16595; AAA64161.1; -.
NON TER 1
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                                                   01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, Calcitermin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 54.5
Matches 6; Conservative
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     PRELIMINARY;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 2.1 kDa profein (Fragment).
unidentified human poliovirus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Enterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE=92144618; PubMed=1737046;
Koike K., Urata Y., Goto S.;
'Proteinsae-catalyzed activation of porcine heart muscle pyruvate dehydrogensse and identification of its cleavage site.";
Biochim. Biophys. Acta 1118:223-230(1992).
SEQUENCE 15 AA; 1757 MW; 9405BFFE4B126598 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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"Primary structure of poliovirus defective-interfering particle genomes and possible generation mechanisms of the particles.";
J. Mol. Biol. 192:473-487(1986).
EMBL, M30221, AAA66829.1;
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Pred. No. 1.5e+03;
0; Mismatches 1; Indels
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         dehydrogenase and identification of its cleavage site.";
                                                                                                                                           1; Indels
                           Biochim. Biophys. Acta 1118:223-230(1992).
SEQUENCE 15 AA; 1787 MW; DB1265CDF7737E16 CRC64;
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71.4%; Pred. No. 1.1e+03;
:ive 1; Mismatches 1;
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MEDLINE=87169734; PubMed=3031313;
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80.0%;
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NON TER 1 1
NON TER 19 19
SEQUENCE 19 AA; 210
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Best Local Similarity
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                                                                                                                                                                                                                        7 EVRSKSD 13
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                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20345063; PubMed=10884408;
Keiler K.C., Shapiro L., Williams K.P.;
turkNas that encode proteolysis-inducing tags are found in all known bacterial genomes: A two-piece tmRNA functions in Caulobacter.";
Proc. Natl. Acad. Sci. U.S.A. 97:7778-7783 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermococcus litoralis.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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"Characterization of 2-ketoisovalerate ferredoxin oxidoreductase, a new and reversible coenzyme A-dependent enzyme involved in peptide fermentation by hyperthermophilic archaea.";
J. Bacteriol. 178:780-787(1996).
SEQUENCE 15 AA; 1549 MW; 0C1766910B222944 CRC64;
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Kolke K., Urata Y., Goto S.;
"Proteinase-catalyzed activation of porcine heart muscle pyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                    Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
Caulobacter.
NCBI_TaxID=155892;
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01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Keto-valine-ferredoxin oxidoreductase alpha-subunit, VOR alpha
                                                                                                                                                                                                                                                                                                                                 Length 13;
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Pred. No. 9.4e+02;
3; Mismatches 2;
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Best Local Similarity 45.5
Matches 5; Conservative
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Caulobacter crescentus
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NCBI_TaxID=2265;
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MEDLINE=96224102; PubMed=8650211;
Busslinger M., Klix N., Pfeffer P., Graninger P.G., Kozmik Z.;
"Deregulation of PAX-5 by translocation of the Emu enhancer of the IgH
                                                                                                                                                                                                                                                                                                        Iida S., Rao P.H., Nallasivam P., Hibshoosh H., Butler M., Louie D.C., Dyomin V., Ohno H., Chaganti R.S.K., Dalla-Favera R.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=96234102; PubMed=8650231;
Buselinger M., Klix N., Pfeffer P., Graninger P.G., Kozmik Z.;
"Deregulation of PAX-5 by translocation of the Emu enhancer of the Ig
locus adjacent to two alternative PAX-5 promoters in a diffuse large-
cell lymphoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Deregulated PAX-5 transcription from a translocated 1gH promoter in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21354098; PubMed=11460166; Pasqualucci L., Neumeister P., Goossens T., Nanjangud G., Chaganti R.S.K., Kuppers R., Dalla-Favera R.; "Hypermutation of multiple proto-oncogenes in B-cell diffuse largecell lymphomas.";
                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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TISSUE=MARGINAL ZONE LYMPHOMA;
Morrison A.M., Jaeger U., Chott A., Haas O.A., Schebesta M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 4; Length 14;
Pred. No. 2.2e+03;
2; Mismatches 4; Indels
                          01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
B cell specific activator protein BSAP (PAX5) (Fragment).
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BMBL, 02539, AAB09533.1; -
BMBL, U56836, AAB16833.1; -
BMBL, AF074913; AAC69188.1; -
BMBL, AF986791; AAC69188.1; -
NOW TER 14
SEQUENCE 14 AA; 1683 MW; E11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             marginal zone lymphoma.";
Blood 0:0-0(1998).
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J. Bacteriol. 170:2247-2253 (1988).
EMBL; M20391; AAA72654.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88198019; PubMed=2834336;
Schallenberg J., Moes M., Truss M., Reiser W., Thomm M., Stetter K.O.,
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Tityus serrulatus (Brazilian scorpton).
Bukaryota; Metazoa; Arthopoda; Chelicerata; Arachnida; Scorpiones; Buthoidea; Buthidae; Tityus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94024945; PubMed=8212046;
Ferreira L.A., Alves E.W., Henriques O.B.;
"Peptide T, a novel bradykinin potentiator isolated from Tityus serrulatus scorpion venom.";
Toxicon 31:941-947(1993).
SEQUENCE 13 AA; 1604 MW; 35770B0644FC02D7 CRC64;
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01-MAY.2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
RNA polymerase subunit B'' (Fragment).
Methanobacterium thermoautocrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
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Pred. No. 2e+03;
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Pred. No. 1.9e+03;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
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Best Local Similarity
Matches 4; Conserv
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01-MAY-2000
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locus adjacent to two alternative PAX_5 promoters in a diffuse largecell lymphoma.";
Proc. Natl. Acad. Sci. U.S.A. 93:6129-6134(1996).
EMBL, U56838, AAB16835.1; -.
NON TER 14 14
SEQÜENCE 14 AA, 1683 MW; E113518FA19953A1 CRC64;
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093LE4;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last amoctation update)
Proteolysis tag (Fragment).
Heliobacillus mobilis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Heliobacteriaceae; Heliobacillus.
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24.5%; Score 24; DB 11; Length 14;
Best Local Similarity 45.5%; Pred. No. 2.2e+03;
Matches 5; Conservative 2; Mismatches 4; Indels
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Williams K.P.

Williams K.D.

SEQUENCE 9 AA; 937 MW; 7CD8D72DCB544AAB CRC64;
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MEDLINE-20063247; PubMed=10592213;
Williams K.P.;
"The tmRNA website.";
Nucleic Acids Res. 28:168-168(2000).
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2 EIHCKHDPFAS 12
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Mutant 5 of the CD Anti-platelet glyc Mouse HeFi antibod A3 derivative #16,

Llama CDR2 region

Mouse antibody var Anti-hIL12 antibod Llama CDR2 region Human anti-HBs ant Llama CDR2 region

AAB39862 AAB52188 AAE10817

AAB39846 AAB67496 AAU82488

H-CDR-2 of anti-id Scaffold protein S Mutant 3 of the CD

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CD23; FCERII; IgE receptor; monoclonal antibody; CII; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria, nephrotic syndrome; glomerulonephritis; psoriasis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy, asthma; rhinitis; czema; insulitis; graft-versus-host disease; COPD; bronchitis; diabetes;
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AAB84980
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 B-cell malignancy; therapy.
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Mus musculus
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 AAY32258;
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 Light chain CDR H2
Murine PSCA antibo
Scaffold protein S
A3 derivative #15,
H. pylori 26 kDa p
CDRH 20 f monoclona
Mouse mAb 1D9 anti
Anti-Staph (HAX) 9
Llama CDR2 region
H-CDR-2 of anti-id
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| SIDS2/gcgdata/geneseq_geneseqp_embl/AA1981_DAT:*
| SIDS2/gcgdata/geneseq_geneseqp_embl/AA1991_DAT:*
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         GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Anti-platelet glyc Human scFv clone 2 Dl2 seFv CDR H2 re Anti-TANGO 268 scF Anti-IL-18 antibod

ALIGNMENTS

99WO-GB01434.

07-MAY-1999; 19-MAY-1998;

18-NOV-1999.

AAB35297 AAB30033 AAY40694-AAB10002

AAR84529 AAO14988 AAW94737 AAU82539 AAR74934

92.9 81.6 71.6 71.4 69.4 66.3 65.3 53.1

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98GB-0009839.

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Anti-cancer specif Tumour antigen ant Anti-hIL12 antibod Anti-hIL12 antibod Anti-hIL12 antibod

AAB39819 AAW1665

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                                                                                                                                                                                                               This sequence represents complementarity determinating region 2 (CDR H2) of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibodies, such as chimeric or humanised antibodies, which comprise unfibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of C11 light and heavy chain C CDRs (see ANY32254-59) to render them capable of binding to the CD23 type II andlecule expressed on heamatopoletic calls. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, clubus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, clubus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, clubus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, colitis, Crohn's disease, Sogrem's syndrome, allergic syndrome, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, colitis, crohn's disease, Sogrem's syndrome, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, cerema, graft-versus-host disease, COPD, insultis, bronchitis (particularly chronic bronchitis) crohn's principle of diabetes), and B-cell malignancies (claimed). They are also useful contractions between CD23 and various ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibodies binding to prostate stem cell antigen inhibit the growth of cancer cells and are used to detect and treat prostate, pancreatic or
                                                                                                              Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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  Shearin J;
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100.0%; Pred. No. 1.4e-09; Midmatches 0; Indels
  Rapson NT,
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Ellis JH,
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                                                                                                                                                                              Claim 1; Page 40; 81pp; English.
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03-MAY-2000; 2000US-0564329
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  Crowe SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNIV CALIFORNIA.
UROGENESYS.
                                          WPI; 2000-053101/04.
N-PSDB; AAZ34743.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-159478/16
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Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 AA;
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Bonnefoy JMP,
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(UROG-) UROGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB35297;
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                                                                                       with prostate stem cell antigen (PSCA) by administering an antibody which selectively binds to PSCA and inhibits the growth of the cancer cells. The PSCA gene is found on human chromosome 8Q24.2. The invention provides the human and murine PSCA protein and coding sequences, which can be used not only in the treatment of, but also in detection and prognosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAB22930-B29939 were used in the production of the proteins of the invention.
                                                             present invention describes a method of treating cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, CTLA-4; scaffold protein; antigen-binding; receptor-binding; SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis; diabetic retinopathy; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful supporting framework and carrying antigen- or receptor binding
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88.2%; Pred. No. 1.2e-06;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                        Score 91; DB 22; Length 19;
Pred. No. 2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                        ch 92.9%; Score 91; DB 1. Similarity 89.5%; Pred. No. 2e-0 17; Conservative 2; Mismatches
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Example 21; Fig 61; 229pp; English.
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Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-665002/64.
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                                                                                                                                                                                                                                                      prostate cancer
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1 RLNSDNFATHYAESVK 16

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AAB10002

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Sequences AAY40680-Y40703 are functionally equivalent derivatives of the A3 peptide (AAY40605) which forms part of a beta sheet. Peptides CC A3 peptide (AAY40605) which forms part of a beta sheet. Peptides CC (AAY40601-Y40609) together form a shighe-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 1 disulfide bond, contains less than 10% alpha helix CC and contains at least 8 le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New scaffold protein, useful for stabilizing antigens used as vaccines
                                                                                                                                                                                                                                                                                                                                                    Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
                                                                                                                                                                                                                                                                                                   A3 derivative #15, beta strand of scaffold protein structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 6; 105pp; English.
                                                                                                                                                             AAY40694 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                               tumour, chemotherapeutic agent.
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3 RLKSDNYATHYAESVKG 19
                             1 RLNSDNFATHYAESVKG 17
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This invention describes a novel method for the detection of a mammalian infection by an acid-resistant microorganism (A) by treating a facel sample with at least two different monoclonal antibodies (MAD) (or their fragments or derivatives) or aptamers (collectively (I)) and detecting formation of a complex (C) between (I) and the corresponding antigen of (A). The first and second (II) bind to epitopes of different antigens (Ag). These epitopes are present, after passage through the intestines, in at least some mammals, and have either: (I) their native structure; or (II) a structure against which an antibody is produced by an animal infected or immunized with (A), or its extract, lysate, derived protein or fragment, or with a synthetic peptide. Practically all mammals display infection by acid-fast bacteria, particularly of the genera Helicobacter, Mycobacterium and Campylobacter, apecifically H. Pylori, H. hepaticus, therapeutically. The method is direct and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible degradation of antigens during passage through the intestines. This sequence represents a fragment of a H. Pylori 26 kDa protein-binding antibody heavy chain complementarity determining region CDR2 which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a faecal sample with two binding reagents for antigens that survive intestinal passage -
                                                                                                                                                 Acid-resistant microorganism; detection; faecal; intestine; infection; monoclonal antibody; heavy chain; complementarity determining region;
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                                                                                                              H. pylori 26 kDa protein-binding antibody heavy chain CDR2 peptide.
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AAB10002 standard; Protein; 19 AA.
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98EP-0120687.
                                                                        (first entry)
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                                                                                                                                                                                                                                                               WO200026671-A1.
                                                                                                                                                                                                                            Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen-antibody specificity exchanger - used in a method to redirect a patient's antibodies against polio:virus to fight HIV infection in the patient
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Pred. No. 0.00014;
3; Mismatches 2; Indels
                                                                                                                                                                                              CDRH2 of monoclonal antibody C1-5.
                                                                        AAR84529 standard; peptide; 19 AA.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 AA;
                                                                                                                                                       06-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1995;
                                                                                                                                                                                                                                                                                                                                                            WO9529938-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saellberg M;
                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-SEP-2002
                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                 AAR84529;
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                                  RESULT 6
                                                       AAR84529
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The invention comprises a method of inhibiting graft rejection, graft versus host disease or chronic rejection of a transplanted graft. The method involves administering an antagonist of CC chemokine receptor 2 (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may be an anti-CCR2 antibody (i.e. containing light and heavy chain complementarity determining regions from various non-human origins). CCR2 is known to be involved in the rejection of transplanted grafts. The method of the invention is useful for inhibiting graft rejection particularly allografts such as kidney, liver, lung, heart-lung, particularly allografts such as kidney, liver, lung, heart-lung, inhibiting graft versus host disease and for inhibiting chronic rejection of a transplanted graft. The present amino acid sequence represents a mouse mAb 1D9 antibody heavy chain complementarity determining region 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody, MAb, lipoteichoic acid; gram positive, bacteria, immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/note= "complementarity determining region (CDR)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting graft rejection, graft versus host disease or chronic rejection of a transplanted graft, involves administering a CCR2
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lung transplant; heart-lung transplant; pancreas transplant; bowel transplant; heart transplant; graft versus host disease; chronic graft rejection; antibody heavy chain; mAb 1D9; CDR2; complementarity determining region 2.
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Pred. No. 0.00045;
4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                   13-APR-2001; 2001US-0835087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.3%;
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Best Local Similarity 70.0-
Best Local 21 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-351265/38.
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The present invention relates to a phage display library of variable heavy domain (VHH or VH) fragments (sdab fragments) derived from liama antibodies. The library is useful for in vitro selection against any antigen of interest as a target. Single domain anti-idiotypic antibody fragments are isolated from the library using phage display technology and an antibody serving as an antigen. Such anti-idiotypic antibody fragments have great potential in evoking the immune system response to pathological antigens and in vaccine development. The large size of the library considerably increases the probability of isolating from it antigen-binding fragments having high affinity to almost any predetermined target (antigen of interest). The library eliminates the development of anti-idiotypic antibodies by immunisation and allows isolation of anti-idiotypic antibodies by immunisation and allows the llama heavy chain domain fragments of the invention.
                                                                                                                                         New phage display library of variable heavy domain antigen-binding fragments derived from llama antibodies, useful for in vitro selection against any antigen of interest as a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H-CDR-2 of anti-idiotype antibody against human anticancer antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel anti-idiotype antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A new anti-idiotype antibody against a human anticancer monoconal antibody is claimed. This antibody contains in its heavy chain 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; complementarity determining region.
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                                                                                                                                                                                                                                         Claim 16; Page 32; 46pp; English.
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(CANA ) NAT RES COUNCIL CANADA
                                             Dubuc G, Narang S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93JP-0272950.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 RLKSDNYATHYAESVKG 19
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Best Local Similarity 58.8
Matches 10; Conservative
                                                                                           WPI; 2002-083093/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 AA;
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                                             Tanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR74934;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a monoclonal antibody (MAb) to lipoteichoic acid of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin variable immunoglobulin comprising at least part of a human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and killing of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipoteichoic acid antibody or characterised by amino acids anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacterial infections.

Sequences AAW94735-39 represent heavy chain variable regions of the anti-lipoteichoic antibody 96-100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                    New antibodies to lipoteichoic acid of gram positive bacteria - used to develop products for the diagnosis, prevention and treatment of infections caused by gram positive bacteria
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Pred. No. 0.00065;
2; Mismatches 2; Indels
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                                                                                                                                                                                      (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED
                                                                                                                                                                                                                                    Stinson JL, Wong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complementarity determining region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 21; Fig 12; 150pp; English
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                                                                                        98WO-US12402.
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Best Local Similarity 70...
Best Local 3 Conservative
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                                                                                                                                                                                                                                    Fischer GW, Schuman RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       guanicoe glama.
                                                                                                                                                                                                                                                                                    WPI; 1999-095329/08.
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                                                                                                                                                                                                                                                                                                           N-PSDB; AAX05581
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W09857994-A2
                                                                                           16-JUN-1998;
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                                             23-DEC-1998
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complemetarity determining regions CDR1 (AAR74929-R74931), CDR2 (AAR74932-R79932-R794931), this is also true of the light chain which has its own CDR1 (AAR74944-R74946 and AAR85774), CDR2 (AAR74947-R74949) and CDR3 (AAR74954). The antibody and DNA encoding it are useful in pharmacological, medical and biochemical fields.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynuclectides encoding binding protein polypeptides specific to ligand, selecting plant cells for preparing array
                                                                                                                      Gaps
                                                                                                                      ö
                                                                                                                                                                                                                                                                                                      Immunoglobulin, antibody, light chain; heavy chain; CDR; FR, conplementearity determining region; framework region; IgBP; transgenic plant; immunoglobulin binding protein array, IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
                                                                                                 16; Length 19;
                                                                                                                     5; Indels
                                                                                                50.0%; Score 49; DB 16
55.6%; Pred. No. 0.21;
tive 3; Mismatches
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                                                                                                                                                                                                                    AAU70371 standard; Peptide; 19 AA.
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                                                                                                                                                                                                                                                                                  Human heavy chain III CDR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-2001; 2001WO-US14349.
                                                                                                                                            2 IRLKSDNYATHYAESVKG 19
                                                                                                                                                        2 IRNKANYYTTEYSASVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIC-) EPICYTE PHARM INC.
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                                                                                                                     Conservative
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                                                                                                 Query Match
Best Local Similarity
Matches 10; Conserv
                                                                              19 AA;
                                                                                                                                                                                                                                                                                                                                                                                WO200183806-A1
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                               Sequence
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The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides encoding different immunoglobulin binding protein (198P) polyrpeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transferded cells, to generate an ISBP that binds to a ligand, and transformed plant cells are selected, and preparing an ISBP array in plant cells. At least one peptide sequence low, ISB sequence identity to a framework region (FR) of a native ISB, ISB, ISB, Kappa or lambda immunoglobulin molecule. The machod is useful for preparing an immunoglobulin binding protein calls especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammalian cells). The CHBP is useful for preparing cells or mammalian cells). The chart eukaryotic cells (e.g. insect cells or mammalian cells). The immunoglobulin derived peptide that may be incorporated into an ISBP of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polyneptides specific to ligand, selecting plant cells for preparing array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                          Immunoglobulin; antibody; light chain; heavy chain; CDR; FR; complementarity determining region; framework region; IgBP; transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23; Length 19;
                                         DB 23; Length 19;
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                                                                       2;
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Pred. No. 0.31;
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                                                                         4; Mismatches
                                         Score 49;
                                                            Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 15, 129pp, English.
                                                                                                                                                                                                                   AAU70380 standard; Peptide; 19 AA.
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                                         50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-2000; 2000US-0563222.
                                                                                                                                                                                                                                                                                                               Mouse heavy chain III CDR 2.
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                                                                                                                                                                                                                                                                                   (first entry)
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                                                                         Conservative
                                                                                                         5 KSDNYATHYAESVKG 19
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5 KTDGGSTXYADSVKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hein MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
                                           Query Match
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               19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200183806-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                   14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hiatt AC,
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             Sequence
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AAU70380
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The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAB29930-B29939 were used in the production of the proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complementarity determining region 2; Campath-1; Campath-1H; antibody; lymphoma; CD52 antigen; loop 2; immunological tolerance; minimal mutant; antibody therapy; antiglobulin response; heavy chain; CDR.
                                                                                                                                                                                                                                                                             Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= K7D
/note= "wild type Lys substituted with Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.9%; Score 46; DB 21; Length 17; 52.9%; Pred. No. 0.59; ive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant 3 of the CDR2 region of the Campath-1H heavy chain.
                                                                                                                                                                                                           Sablon
                                                                                                                                                                                                           Hoogenboom H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
5
                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 14; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW23392 standard; peptide; 19 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 RLKSDNYATHYAESVKG 19
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les 9; Conservative
                                                                                                                                                                          (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                          Desmet J, Hufton S,
                                                                                                                                                                                                                                             WPI; 2000-665002/64.
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                                 WO200060070-A1.
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                                                                                                     01-APR-1999;
                                                                                                                                      01-APR-1999;
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                                                                   12-OCT-2000
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A new anti-idiotype antibody against a human anticancer monoconal antibody is claimed. This antibody contains in its heavy chain 3 complemetarity determining regions CDR1 (AAR74929-R74911), CDR2 (AAR74932-R794935) and CDR3 (AAR74936-R74939), this is also true of the light chain which has its own CDR1 (AAR74944-R74946 and AAR8774), CDR2 (AAR74947-R74949) and CDR3 (AAR74954). The antibody and DNA encoding it are useful in pharmacological, medical and biochemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                             H-CDR-2 of anti-idiotype antibody against human anticancer antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, CTLA-4; scaffold protein; antigen-binding; receptor-binding;
SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
diabetic retinopathy; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel anti-idiotype antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.
                                                                                                                                                                                                                                                                               Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; complementarity determining region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 16
Pred. No. 0.45;
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                                                                                                                                      AAR74933 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 2; 28pp; Japanese.
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55.6%;
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RNKANDYTTEYSASVKG 19
                                                                                                                                                                                                          (first entry)
                RLKSDNYATHYAESVKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-182987/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HAGI/) HAGIWARA Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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Matches

RESULT 14 AAB30034

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Gaps

Tone M, Waldmann H, Walsh L;

Gilliland LK,

Modified therapeutic antibody having reduced affinity for its antigen - can induce immunological tolerance, e.g. to Campath-1 monoclonal antibodies used in antibody therapy of lymphoma and WPI; 1997-435093/40. Frewin MR, 

complementarity determining (CDR) region 2 of the humanised antibody campath-1. Campath-1H. Campath-1H heavy chain sequence encodes human complementarity determining (CDR) regions 2 of the humanised antibody campath-1H. Campath-1H heavy chain sequence encodes human is protein at all positions, except the 3 CDR regions. Campath-1 antibodies have been used to induce remissions in lymphoma and leukemia patients and for the treatment of rheumatoid arthritis and vasculitis. The target antigen is CDS2, which is a GPI-anchored cell-surface glycoprotein of lymphocytes and monocytes. Loop 2, represented by residues 4-9 of the present sequence, is important for binding to CDS2. Mutations were made within this region so as to abolish binding of the antibody to CDS2, within this region so as to abolish binding of the antibody to CDS2, which reduces affinity for the antigen, and induces immunological tolerance. The present mutant contains a single charge difference from Lys to Asp. The positive charge of Lys is thought to interact with the the papel and this alphale mutation may destroy antigen binding. Antibody therapy is often limited by an anti-antibody (antiglobulin) response preventing retreatment with the antibody. The minimal mutants or patients may be used to induce tolerance to the therapeutic antibody in patients. They can also be used in the manufacture of medicines for induction of tolerance. Peptides AAW23390-95 represent "minimal" mutant sequences of the Claim 12; Fig 1; 43pp; English. 19 AA; leukaemia Sequence

0; Gaps Score 45; DB 18; Length 19; Pred. No. 0.98; 1; Mismatches 7; Indels Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative

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2 IRLKSDNYATHYAESVKG 19

2 IRDKADGYTTEYNPSVLG 19 ð 셤 Search completed: April 22, 2003, 13:48:26 Job time : 74 secs

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TELEPHONE: 212-527-7659
TELEFAX: 212-753-6237
TELEX: 236687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
US-09-839-666-4
 RESULT 1
 Sequence 164, App
Sequence 164, App
Sequence 4, Appl
Sequence 85, Appl
Sequence 37, Appl
Sequence 26, Appl
Sequence 26, Appli
Sequence 26, Appli
Sequence 20, Appli
Sequence 200, Appli
Sequence 200, Appli
Sequence 200, Appli
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Sequence 4, Appli
Sequence 115, App
Sequence 6, Appli
Sequence 14, Appli
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Sequence 18, Appl
Sequence 98, Appl
Sequence 60, Appl
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                                                                April 22, 2003, 13:49:38; Search time 41 Seconds
- (Without alignments)
37.133 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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        GenCore version 5.1.4 p5 4578 (c) 1993 - 2003 Compugen Ltd.
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US-09-192-854-60
US-09-192-854-164
US-09-192-854-164
US-09-125-4604-14
US-09-125-4604-164
US-09-192-854-37
US-09-192-854-37
US-09-192-854-37
US-09-192-854-37
US-09-192-854-37
US-09-988-51A-8
US-09-988-51A-8
US-09-988-51A-8
US-09-988-51A-20
US-09-988-51A-20
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US-09-192-854-115
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US-09-968-561A-14
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US-09-835-087-18
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                                                                                                                                                                                    301932 segs, 80129803 residues
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Maximum Match 100%
Listing first 45 summaries
                                                - protein search, using sw model
                                                                                                                                1 EIRLKSDNYATHYAESVKG 19
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Gapop 10.0 , Gapext 0.5
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ZIP: 10022

COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTESE for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/839,666
FILING DATE: 19-Apr-2001
CLASSIFICATION NUMBER: US/09/839,666
PRIOR APPLICATION NUMBER: OP/37,085
APPLICATION DATA:
APPLICATION NUMBER: 08/737,085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SALLBERG, MATTI
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
US-09-968-561A-38

US-09-968-561A-68

US-09-968-561A-14

US-09-968-561A-92

US-09-968-561A-12

US-09-968-561A-12

US-09-968-561A-12

US-09-968-561A-134

US-09-968-561A-146

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US-09-968-561A-146

US-09-968-561A-128

US-09-968-561A-128

US-09-968-561A-128

US-09-968-561A-128

US-09-968-561A-128

US-09-968-561A-218

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ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE:
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXCHANGER NUMBER OF SEQUENCES: 23
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Patent No. US2002025513A1
GENERAL INFORMATION:
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; Batent No. US20020068276A1
; GABERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/22916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT APPLICATION NUMBER: 60/066,729
; BARLIER APPLICATION NUMBER: 60/066,729
; BARLIER PILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-60
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Pred. No. 0.22;
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                                                                                                                                                                             Score 48; DB 9; Length 17;
Pred. No. 0.22;
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Pred. No. 0.45;
                                                                                                                                                                                                                                                                             3; Mismatches
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52.9%;
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52.9%;
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Best Local Similarity 52.>
Best Local Similarity
9; Conservative
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                                                                                                                                                                                                                      Best Local Similarity 52.9
Matches 9; Conservative
                                                      ; ORGANISM: Homo sapiens
US-09-968-561A-98
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Best Local Similarity
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US-09-968-561A-98

US-09-968-561A-98

Sequence 98, Application US/09968561A

Patent No. US20020164642A1

GENERAL INFORMATION:

APPLICANT: Tomlineon, Ian M

APPLICANT: Winter, Gregory

TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands

FILE REFERENCE: 3003-10.3B

CURRENT PLICATION NUMBER: US/09/968,561A

FRIOR FILING DATE: 1997-11-0.0

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-21

PRIOR FILING DATE: 1997-11-21

PRIOR FILING DATE: 1997-11-21

PRIOR FILING DATE: 1997-11-20

PRIOR PLICATION NUMBER: US 60/066,729

PRIOR APPLICATION NUMBER: US 60/511,939

PRIOR PLICATION NUMBER: US 60/511,939

PRIOR PLICATION NUMBER: US 60/511,939

PRIOR PLICATION NUMBER: US 60/511,939

PRIOR FILING DATE: 1990-10-20

PRIOR PLICATION NUMBER: US 60/511,939

PRIOR PLICATION NUMBER: US 60/66,729

PRIOR PLICATION NUMBER: US 60/66,729
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; OTHER INFORMATION: CDR2 of murine mAb 1D9 heavy chain variable region
US-09-835-087-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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US-09-835-087-18
# Sequence 18, Application US/09835087
# Sequence 18, Application US/09835087
# Sequence 18, Application US/09835087
# Settle No. US20020042370A1
# GENERAL INFORMATION:
# APPLICANT: WAYNE W. HANCOCK
# TITLE OF INVENTION:
# PRIOR PAPLICATION NUMBER:
# PRIOR APPLICATION NUMBER:
# PRIOR PAPLICATION NUMBER:
# PRIOR PAPLICATI
                                                                                                                                                                                                                           Score 68; DB 10; Length 19;
Pred. No. 0.00017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65; DB 10; Length 19;
Pred. No. 0.00051;
                                                                                                                                                                                                                                                                                                        3; Mismatches
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) MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-839-666-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.6%;
Matches 12; Conservative
                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VRSKSFNYATYYADSVKG 19
                                                                                                                                                                                                                                                                                                                                                                                               2 IRLKSDNYATHYAESVKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Mus Musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: DOMAIN
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US-09-968-561A-56
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                                                                                                                                                                                                                      APPLICANT: Winter, Greg
APPLICANT: Winter, Greg
APPLICANT: Comlinson, Ian
TITLE OF INVENTION: Methods for Selecting Functional Peptides
FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
BARLIER FILING DATE: 1997-11-21
SOFTWARE: PATENTIN NOS: 212
SOFTWARE: PATENTIN VOS: 2.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.9%; Score 45; DB 10; Length 19; 55.6%; Pred. No. 0.73; tive 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 17;
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  Indels
  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: GILLILAND, LISA K
APPLICANT: TONE, MASAHIDE
APPLICANT: FREWIN, MARK R
APPLICANT: FREWIN, MARK R
APPLICANT: WALSH, LOUISE
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REPERENCE: PP/NT/2794 US
CURRENT APPLICATION NUMBER: US/09/125,460A
CURRENT FILING DATE: 1998-08-19
PRIOR FILING DATE: 1997-02-20
PRIOR FILING DATE: 1996-02-20
PRIOR FILING DATE: 1996-02-20
PRIOR FILING DATE: 1996-02-20
PRIOR FILING DATE: 1996-02-20
SOFTWARE: PATCHIN VOR: 7
SOFTWARE: PATCHIN VOR: 7
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1; Mismatches
                                                                                                                                                              Sequence 164, Application US/09192854
Patent No. US20020068276A1
GENERAL INFORMATION:
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Patent No. US20020046578A1
GENERAL INFORMATION:
APPLICANT: WALDMANN, Herman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.9%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 64.3
Matches 9; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 SDNYATHYAESVKG 19
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                                      SDNYATHYAESVKG 19
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US-09-192-854-164
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                                                                                                                                                   US-09-192-854-164
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LENGIH: 19
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Matches
Matches
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Gequence 56, Application US/09968561A

Patent No. US20020164642A1

GENERAL INFORMATION:

APPLICANT: Tomilinson, Ian M

APPLICANT: Winter, Gregory

TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands

TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands

CURRENT APPLICATION NUMBER: US/09/968,561A

CURRENT APPLICATION NUMBER: 2001-10-01

PRIOR APPLICATION NUMBER: GB 9722131.1

PRIOR FILING DATE: 1997-10-20
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45.9%; Score 45; DB 10; Length 19;
Best Local Similarity 50.0%; Pred. No. 0.73;
Matches 9; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Weshington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

ZIP: 2006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: PESTENCE OF WINGOWS VERSION 2.0
CURRENT APPLICATION NUMBER: US/09/730,857
FILING DATE: 07-Dec-2000
CLASSIFICATION NUMBER: US/09/730,857
PRIOR APPLICATION DATA:
APPLICATION UNTRES: 09/416,557

APPLICATION UNTRES: 09/416,557
Sequence 85, Application US/09730857

Patent No. US20020083396A1

GENERAL INFORMATION:

MACBUROCO, YOSHINIO

Yamada, YOSHINI

Sato, Koh

TSUCHIYA, Masayuki

Yamazaki, Tafsumi

TITLE OF INVENTION:

Interleukin-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IRLKSDNYATHYAESVKG 19
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                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS
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Sequence 8, Application US/09968561A

Sequence 8, Application US/09968561A

Patent No. US20020164642A1

GENERAL INFORMATION:

APPLICANT: Tomlinson, Ian M

APPLICANT: Tomlinson, Ian M

APPLICANT: Winter, Gregory

TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands

FILE REFERENCE: 8039/1073B

CURRENT APPLICATION NUMBER: US/09/968,561A

CURRENT PELING DATE: 1997-10-20

PRIOR FILING DATE: 1997-11-3

PRIOR FILING DATE: 1997-11-3

PRIOR APPLICATION NUMBER: US 60/066,729

PRIOR APPLICATION NUMBER: US 60/066,739

NUMBER OF SEQ ID NOS: 350

NUMBER OF SEQ ID NOS: 350

NUMBER OF SEQ ID NOS: 350
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Us.09-798-058-6
Us.09-798-058-6
Sequence 6, Application US/09798058
Fatent No. US20020098523A1
GERERAL INFORMATION:
APPLICANT: Vaughan, Tristan John
APPLICANT: Wilton, Alison Jane
APPLICANT: Wilton, Alison Jane
FAPLICANT: Main, Sarah Helan
ITTLE OF INVENTION: Human antibodies against eotaxin and their use
FILE REPRENCE: 84632-00010
CURRENT APPLICATION NUMBER: US/09/798,058
CURRENT FILING DATE: 2001-08-29
FRICH RELING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 20
SOUTHARR: PatentIN Ver. 2.1
SEQ ID NO 6
LENGTH: 17
                                                                                                                               ö
                                                                             Query Match 43.9%; Score 43; DB 10; Length 17; Best Local Similarity 47.1%; Pred. No. 1.3; Matches 8; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 10; Length 17;
Pred. No. 1.9;
1; Mismatches 4; Indels
                                                                                                                                                                                                          1 RISGNSGSTFYADSVKG 17
                                                                                                                                                                             3 RLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 61.5
Matches 8; Conservative
          ; ORGANISM: Homo sapiens US-09-828-708-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Homo sapiens
US-09-798-058-6
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5 DGSIKHYADSVKG 17
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LENGTH: 17
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Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditcel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particifile REPRENCE: 1361-005US1
CURRENT FILIA DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020068276A1
Patent No. US20020068276A1
GENERAL INFORMATION:
APPLICANT: Wincer, Greg
FAPLICANT: Wincer, Greg
FILE REFERENCE: 3789/72916
CURRENT FAPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER RPLICATION NUMBER: 60/066,729
FARLIER FILING DATE: 1999-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                             DB 9; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1998-10-20
PRIOR PILING DATE: 1998-10-20
PRIOR PILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PATENTIN VOMBER: US 09/511,939
SOFTWARE: PATENTIN VOMBER: 2000-02-24
SEQ ID NO 56
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
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Best Local Similarity 47.1%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 RLKSDNYATHYAESVKG 19
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1 RITPAGHRTYYADSVKG 17
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                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Homo sapiens
US-09-192-854-37
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US-09-192-854-37
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LENGTH: 17
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                                                              Length 17;
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                                                              Score 41; DB 3
Pred. No. 2.8;
1; Mismatches
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Job time: 42 secs
                                                              Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
      ; ORGANISM: Homo sapiens
US-09-968-561A-206
                                                                                                                                           10 ATHYAESVKG 19
                                                                                                                                                                8 ATRYADSVKG 17
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Sequence 2000, Application US/09968561A  
Sequence 2000, Application US/09968561A  
Retent No. US20020164642A1

GENERAL INFORMATION:

APPLICANT: Fonlinson, Iam M
APPLICANT: Winter, Gregory
ITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REPRENCE: 8019/1073B
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT APPLICATION NUMBER: US 9722131.1
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR PRILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR PRILING DATE: 1997-11-13
PRIOR PRILING DATE: 1997-11-21
PRIOR PRILING DATE: 1998-10-20
SOFTWARE PRILING DATE: 1998-10-20
SOFTWARE PRILING DATE: 1998-10-20
SOFTWARE PRILING DATE: 1997-11-31
PRIOR PRILING DATE: 1998-10-20
SOFTWARE PRILING DATE: 1997-11-31
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80.0%; Pred. No. 2.8;
tive 1; Mismatches 1; Indels
  Score 41; DB 9; Length 17; Pred. No. 2.8;
                                         3; Indels
Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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4 SEGWPTIYADSVKG 17
                                                                               6 SDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-200
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US-09-968-561A-206
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Sequence 86, Appl
Sequence 65, Appl
Sequence 65, Appl
Patent No. 5496552
Sequence 16, Appl
Patent No. 5169815
Sequence 81, Appl
Sequence 83, Appl
Sequence 83, Appl
Sequence 90, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 61, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 62, Appl
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Pred. No. 8.6e-05;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08737085A
Patent No. 5869232
GENERAL INFORMATION
APPLICANT: SALIBERG, MATTI
TITLE OF INVENTION: EXCHANGER
INVERSE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARRY & DARBY PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 805 Third Avenue
CITY: New York
STREET: New York
COUNTRY: USA
CONTUTER: NEADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMERE: US/08/737,085A
FILING DATE: 27-DEC-1996
US-08-285-936-54
US-08-487-860-54
US-08-104-744-86
US-08-704-744-86
US-08-290-7938-65
5496552-4
US-09-406-532-16
US-09-406-532-16
US-09-406-532-16
US-08-208-886C-81
US-08-208-886C-81
US-08-704-744-90
US-08-704-744-90
US-08-36-953A-21
US-08-36-953A-21
US-08-36-953A-21
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                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38,475
ER: 3846/0C569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Green, Reza
REGISCRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-227-7659
TELEFAX: 212-53-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.48;
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 23669
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 19 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 69.4
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide US-08-737-085A-4
 US-08-737-085A-4
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                                                                                                                 April 22, 2003, 13:47:08 ; Search time 14 Seconds (without alignments) 39.931 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4,
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-246-258-4
US-09-236-258-4
US-09-839-666-4
US-09-839-666-4
US-08-976-966-78
US-08-976-288A-78
US-08-976-288A-78
US-08-976-288A-78
US-08-918-970B-6
US-08-918-970B-6
US-08-918-970B-6
US-08-918-970B-6
US-08-918-970B-6
US-08-95-95-95-96
US-08-650-262-14
US-08-953-451B-33
US-08-053-451B-33
US-08-053-451B-33
US-08-053-451B-33
US-08-053-451B-33
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US-08-053-451B-34
US-09-170-769A-11
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.08-480-434-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                   - protein search, using sw model
                                                                                                                                                                                                                            1 EIRLKSDNYATHYAESVKG 19
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Gapop 10.0 , Gapext 0.5
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98
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                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 19
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Maximum DB
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Length 19;
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CITY: New York
CUMPRY: USA
ZIP: 10022
COMPUTRY: USA
ZIP: 10022
COMPUTRY: USA
COMPUTRY: BALGALE FORM:
MEDIUM TYPE: Diskette
COMPUTRY: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PESELSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/839,666
FILING DATE: 19-APL-2001
CLASSIFICATION: AUNKNOWN:
PRIOR APPLICATION DATA:
APPLICATION UNDBER: 08/737,085
FILING DATE: CURROWN:
ATTORNEY/AGENT INFORMATION:
                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASEUSC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/532,106
FILING DATE: 21-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/737,085A
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09839666
Patent No. 6469143
GENERAL INFORMATION:
APPLICANT: SALIBERG, MATTI
TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
EXCHANGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; I
8.6e-05;
                                                                                                                                                                                                                                                     NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 68; DB 4
Pred. No. 8.6e-
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-532-106-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                TELEPAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
    ZIP: 10022
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 IRLKSDNYATHYAESVKG 19
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Pred. No. 8.68-05;
2; Indels
                                                                                                   Sequence 4, Application US/09246258
; Batent No. 6040137
; GENERAL INFORMATION:
    APPLICANT: SALIBERG, MATTI
    TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
    TITLE OF INVENTION: EXCHANGER
    NUMBER OF SEQUENCES: 23
    CORRESPONDENCE ADDRESS:
    STRRET: 805 Third Avenue
    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09532106
Patent No. 6245895
GENERAL INFORMATION:
APPLICANT: SALIBERG, MATTI
TITLE OF INVENTION: EXCHANGER
                                                                                                                                                                                                                                                                                                                                                        ZUP. 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/246,258
FILMO DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/737,085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATORNEY AGENT INPORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REPRENCE/DOCKET NUMBER: 3846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
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2 VRSKSFNYATYYADSVKG 19
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-09-246-258-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
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RESULT 7
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Patent No. 5792822

GENERAL INFORMATION:
APPLICANT: Cariani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padian Dr., Jerry A.
APPLICANT: Padian Dr., Buardo A.
TITLE OF INVENTION: Analogue Peptides with Specificity
TITLE OF INVENTION: and Therapeutic Methods.
NUMBER OF SEQUENCES: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                 69.4%; Score 68; DB 4; Length 19; ilarity 72.2%; Pred. No. 8.6e-05; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRI: ...

ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM PC compatible
COMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,696C
FILING DATE: 11.16-92
CLASSIFICATION 1456
ATTORNEY/AGENT INCRMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REPERENCOPCKET NUMBER: 966 38227
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 148-6688
TELEFRAK: (510) 748-6688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY; SCHROEDER & POPLAWSKI
STREET: 444 South Flower Street, Suite 2000
STATE: California
                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
TELEFAX: 212-753-6237
TELEX: 236697
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EIRLKSDNYATHYAESVKG 19
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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UN-US-119-91000

| Patent No. 5804107
| Patent No. 5807
| Patent No. 5907
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US-60-118-970B-5

1 Sequence 5, Application US/08318970B

1 Patent Wo. 5589573

2 Patent Wo. 5589573

2 Patent Wo. 5589573

2 Patent WO. 5589573

3 PAPLICANT: Hideaki HAGIWARA, et al.

APPLICANT: Hideaki HAGIWARA, et al.

TITLE OF INVENTION: AMINO ACID SEQUENCES COPING THOSE SEQUENCES

TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES

TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES

ADDRESSEE: Law Office of Sherman and Shalloway

STREET: 413 N. Washington Street

CITY: Alexandria

STATE: Virginia

COMPUTER: Machineton Street

COMPUTER: Dall System 210; Intel 80 285 Microprocessor

COMPUTER: Dall System 210; Intel 80 285 Microprocessor

COMPUTER: Dall System 210; Intel 80 285 Microprocessor

COMPUTER: Word Perfect, Version 5.1

CURRENT APPLICATION NUMBER: 10/08/316, 970B

FILING DATE: October 6, 1994

CLASSIFICANION NUMBER: 26,588

REPERENCE/OCEST NUMBER: 85,588

REPERENCE/OCEST NUMBER: 86,588

REPERENCE/OCEST NUMBER: 86,588

REPERENCE/OCEST NUMBER: 96,988

REPERENCE/OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
50.0%; Score 49; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 0.1;
Matches 10; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: H-CDR2-2
; OTHER INFORMATION: hypervariable region
US-08-318-970B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: H-CDR2-3
OTHER INFORMATION: hypervariable region
US-08-318-970B-6
                       REFERENCE/DOCKET NUMBER: S-23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 845-2282
TELEPAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
REGISTRATION NUMBER: 26,588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 IRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 IRNKANYYTTEYSASVKG 19
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Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-08-318-970B-5
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Sequence 6, Application US/08318970B

Patent No. 5589573

GENERAL INFORMATION:

APPLICANT: Hideaki HAGIWARA, et al.

APPLICANT: Hideaki HAGIWARA, et al.

TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-IDIOTYPIC

TITLE OF INVENTION: AND DNA BASE SEQUENCES HUMAN MONOCLONAL

TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Office of Sherman and Shalloway

STREET: Alaxandria

STATE: Virginia

STATE: Virginia

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: Dell System 210; Intel 80 285 Microprocessor
OFREATING SYSTEM: MS DOS 3.3
SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,970B
FILING DATE: October 6, 1994
CLASSIFICATION: 5.30
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.3%; Score 66; DB 4; Length 19;
Best Local Similarity 68.4%; Pred. No. 0.00018;
Matches 13; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                    MEDIUM TYPE: FLOPPY GIBE

COMPEDIEN: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOCTAARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION NUMBER: 08/129,930
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: No. 6315997ember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amc21 Ph.D.
NAME: Viviana Amc21 Ph.D.
NEGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 20,930
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (213) 489-4210
          444 South Flower St., 19th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: n.a.
INFORMATION FOR SEQ ID NO: 78
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EIRLKSDNYATHYAESVKG 19
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                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
             STREET: 444 South FILTY: Los Angeles STATE: California COUNTRY: USA
                                                                                                                                          90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-976-288A-78
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JOS-264-02 22, Application US/08264093

Sequence 22, Application US/08264093

Patent No. 5639863

GENERAL INFORMATION:

APPLICANT: Michael D. Dan

TITLE OF INVENTION: HUWAN MONOCLONAL ANTIBODIES SPECIFIC TO

TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE

TITLE OF INVENTION: ANTIGEN

NUMBER OF SEQUENCES: 26

CORRESONDENCE ADDRESS:

ADDRESSEE: Ridout & Maybee

STREET: 2300 Richmond-Adelaide Centre

STREET: 101 Richmond Street West

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: MSH 2J7

COMPUTER: BADABLE FORM:

MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage

COMPUTER: ASSTEM MS-DOS 6.00

SOFTWARE: ASCII Editor

CURRENT APPLICATION NUMBER: US/08/264,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
TITLE OF INVENTION: Interleukin-8
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
DERRATING SYSTEM: DOS
SOFTWARE: FRESENCE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/416,557
FILING DATE: 12-October-1999
CLASSIFICATION NUMBER: 08/765,783
APLICATION NUMBER: 08/765,783
FILING DATE: 7-March-1997
ATORNEY/AGENT INFORMATION:
NAME: MATEANIGE, KARLE H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.10
TELLEPAK: 202-887-1500
TELLEPAK: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
45.9%; Score 45; DB 4;
Best Local Similarity 50.0%; Pred. No. 0.45;
Matches 9; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-09-416-557-85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                         APPLICANT: Matsushina, Kouji
APPLICANT: Matsumoto, Yoshihiro
APPLICANT: Yamada, Yoshiki
APPLICANT: Yamada, Yoshiki
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Tatsumi
TTTLE OF INVENTION: Interleukin-8
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,783A
FILIASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 2
Pred. No. 0.45;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35029-20001.20
                                                                                                                                                       Sequence 85, Application US/08765783A Patent No. 5994524 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsushima, Kouji
Matsumoto, Yoshihiro
Yamada, Yoshiki
Sato, Koh
Tsuchiya, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 85, Application US/09416557
Patent No. 6245894
GENERAL INFORMATION:
APPLICANT: Matsushima, Kouji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MAISANIGE, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 3502;
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 IRLKSDNYATHYAESVKG 19
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                                  2 IRNKANLYTTDYSASVKG 19
      2 IRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0°
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-765-783A-85
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APPLICANT:
APPLICANT:
                                                                                                                                    US-08-765-783A-85
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US-09-416-557-85
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Patent No. 5866124

GENERAL INFORMATION:
APPLICANT: Pluschke, Gerd
APPLICANT: Pluschke, Gerd
APPLICANT: Murray, Brendan
TITLE OF INVENTION: Genetically engineered antibodies
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5866124artis Corporation
STREET: 59 Route 10
CITY: Bast Hanover
STATE: NJ
COUNTRY: USA
ZIP: 07936-1080
COMPUTRY: USA
COUNTRY: IBM PC compatible
COMPUTRY: IBM PC compatible
COMPUTRY: Bast Hanover
STATE: NJ
COUNTRY: USA
COUNTRY: NSA
COMPUTRY: NSA
COMPUTRY: SAPELEATION PRESSES
APPLICATION NUMBER: US/08/650,262
APPLICATION NUMBER: US/08/650,262
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                                                                                   Score 39, DB 2; Length 14;
Pred. No. 3;
2; Mismatches 4; Indels
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Pred. No. 3.7;
5; Mismatches
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Patent No. 5562903
GENERAL INFORMATION:
APPLICANT: Co, Loibner
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 32
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PILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 92810188.0
FILING DATE: 17-MAR-1992

* ATTORNEY/AGENT INFORMATION:
NAME: Henry P. No. 5866124ak
REGISTRATION NUMBER: 33200
REGISTRATION NUMBER: 4-18995/A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
"TELECOMMUNICATION INFORMATION"
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Best Local Similarity 43.6
Matches 7; Conservative
                                                                                          Query Match 39.8
Best Local Similarity 53.8
Matches 7; Conservative
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2 NKYTTEYSASVKG 14
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HYPOTHETICAL: N
                                 US-08-452-724A-41
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US-08-053-171-31
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US-08-650-262-14
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US-08-452-724A-41
Sequence 41, Application US/08452724A
Sequence 41, Application US/08452724A
Sequence 41, Application US/08452724A
FEMERAL No. 5830650
Sequence 41, Application US/08452724A
SERENT OF INVENTION:
MUNISER OF INVENTION:
MUNISER OF INVENTION:
MUNISER OF SEQUENCES:
MUNISER DESER:
MUNICAL ADDRESS:
MUNICAL AD
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/Ms-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,724A
FILING DATE: 30-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/930,600
FILING DATE: 05-APR-1991
RIGH APPLICATION DATA:
APPLICATION NUMBER: US 07/930,600
FILING DATE: 05-APR-1991
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/505,314
FILING DATE: 05-APR-1991
RIGHT DATE: 05-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E
RESERRATION NUMBER: 22,592
REPERENCE/DOCKET NUMBER: RC90-01AZ
FILING DATE:
CLASSIFICATION: 536
FRIOR APPLICATION DATA: NO. 5639863 applicable
ATTORNEY/AGENT INPORMATION:
NAME: Lake, James R.
RECISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELEPAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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Best Local Similarity 50.0
Matches 8; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE
ADDRESSEE
Townsend and Townsend Khourie and Crew
STREET: 3/9 Lytcon Avenue
CTHF: Palo Alto
CTHF: Palo Alto
CALICOTIA
STREET: 43101
COMPUTER READALE FORM:
MEDIUNT THE PROCOMPLIA
COMPUTER: PROPEN ALTO
SUPPLICATION NUMBER: PC-DOS/NB-LOS
SOFTARE: PARENTIN RESIDENT: 44
COMPUTER: PROCOMPLIA
SPELICATION NUMBER: 10,0 Version #1.25
CTASSITICATION NUMBER: 130,033
TELECOMPUTATION NUMBER: 130,033
TELECOMPUTATION NUMBER: 130,233
REFERENCE/DOCKT NUMBER: 30,233
REFERENCE/DOCKT NUMBER: 130,233
REFERENCE/DOCKT NUMBER: 130,233
REFERENCE/DOCKT NUMBER: 130,233
REPRENCE/DOCKT NUMBER: 130,233
REPRENCE/DOCKT NUMBER: 130,240
TELECOMPUTER: PEPPI CALICO
TELECOMPUTER: PEPPI CALICO
TELECOMPUTER: PEPPI CALICO
TELECOMPUTER: PC-DEC CALICO
TOPER: PC-DEC CALICO
TELECOMPUTER: PC-DEC CALICO
TOPER: PC-DEC CALICO
TELECOMPUTER: PC-DEC CALICO
TOPER: PC-DEC CALICO
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Search completed: April 22, 2003, 13:50:14 Job time : 15 secs

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APPLICANT: Barbas III, Carlos F.
APPLICANT: Shabar Doron
APPLICANT: Shabar Doron
APPLICANT: Rader, Doron
APPLICANT: List, Benjamin
APPLICANT: List, Benjamin
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: PROBUG ACTIVATION USING CATALYTIC ANTIBODIES
FILE REFERENCE: PLF0011S
CURRENT APPLICATION NUMBER: US/09/318,661
CURRENT APPLICATION NOWBER: 1999-05-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
                   SEQ ID NO 4
LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-318-661-4
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                                                                                                                             April 22, 2003, 12:48:49; Search time 16.625 Seconds (without alignments) 33.626 Million cell updates/sec
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Sequence 1
Sequence 1
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Sequence 2
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Sequence 2
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
                                 GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-318-661-4

US-09-318-661-2

US-08-466-272A-1

US-08-466-272A-1

US-08-471-771-1

US-09-130-783-1

US-08-130-783-1

US-08-483-749A-2

US-08-483-749A-2

US-08-483-749A-2

US-08-767-128-26

US-08-767-128-26

US-08-192-102-5

US-08-192-861A-5

US-08-192-861A-5

US-08-192-861A-5

US-08-192-861A-5

US-08-192-645-45

US-08-192-645-45

US-08-681-432-2

US-08-681-432-2

US-08-737-085A-4

US-09-833-666-4
                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   protein search, using sw model
                                                                                                                                                                                                                                   1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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98
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                   OM protein
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                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                    Run on:
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No.
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   24, Appl
78, Appl
78, Appl
13, Appl
113, Appl
113, Appl
114, Appl
2, Appl
2, Appl
118, Appl
119, Appl
2, Appl
3, Appl
119, Appl
2, Appl
3, Appl
33, Appl
21, Appl
2, Appl
33, Appl
21, Appl
33, Appl
33, Appl
21, Appl
33, Appl
33, Appl
21, Appl
33, Appl
34, Appl
34, Appl
36, Appl
37, Appl
38, Appl
38, Appl
39, Appl
31, 
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Patent No. 6268488

GENERAL INFORMATION:
APPLICANT: Barbas III, Carlos F.
APPLICANT: Shabat, Doron
APPLICANT: Larie, Benjamin
APPLICANT: List, Benjamin
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: PROBRUG ACTIVATION USING CATALYTIC ANTIBODIES
FILE REFERENCE: PLF0011S
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: residue sequence of catalytic fragment
                                                                                                                       Sequence
Sequence
Sequence
Sequence
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Sequence
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US-08-767-128-24
US-08-767-128-36
US-08-77-69(C-78
US-08-129-930B-78
US-08-976-288A-78
US-08-976-288A-78
US-08-976-288A-13
US-08-976-288A-13
US-08-976-288A-13
US-08-976-288A-14
US-08-976-268-14
US-08-976-269-14
US-08-765-469-14
US-08-765-469-18
US-08-765-469-18
US-08-765-469-18
US-08-765-469-18
US-08-765-469-18
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US-08-525-539A-33
US-07-942-245-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-09-318-661-2
; Sequence 2, Application US/09318661
; Patent No. 6268488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 EIRLKSDNYATHYAESVKG 221
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linear
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-478-857-1
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                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bosslet, Klaus
APPLICANT: Bosslet, Klaus
APPLICANT: Ffleiderer, Peter
APPLICANT: Ffleiderer, Peter
APPLICANT: Seeman, Gerhard
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
TITLE OF INVENTION: Preparation Thereof and the Use Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STREET: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                         Length 298;
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                                                                                                  Score 95; DB 4; Length 230
Pred. No. 7.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.C.

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,661

FILING DATE: 06-JUNE-1995

CLASSIFICATION: 530

PROGRATION NUMBER: US 07/957,827

FILING DATE: 08-OCT-1992

CLASSIFICATION: 330

ATTORNEY/AGENT INFORMATION:

NAME: FORMAN, DAVIG S.

REGISTRATION NUMBER: 35,694

REFERENCE/POCKET NUMBER: 35,694

REFERENCE/POCKET NUMBER: 35,694

REFERENCE/POCKET NUMBER: 35,694

TELERPHONE: 202-408-4000
                                                                                                                   Query Match 96.9%; Score 95; DB Best Local Similarity 94.7%; Pred. No. 7.8e Matches 18; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/08468661
; Patent No. 5639621
; GENERAL INFORMATION:
                                                                                                                                                                                                                      205 EIRLRSDNYATHYAESVKG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                   1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 115 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 94.7
Matches 18; Conservative
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                                     ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-318-661-2
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SEQ ID NO 2
LENGTH: 298
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RESULT 4

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| Use for $2.72.1
| Sequence 1, Agolication US/08466272A
| Peacur No. 5674394
| Peacur No. 56674394
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Gaps

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Sequence 1, Application US/09130783
Patent No. 6030797
GENERAL INCRMATION:
APPLICANT: Besslet, Klaus
APPLICANT: Belaiderer, Peter
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Monoclonal Antibodies Against
TITLE OF INVENTION: Preparation Thereof and the Use Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 93; DB 3; Length 115;
Pred. No. 5.7e-08;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                      Length 115;
                                                                                                                                                                                                                                                                                                    94.9%; Score 93; DB 2; Length 115
94.7%; Pred. No. 5.7e-08;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
COUNTRY: USA
I 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130.707
FILING DATE:
CLARGETTER
                              05552-1227-01000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,771
FILING DATE:
                       REFERENCE/DOCKET NUMBER: 0555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-400
TELEFAX: 202-408-400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Forman, David S.
REGIGTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
REGISTRATION NUMBER: 33,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 94.7%;
Matches 18; Conservative
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                                                                                                                                                             LENGTH: 115 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-471-771-1
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.74
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-09-130-783-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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US-09-130-783-1
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Patent No. 5837824

GENERAL INFORMATION:
APPLICANT: Bosslet, Klaus
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Monoclonal Antibodies Against
TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
TITLE OF INVENTION: Preparation Thereof and the Use Thereof
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.9%; Score 93; DB 1; Length 115; 94.7%; Pred. No. 5.7e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PAPELICATION DATA:
APPLICATION NUMBER: US/08/471,771
FILING DATE: 06-UNTE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/957,827
FILING DATE: 08-OCT-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,857
                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA
APPLICATION DATE: US 07/957,827
FILING DATE: 08-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: BUGALSKY, LAWRENCE B.
REGISTRATION NUMBER: 35,086
REGISTRANCE/DOCKET NUMBER: 02481-1227-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                     ZIP: 2005-3315
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Forman, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 EIRLKSNNYATHYAESVKG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 115 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                          FILING DATE:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-478-857-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-471-771-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Gaps

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COUNTRY: USA
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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50 EIRLKSNNYATHYAESVKG 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (510) 621-281
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                               RESULT 9
US-08-483-749A-2
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0
                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: LOPEZ, OSVALDO
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY PETER
APPLICANT: GOBBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.9%; Score 93; DB 3; Length 120; 94.7%; Pred. No. 6e-08; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFTCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFTCATION 1424
PRIOR APPLICATION DATA:
APPLICATION WIMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION DATA: 06/41,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA: 08/46,798
FILING DATE: 05-JUN-1995
ATTONEY/AGENT INFORMATION:
NAME: CARLE, CHARLES G.
REGISTAATION NUMBER: 35,093
REFERENCE/DOCKT NUMBER: 8448.49USF1
TELECOMMUNICATION: INFORMATION:
TELECOMMUNICATION: 1870RMATION:
TELECOMMUNICATION: 1870RMATION:
TELECOMMUNICATION: 1870RMATION:
TELECOMMUNICATION: 1870RMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 55402
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
                                                                                                             RESULT 8
US-08-77-128-28
Sequence 28, Application US/08767128
Fatent No. 6111079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                    46 EIRLKSNNYATHYAESVKG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Lacal Similarity 94.73
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: internal ORIGINAL SOURCE: US-08-767-128-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MN
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1 EIRLKSDNYATHYAESVKG 19

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Gaps
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US-08-483-749A-10
is Sequence 10, Application US/08483749A
is Sequence 10, Application US/08483749A
is Part No. 6054561
is GENERAL INFORMATION:
is APPLICANT: RING, DAVID B.
is TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
ITILE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
is NUMBER OF SEQUENCES:
is ADDRESSEE: CHIRON CORPORATION
is STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
is COUNTRY: USA
is COMPUTER: CA
is COMPUTER: FORM:
is COMPUTER: IBM PC compatible
is COMPUTER: IBM PC COMPATIONS
Sequence 2, Application US/08483749A

Patent No. 6054561

GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
CITY: EMERYVILLE
STATE: CANCER CONTINUE
STATES CANCER CONTINUE
STATES CANCER CONTINUE
STATES CANCER CANCE
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Pred. No. 6.1e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE PATENT PC-DOS/MD-LOG
SOFTWARE PATENTIN ROLEAGE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-JUN 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REGISTRATION NUMBER: 36,914
RETERENCE/DOCKET NUMBER: 0508.008
TELECOMMUNICATION INFORMATION:
TELECHONE: (510) 601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Gaps
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APPLICANT: Us, Unming
APPLICANT: Us, Usek, Jan
APPLICANT: Us, Care
APPLICANT: Chight, David M.
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: ANTI-THE ANTIBODIES AND ASSAYS EMPLOYING
TITLE OF INVENTION: ANTI-THE ANTIBODIES AND ASSAYS EMPLOYING
TITLE OF INVENTION: ANTI-THE ANTIBODIES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: 19
CORRESPONDENCE ADDRESS: 19
CORRESPONDENCE ADDRESS: 19
CONDITE: Leatington
STREET: Two Militia Drive
CITY: Leatington
STREET: Two Militia Drive
COMPUTER: IBP PC compatible
COMPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.1%; Score 80.5; DB 3; Length 119; Best Local Similarity 89.5%; Pred. No. 6.2e-06; Matches 17; Conservative 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-192-102-5
; Sequence 5, Application US/08192102
; Patent No. 5656272
                                                        REFERENCE/DOCKET NUMBER: 86
TELECOMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEPHONE: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 EVRLKS-NYATHYAESVKG 67
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                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: S
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        internal
                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO FRACMENT TYPE: i ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-767-128-26
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Patent No. 6111079

GENERAL INPORMATICALION

APPLICANT: WYLE, OSVALDO

APPLICANT: MORRAY, PETER JOSEPH

APPLICANT: GORBEL, PETER JOSEPH

APPLICANT: MURRAY, PETER JOSEPH

APPLICANT: MURRAY, PETER JOSEPH

TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND

TITLE OF INVENTION: NUCLECTIDES CODING THEREFORE

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt

STREET: 3100 No. 6111079west Center, 90 South Seventh St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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86.7%; Score 85; DB 3; Length 114;
Best Local Similarity 84.2%; Pred. No. 1.1e-06;
Matches 16; Conservative 2; Mismatches 1; Indels
CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRANICH NUMBER: 05.08.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
TELEPAX: (510) 655-3542
INFORMATION ER SEQ ID NO: 10:
SEQUENCE (TRARATERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-749A-10
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CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIPRICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-UNI-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-CCT-1995
PRIOR APPLICATION NUMBER: 08/462,798
FILING DATE: 05-UNI-1995
ATTORNEY/AGENT INFORMATION:
NAMB: CARTER, GLARIBER: 35,093
REGISTRATION NUMBER: 35,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 55402
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EIRLKSDNYATHYAESVKG 19
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US-08-767-128-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MI
COUNTRY:
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Patent No. 5919452
GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: GENERACH, John
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: METHODS OF TREATING TNF - MEDIATED DISEASE USING
TITLE OF INVENTION: CHIMERIC ANTI-TNF ANTIBODIES (As Amended)
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 75.5%; Score 74; DB 1; Length 119; Best Local Similarity 84.2%; Pred. No. 7e-05; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEN PC compatible
CORRATE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/192,861A
PRIOR APPLICATION NUMBER: US/08/192,861A
PRIOR APPLICATION NUMBER: US/08/193,413
APPLICATION NUMBER: US/08/13,413
APPLICATION NUMBER: US/08/13,413
FILING DATE: 20-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,406
FILING DATE: 20-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,852
FILING DATE: 11-SEP-1992
PRIOR APPLICATION NUMBER: US 07/943,606
FILING DATE: 18-MAR-1992
PRIOR APPLICATION NUMBER: US 07/853,606
FILING DATE: 18-MAR-1992
PRIOR APPLICATION NUMBER: US 07/853,606
FILING DATE: 18-MAR-1991
PRIOR APPLICATION NUMBER: US 07/670,827
PRIOR APPLICATION NUMBER: US 07/670,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                     FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/670,827
FILING DATE: 18-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: BYOOK, DAVIG B.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 5:
SEQUENCE (617) 861-9540
INFORMATION FOR SEQ 1D NO: 5:
SEQUENCE CHARACTERISTICS:
03,638,606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 EIRSKSINSATHYAESVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-324-799-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Lexington
STATE: Massachusetts
   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-08-192-861A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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Pred. No. 7e-05;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter E.
APPLICANT: Ghrayeb, John
APPLICANT: Ghrayeb, John
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: ANTI-TINF ANTIBODIES AND PEPTIDES
TITLE OF INVENTION: OF HUMAN TUMOR NECROSIS FACTOR
NUMBER OF SEQUENCES: 19
CORRESPONDENCE HAMILTON, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: DIALY
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPUTER:
COMPUTER: DATE: DCT-1994
RICK APPLICATION NUMBER: US/08/124,799
FILING DATE: 18-OCT-1994
RICK APPLICATION NUMBER: 08/192,093
FILING DATE: 04-FEB-1994
RICK APPLICATION NUMBER: 08/192,102
FILING DATE: 04-FEB-1994
RICK APPLICATION DATA:
APPLICATION NUMBER: 08/192,861
FILING DATE: 04-FEB-1994
RICK APPLICATION DATA:
APPLICATION NUMBER: US/08/13,413
FILING DATE: 02-FEB-1993
RILING DATE: 02-FEB-1993
TELLING DATE: 18-MAR-1991
ATTORNEY FAGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: NYU93-01M3
TELECHONE: (617) 861-6240
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFFLING DATE: 29-UAN-FILING DATE: 29-UAN-FILING DATE: 29-UAN-FILING APPLICATION NUMBER: US 07/943,852
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 EIRSKSINSATHYAESVKG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-192-102-5
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Search completed: April 22, 2003, 12:55:43 Job time : 17.625 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.5%; Score 74; DB 2; Length 119; Best Local Similarity 84.2%; Pred. No. 7e-05; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter E.
APPLICANT: Ghrayeb, John
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scort A.
TITLE OF INVENTION: OF HUMAN TUMOR NECROSIS FACTOR
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Lexington

STATE: Lexington

STATE: Massachusetts

CONTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

APPLICATION NUMBER: US/09/133,119

FILING DATE: 10-DEC-1995

FILING DATE: 10-DEC-1994

FRIOR APPLICATION NUMBER: US/192,093

FILING DATE: 04-FEB-1994

PRIOR APPLICATION NUMBER: US/192,102

FILING DATE: 04-FEB-1994

PRIOR APPLICATION NUMBER: US/192,102

FILING DATE: US/FEB-1994

PRIOR APPLICATION NUMBER: US/FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: 22,592
REFERENCE/DOCKET NUMBER: 72,592
REFERENCE/DOCKET NUMBER: 72,592
REFERENCE/DOCKET NUMBER: 72,592
TELEPANICATION INFORMATION:
TELEPANICATION 1861-6240
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 04-FEB-1994
PRIOR APPLICATION DATE: 08/192,861
PRIOR APPLICATION DATE: 08/013,413
FILING DATE: 02-FEB-1993
PRIOR APPLICATION NUMBER: US 08/010.406
APPLICATION NUMBER: US 08/010.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 08/010,406
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; Sequence 5, Application US/09133119
; Patent No. 6277969
; GENERAL INFORMATION:
APPLICANT: Le, Juuming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EIRLKSDNYATHYAESVKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 EIRSKSINSATHYAESVKG 68
                                                                                                                                                                                                                                                     LENGTH: 119 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-192-861A-5
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Gaps
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FILING DATE: 29-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,852
FILING DATE: 11-SEP-1992

PRIOR APPLICATION NUMBER: US 07/853,606
FILING DATE: 18-MAR-1992

PRIOR APPLICATION NUMBER: US 07/670,827
FILING DATE: 18-MAR-1991

APPLICATION NUMBER: US 07/670,827
FILING DATE: 18-MAR-1991

APPLICATION NUMBER: US 07/670,827
FILING DATE: 18-MAR-1991

ATTONNEY/AGRWT INFORMATION:

REGISTRATION NUMBER: 22,592

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: NYU93-01M4A

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 11.9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-133-119-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 EIRSKSINSATHYAESVKG 68
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Best Local Similarity 84.2
Matches 16; Conservative
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Sequence Sequence

Appli Appli Appli Appli Appl

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence

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US-08-483-7494-16

US-08-253-877C-10

US-08-253-877C-10

US-08-253-877C-20

US-08-452-1644-10

US-08-603-024-4

US-08-603-024-4

US-08-603-024-27

PCT-US93-11611-2

PCT-US93-11611-2

US-08-231-1611-2

US-08-211-210

US-08-211-210

US-09-211-207-10

US-09-211-207-10

US-09-211-207-10

US-09-211-207-10

US-09-211-207-10
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Best Local Similarity 88.5-
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
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119, App
4, Appli
20, Appl
14, Appl
4914, Ap
3, Appli
11, Appli
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                                                 April 22, 2003, 12:48:49 % Search time 7.875 Seconds (without alignments) 33.626 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
      GenCore version 5.1.4 p5 4578 (c) 1993 - 2003 Compugen Ltd.
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US-08-478-857-3
                                                                                                                                      262574 seqs, 29422922 residues
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                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                   - protein search, using sw model
                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
            Copyright
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                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: TELOPY disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
CORFRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 212-278-0400
Sequence 27, Application US/08672345C
Patent No. 5948658
GENERAL INFOATION:
APPLICANT: Landary Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
CORRESPONDED ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
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STREET: 1185 Avenue of the Americas
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TOPOLOGY: linear MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                  Score 44; DB 4; Length 9;
Pred. No. 1.9e+05;
US-09-214-095D-27
; Sequence 27, Application US/09214095D
; Patent No. 6280897
; GENERAL INFORMATION:
; APPLICATION:
; TILLE OF INVENTION:
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT PILIAGD AND: 129-07-19
; NUMBER OF SEQ ID NOS: 121
; SEQ ID NO 27
; SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER FRAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: PACHILIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-UUN-1996
CLASSIFICATION: 435
ATTORNEY/AGBNT INPORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INPORMATION:
TELEPHONE: 212-278-0400
TELEFRAX: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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88.9%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 88.9
Matches 8; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
COINTRY: USA
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    1 QQLVEYPFT 9

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US-08-672-345C-8
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Pred. No. 0.16;
0; Mismatches 1; Indels
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Batent No. 6280987

GENERAL INFORMATION:

APPLICANT: Landry, Donald

TITLE OF INVENTION:

FILE REFERENCE: 51400-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/214,095D

CURRENT PILING DATE: 1999-07-19

NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patentin version 3.0

SEQ ID NO 8

SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: ABACHILE POSAMS-DOS
SOCTAME: Patentin Release #1.0, Version #1.30
SOUTHARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE: 24-JUN-1996
FLING DATE: 21-2-391-0525
FREERPONE: 212-278 0-0400
TELEFRAX: 212-391-0525
FINFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
FUNCH THE SECOND SEQ ID NO: 98:
FUNCH THE SECOND SEQ ID NO: 98:
FUNCH THE SECOND SEQ ID NO: 98:
FUNCH THE SECOND 
Sequence 98, Application US/08672345C
Patent No. 594858
GENERAL INPORATION:
APPLICATE Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                             ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.7%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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ORGANISM: Murinae gen. sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 91.7
Best Local Similarity 88.9
Matches 8; Conservative
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Pred. No. 1.9e+05;
1; Mismatches 2; Indels
66.7%; Pred. No. 1.9e+05;
tive 1; Mismatches 2; Indels
                                                                                                                                                                                          Sequence 21, Application US/09214095D
Fatent No. 6280307
GENERAL INFORMATION:
APPLICANT: Landry, Donald
ITILE OF INVENTON:
CURRENT APPLICANT: 51400-A-PCT-US
CURRENT FALING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New iol.

COUNTRY: USA
ZIF: 1036
COMPUTER READABLE FORM:
MEDIUM TYPE: Bloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA: 20.08/672,345C
FILING DATE: 24-UN-1996
CIASSIFICATION HABE: 26.78
FILING DATE: 20.00 P.
REGISTRATION WINBER: 28,678
REFERENCY DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHOME: 212-738-0400
TELEPHOME: 212-739-0525
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TENETAL: 113 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Cooper and Dunham LLP
1185 Avenue of the Americas
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 66.7
Matches 6; Conservative
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Murinae gen.sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
                                                           1 QQLVEYPFT 9
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1 QHFVDYPFT 9
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                                                                                                                                                                                      US-09-214-095D-21
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US-08-672-345C-5
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Pred. No. 0.16;
0; Mismatches 1; Indels
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| Sequence 21, Application US/08672345C
| Patent No. 594865B
| GENERAL INFORMATION:
| APPLICANT: Landry Donald, W. TITLE OF INVENTION: AWTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
| CORRESPONDENCE ADDRESS: ADDRESSEE: Cooper and Dunham LLP STREET: 1185 Avenue of the Americas CITY: New York STATE: New York
| STATE: New York COUNTRY: USA
                                                                                                                                Sequence 108, Application US/09214095D
Patent No. 6280987;
GERREAL INFORMATION:
APPLICANT: Landry. Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFRENCE: 51400-A-PCT-US
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SEQ ID NO 108
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Flopyy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FLING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TBLECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.7%;
88.9%;
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Best Local Similarity 88.5
Matches 8; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
strandEdness: single
process: process: process:
molEctua Type: peptide
US-08-672-345C-21
                                94 QOFVEYPFT 102
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94 QQFVEYPFT 102
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; ORGANISM: Murine
US-09-214-095D-108
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US-09-214-095D-108
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E: Cooper and Dunham LLP
1185 Avenue of the Americas
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US-08-672-345C-97
'Sequence 97, Application US/08672345C
'Patent No. 5948658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212.391-0525
INPORMATION FOR SEQ ID NO: 95: SEQUENCE CHARACTERISTICS: LENGTH: 113 amino acide TYPE: amino acide STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 97
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-672-345C-95
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         COUNTRY:
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                                                                                  75.0%; Score 36; DB 2; Length 113; 66.7%; Pred. No. 5.6; 2; Indels ive 1; Mismatches 2; Indels
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66.7%; Pred. No. 5.6;
cive 1; Mismatches 2; Indels
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CIASSIFICATION: 435
FILING DATE: 24-JUN-1996
FILING DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-08-672-345C-95
US-08-672-345C-95
Sequence 95, Application US/08672345C
Sequence 95, Application US/08672345C
Sequence 100 
                                       Query Match
Best Local Similarity 66.73,
Sample 6; Conservative
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Matches 6; Conservative
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STATE: New York
COUNTRY: USA
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94 QHFVDYPFT 102
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94 QHFVDYPFT 102
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STATE: New York
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US-08-672-345C-7
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US-08-672-345C-5
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ZIP: 10036

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C

PILING DATE: 24-JUN 1996

CLASSIFICATION: 435

ATYONEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678

TELEBPHONE: 212-278-0400
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
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                                                          Score 36; DB 2; Length 113;
Pred. No. 5.6;
1; Mismatches 2; Indels
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Sequence 7, Application US/09214095D

Sequence 7, Application US/09214095D

GENERAL INFORMATION:

APPLICANT: Landry, Donald

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

FILE REFERENCE: 51400-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/214,095D

CURRENT FILING DATE: 1999-07-19

NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patentin version 3.0

SEQ ID NO 7
                                                                                                                                                                                                                                           RESULT 13
US-09-214-095D-5
Sequence 5, Application US/09214095D
Sequence 5, Application US/09214095D
Sequence 6, Application US/09214095D
Sequence 7, Application US/09214095D
SERVERAL INFORMATION:
SERVERAL INFORMATION:
STILE OF INVENTION:
STILE REFERENCE:
STATOS APPLICATION NUMBER: US/09/214,095D
CURRENT FILIAG DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SEQ ID NO 5
SEQ ID NO 5
LENGTH: 113
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US-09-214-095D-100
1S-09-214-095D-100
1 Sequence 100, Application US/09214095D
1 Patent No. 6280987
2 GENERAL INFORMATION:
2 APPLICANT: Landry, Donald
2 TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
                                                             Query Match 75.0%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 6; Conservative
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ORGANISM: Murinae gen. sp
US-09-214-095D-7
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US-09-214-095D-5
MOLECULE TYPE: peptide
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94 OHFVDYPFT 102
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US-08-672-345C-97
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Sequence 6, Appli
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Sequence 95, Appli
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Sequence 97, Appli
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Sequence 96, Appl
Sequence 97, Appl
Sequence 5, Appli
Sequence 6, Appli
Sequence 7, Appli
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Sequence 8, Appli
Sequence 98, Appl
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Seguence 25, App]
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Sequence 104, A
Sequence 112, A
                                                              April 22, 2003, 12:48:49; Search time 14 Seconds (without alignments) 33.626 Million cell updates/sec
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Sequence
Sequence
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          GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-09-214-095D-22
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US-09-214-095D-108
US-09-214-095D-108
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US-09-214-095D-108
US-08-672-345C-9
US-09-214-095D-100
US-09-214-095D-119
US-09-214-095D-119
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US-09-214-095D-119
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Maximum Match 100%
Listing first 45 summaries
                                              - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length
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                                      Sequence Seq
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Pred. No. 1.3e-06;
1; Mismatches 0; Indels
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APPLICANT: Landary Donald, W.

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDER: Cooper and Dunham Lip-
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: New York
STATE: New York
COUNTRY: USA
ZIP: Plopy disk
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION NUMBER: US/08/672,345C
FILING DATE: 212-310-0525
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERESTICS:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERESTICS:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERESTICS:
INFORMATION acids
TELENGTH: A maino acids
US-09-214-095D-43
US-09-214-095D-19
US-09-114-095D-116
US-08-672-345C-9
US-08-672-345C-9
US-09-214-095D-9
US-09-214-095D-9
US-08-672-245-28
US-07-942-245-28
US-08-677-877B-89
US-08-477-877B-89
US-08-678-194-6
US-08-678-194-6
US-08-690-011-6
US-08-690-011-6
US-08-903-011-6
US-08-903-011-6
US-08-903-011-6
US-08-903-011-6
US-08-903-011-6
US-08-917-877B-87
US-08-917-877B-87
US-08-477-877B-88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/08672345C Patent No. 5948658 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.1%;
93.8%;
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Best Local Similarity 93.0
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
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Query Match 95.1%; Score 77; DB 2; Length 113; Best Local Similarity 93.8%; Pred. No. 9.9e-06; Matches 15; Conservative 1; Mismatches 0; Indels
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| Sequence 8, Application US/08672345C
| Patent NO. 5948658
| GENERAL INFORMATION:
| APPLICANT: Landry Donald, W. ATTILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
| CORRESPONDENCE ADDRESS: 108
| CORRESPONDENCE ADDRESS: 108
| CORRESPONDENCE ADDRESS: 108
| CORRESPONDENCE ADDRESS: 108
| COUNTRY: USA | COMPATION: New York COUNTRY: USA | COMPATION: STATE: 10036 | COMPATION: STATE: 10036 | COMPATION: ID OF COMPATION: NAS: 10036 | COMPATION: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 95.1%; Score 77; DB 4; Length 16; Best Local Similarity 93.8%; Pred. No. 1.3e-06; Matches 15; Conservative 1; Mismatches 0; Indele
                                                                                Sequence 25, Application US/09214095D

Sequence 25, Application US/09214095D

Batent No. 620087

GENERAL INFORMATION:

APPLICANT: Landry, Donald

TITLE OF INVENTION:

FILE REFERENCE: 51400-A-PCT-US

CURRENT FILING DATE: 1999-07-19

NUMBER OF SEQ ID NOS: 121

SOFTWARE: PatentIn version 3.0

SEQ ID NO 25

LENGTH: 16
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Murinae gen. Sp.
US-09-214-095D-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSSKSLLYKDGKTYLN 16
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MOLECULE TYPE: protein
                                                                            US-09-214-095D-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-08-672-345C-8
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Pred. No. 1.3e-06;
1; Mismatches 0; Indels
   US-US-672-345C-25

Sequence 25, Application US/08672345C

Patent No. 5948658

GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
COUNTRY: New York
STREET: New York
COUNTRY: New York
STREET: New York
COUNTRY: New York
CONFUTER: FADDBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EADDBLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: EADBLE FORM:
MEDIUM TYPE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-UTN-1996
CLASSIFICATION NUMBER: 28,678
REGISTRATION NUMBER: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
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UG-09-214-095D-22
Sequence 22, Application US/09214095D
Fatent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TILE OF INVENTOR: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
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93.8%;
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; ORGANISM: Murinae gen. sp.
US-09-214-095D-22
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Best Local Similarity 93.9
Matches 15; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-672-345C-25
US-08-672-345C-25
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LENGTH: 16
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                                       Indels
                                                                                                                                                                                                                        ## Sequence 108, Application US/09214095D
| Patent No. 6280997
| GENERAL INFORMATION:
| APPLICANT: Landary, Donald
| TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
| TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
| CURRENT APPLICATION NUMBER: US/09/214,095D
| CURRENT FILING DATE: 1999-07-19
| SOFTWARE: Patentin version 3.0
| SEC ID NO 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
STREET: 1185 Avenue of the Americas
STATE: New York
CUNTRY: USA
STATE: New York
COUNTRY: USA
STATE: New York
COMPUTER: READABLE FORM:
MEDILUM TYPE: Floppy disk
COMPUTER: ParentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: 24-JUW-1996
CLASSIFICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUW-1996
CLASSIFICATION NUMBER: 24.70W-1996
TELEPOMNICATION NUMBER: 0575/51400
TELEPHONE: 212-2391-0525
INFORMATION FOR SEQ ID NO: 19:
SECTION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
                Pred. No. 9.9e-06;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
         Best Local Similarity 93.8%;
Matches 15; Conservative
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Best Local Similarity 93.8%;
Matches 15; Conservative
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LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                     24 RSSKSLLYEDGKTYLN 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 RSSKSLLYEDGKTYLN 39
                                                                            1 RSSKSLLYKDGKTYLN 16
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ORGANISM: Murine
                                                                                                                                                                                                          US-09-214-095D-108
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US-08-672-345C-19
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Pred. No. 9.9e-06;
1; Mismatches 0; Indels
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                                                                                                                                                 Sequence 98, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT LANGTY DONAIG, W.
ITILE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPRAN: 212-39-0625
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LEMGTH: 113 amino acids
STRANDEDNESS: Bingle
TYPE: amino acid
STRANDEDNESS: Bingle
MINDENTER: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Landry, Donald
TILLE OP INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOPTWARE: Patentin version 3.0
LENGTH: 113
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93.8%;
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1 RSSKSLLYKDGKTYLN 16
                       24 RSSKSLLYEDGKTYLN 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 RSSKSLLYEDGKTYLN 39
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ORGANISM: Murinae gen. sp
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; MOLECULE TYPE: peptide
US-08-672-345C-98
                                                                                                                            US-08-672-345C-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-214-095D-8
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                                                                                                                    Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.6%; Score 75; DB 4; 1
87.5%; Pred. No. 2.8e-06;
                                                                                                                       Score 75; DB 4; 1
Pred. No. 2.8e-06;
                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-09-214-095D-28

Sequence 28, Application US/09214095D
Patent No. 6280387
GENERAL INFORMATION:
FIGUREAL INFORMATION:
CURRENT APPLICATION UNMERE: US/09/214,095D
CURRENT APPLICATION UNMER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
SERVING SEQ ID NOS: LENGTH: 16
                                                                                                                                                                          2; Mismatches
                                                                                                                    Query Match 92.6%;
Best Local Similarity 87.5%;
Matches 14; Conservative
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; ORGANISM: Murinae gen. sp.
US-09-214-095D-28
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                  TYPE: PRT; ORGANISM: Murinae gen. sp. US-09-214-095D-19
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Pred. No. 2.8e-06;
2; Mismatches 0; Indels
                                           Score 75; DB 2; Length 16;
Pred. No. 2.8e-06;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                             | Sequence 28, Application US/08672345C
| Sequence 28, Application US/08672345C
| Patent No. 5948658
| GENERAL INFORMATION:
| APPLICANT: Landry Donald, W. APPLICANT: Landry Donald, W. NUMBER OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
| CORRESPONDENCE ADDRESS: ADDRESSE: COOPERS OF ADDRESSE: Cooper and Dunham LLP STREET: 1185 Avenue of the Americaff CITY: New York STATE: New York STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-09-214-095D-19
; Sequence 19, Application US/09214095D
; Patent NO. 6280987;
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REPERBUCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUM-1996
CLASSIFICATION: 435
ATTOMNEY/AGENT INPORMATION:
NAME: White: 28,679
REGISTRATION NUMBER: 28,679
REGISTRATION NUMBER: 28,679
TELEPHONE: 212-278-0400
TELEPHONE: 212-39-0525
INFORMATION POR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
TENDATH: 16 amino acids
                                                92.6%;
87.5%;
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87.5%;
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Best Local Similarity 87.5
Matches 14; Conservative
                                           Query Match
Best Local Similarity 97.5
Matches 14; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-28
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US-08-672-345C-28
US-08-672-345C-19
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Search completed: April 22, 2003, 12:55:40 Job time : 14 secs
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                                                                                                                                                                                                                   0; Indels
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COMPUTER READBLE FORM:
MCDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: A4-UN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White. John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 113 amino acids
TYPE: amino acid
TYPE: amino acid
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APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
                                                                                                                                                                        Score 75; DB 2;
Pred. No. 2.1e-05;
                                                                                                                                                                                                               2; Mismatches
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; Sequence 6, Application US/08672345C
; Patent No. 5948658
                                                                                                                                                                      92.6%;
SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-5
                                                                                                                                                                 Query Match
Best Local Similarity 87.5
Matches 14; Conservative
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Matches 14; Conservative
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; MOLECULE TYPE: protein
US-08-672-345C-6
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                                                                                                                                               CUMPLIATE USAGE

CUMPLIER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 24.0UN-1996
CLASSIFICATION WINBER: 24.0UN-1996
CLASSIFICATION WINBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELEFANCE/DOCKET UNBER: 0575/51400
TELEFANCE/DOCKET UNBER: 0575/51400
TELEFANCE/DOCKET UNBER: 0575/51400
TELEFANCE/DOCKET UNBER: 0575/51400
                                                                 STREET: 1185 Avenue of the Americas
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 113 amino acids
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Best Local Similarity 87.5
Matches 14; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS: si
                                                                                       CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                              New York
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COUNTRY: U.O..

ZIP: 10036
COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NOWBER: US/08/672,345C
FILING DATE: 24-UTW-1996
CLASSIFICATION: 435
ATTONENT INFORMATION:
NAME: White, John P.
REGISCHATION NOWBER: 28,678
REGISCHATION NOWBER: 28,678
REGISCHATION NOWBER: 28,678
REGISCHATION NOWBER: 28,678
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION 
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Sequence, 23, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
             US-08-963-825-18

US-09-50-811-18

US-09-548-608-18

US-09-585-887-9

US-09-289-578-9

5240838-5

US-09-188-930-336

US-09-188-930-336

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US-09-188-948-5

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; MOLECULE TYPE: peptide
US-08-672-345C-23
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STATE: New York
COUNTRY: USA
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97, Appl
98, Appl
6, Appli
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104, App
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112, App
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                  April 22, 2003, 12:48:49; Search time 6.125 Seconds
(without alignments)
33.626 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
             GenCore version 5.1.4 p5 4578 (c) 1993 - 2003 Compugen Ltd.
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US-09-214-095D-23

US-09-214-095D-29

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US-08-672-345C-6

US-08-672-345C-9

US-08-672-345C-9

US-08-672-345C-9

US-08-672-345C-9

US-08-672-345C-9

US-09-214-095D-10

US-09-214-095D-10

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US-09-214-095D-80
                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                    262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
                          Copyright
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No.
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Gaps

Gaps

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Query Match 100.0%; Score 31; DB 4; Length 7; Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 31; DB 2; Length 7; 100.0%; Pred. No. 1.9e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-214-095D-23
; Sequence 23, Application US/09214095D
; Sequence 23, Application US/09214095D
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SEQ ID NO 23
; LENGRH: 7
; LENGRH: 7
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Fatent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT APPLICATION NUMBER: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SEQ ID NO 26
SEQ ID NO 26
       NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMNUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-23
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; ORGANISM: Murinae gen. sp.
US-09-214-095D-26
                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LMSTRAS 7
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                                                                                                                                                                                                                                                                      COUNTRY: COUNTRY: COUNTRY: COUNTRY: COUNTRY READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
ATIONS DATE: 24-JUN-1996
CLASSIFICATION: 435
ATIONEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRANION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0525
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WS-08-672-345C-29
Sequence 29, Application US/08672345C
Sequence 29, Application US/08672345C
Sequence 29, Application US/08672345C
Sequence 29, Application US/08672345C
TOTALE OF INVENTION:
TITLE OF INVENTION:
TITLE OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
AUTHORISE OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER TEADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
US-08-672-345C-26

Sequence 26, Application US/08672345C

Sequence 26, Application US/08672345C

Patent No. 59486EN

PATENTIANT: Landry Donald, W.

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:

ADDRESSE: Cooper and Dunham LLP

STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1185 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                    CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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Best Local Similarity 100.0%; Pred. No. 1.3; Matches 7; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: si
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                                                                                   55 LMSTRAS 61
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55 LMSTRAS 61
                                                     1 LMSTRAS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                  Length 7;
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                                                                                                   Sequence 29, Application US/09214095D
Sequence 29, Application US/09214095D
Sequence 29, Application US/09214095D
Sequence 29, Application US/09214095D
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION:
FILE REPERENCE: S1400-A-PCT-US
CURRENT FILING DATE: 1999-07-19
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SSP ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SUPPLICES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 31; DB 4; I
100.0%; Pred. No. 1.9e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Cooper and Dunham Lip
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08672345C Patent No. 5948658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                            ORGANISM: Murinae gen. sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                    US-09-214-095D-29
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100.0%; Score 31; DB 2; Length 113;

Query Match

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0
Sequence 7, Application US/08672345C

Patent No. 554865B

GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 05.75/51400
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPRORE, 212-278-0400
TELEPRORE, 212-391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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Patent No. 5948658
GENERAL INFOATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
CORRESPONSECUENCES: ADDRESSE:
ADDRESSEE: Cooper and Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 31; DB 2;
100.0%; Pred. No. 1.3;
tive 0; Mismatches 0
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T: 1185 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
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Query Match 100.0%; Score 31; DB 2; Length 113; Best Local Similarity 100.0%; Pred. No. 1.3; Matches 7; Conservative 0; Mismatches 0; Indels
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Patent No. 5948658
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSPEL Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                         | Sequence 97. Application US/08672345C
| Sequence 97. Application US/08672345C
| Patent No. 5948658
| GENERAL INFORMATION:
| APPLICANT: Landry Donald, W. |
| TITLE OF INTENTION: ANTI-COCAINE CATALYTIC ANTIBODY NUMBER OF SEQUENCES: 108
| CORRESPENCES: 108 ADDRESS: ADDRESSE: Cooper and Dunham LLP STREET: 1185 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA | CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * COMPUTER READBLE FORM:

**MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUM-1996
CLASSIFICATION: 435
ATTONENY/AGENT INFORMATION:
NAME: White: 0ah P:
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELEPRA: 212-278-0400
TELEPRA: 212-39-0525
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
TOWATH: 113 amino acids
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                    RESULT 11
US-08-672-345C-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIREE:: LIBS AVENUE OF THE AMERICAS STATE: New York STATE: New York COUNTRY: USA ZIP: 10036
COMPUTER READABLE FORM: MEDIUM TYEE: Floppy disk COMPUTER: IBM PC Compatible OPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/672,345C FILING DATE: 24-JUN-1996 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: White, John P. REGISTRATION NUMBER: 28,678 REFERENCE/DOCKET NUMBER: 0575/51400 TELEPHONE: 212-278-9400
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTONENYAGENT INFORMATION:
NAME: White, John P. REGISTRACE DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NO: 8:
CELECOMMATION FRO ID NO: 8:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDENSS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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Patent No. 5948658
GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 96: SEQUENCE CHARACTERISTICS: LENGTH: 113 amino acide TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 7; Conservative
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US-09-214-095D-8
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Patent No. 6280987
GENERAL INFORMATION
GENERAL REPREBENCE: 51400-A-PCT-US
GUNRENT APPLICATION NUMBER: US/09/214,095D
GUNRENT FILING DATE: 1999-07-19
GENERAL PRICE PATENTION
GENERAL PRICE PATENTION
GENERAL PRICE PATENTION
GENERAL PATE
COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMATION SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LINFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LIENGTH: 113 amino acids
TYPE: amino acids
TYPE: AMINORMERS: Single
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Patent No. 6200967
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION:
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
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; ORGANISM: Murinae gen. sp.
US-09-214-095D-6
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US-09-214-095D-7
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